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(54) Title: BINARY PREDICTION TREE MODELING WITH MANY PREDICTORS

(57) Abstract:



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BINARY PREDICTION TREE MODELING WITH MANY PREDICTORS

FIELD OF THE INVENTION

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The field of this invention is the application of classification tree models incorporating Bayesian analysis to the statistical prediction of binary outcomes.

BACKGROUND OF THE INVENTION

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Bayesian analysis is an approach to statistical analysis that is based on the Bayes's law, which states that the posterior probability of a parameter p is proportional to the prior probability of parameter p multiplied by the likelihood of p derived from the data collected. This increasingly popular methodology represents an alternative to the traditional (or frequentist probability) approach: whereas the latter attempts to establish confidence intervals around parameters, and/or falsify a-priori null-hypotheses, the Bayesian approach attempts to keep track of how a-priori expectations about some phenomenon of interest can be refined, and how observed data can be integrated with such a-priori beliefs, to arrive at updated posterior expectations about the phenomenon.

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SUMMARY OF THE INVENTION

This invention discusses the generation and exploration of classification tree models, with particular interest in problems involving many predictors. Problems involving multiple predictors arise in situations where the prediction of an outcome is dependent on the interaction of numerous factors (predictors), such as the prediction of clinical or physiological states using various forms of molecular data. One motivating application is molecular phenotyping using gene expression and other forms of molecular data as predictors of a clinical or physiological state.

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The invention addresses the specific context of a binary response Z and many predictors x_i ; in which the data arises via case-control design, *i.e.*, the numbers of 0/1 values in the response data are fixed by design. This allows for the successful relation of large-scale gene expression data (the predictors) to binary outcomes, such as a risk group or disease state. The invention elaborates on a Bayesian analysis of this particular binary context, with several key innovations.

The analysis of this invention addresses and incorporates case-control design issues in the assessment of association between predictors and outcome with nodes of a tree. With categorical or continuous covariates, this is based on an underlying non-parametric model for the conditional distribution of predictor values given outcomes, consistent with the case-control design. This uses sequences of Bayes' factor based tests of association to rank and select predictors that define significant "splits" of nodes, and that provides an approach to forward generation of trees that is generally conservative in generating trees that are effectively self-pruning. An innovative element of the invention is the implementation of a tree-spawning method to generate multiple trees with the aim of finding classes of trees with high marginal likelihoods, and where the prediction is based on model averaging, *i.e.*, weighting predictions of trees by their implied posterior probabilities. The advantage of the Bayesian approach is that rather than identifying a single "best" tree, a score is attached to all possible trees and those trees which are very unlikely are excluded. Posterior and predictive distributions are evaluated at each node and at the leaves of each tree, and feed into both the evaluation and interpretation tree by tree, and the averaging of predictions across trees for future cases to be predicted.

To demonstrate the utility and advantages of this tree classification model, several embodiments are provided. The first concerns the prediction of levels of fat content (higher than average versus lower than average) of biscuits based on reflectance spectral measures of the raw dough. The second and third examples concern gene expression profiling using DNA microarray data as predictors of a clinical states in breast cancer. The clinical states include estrogen receptor ("ER") prediction, tumor recurrence, and lymph node metastases. The example

of ER status prediction demonstrates not only predictive value but also the utility of the tree modeling framework in aiding exploratory analysis that identify multiple, related aspects of gene expression patterns related to a binary outcome, with some interesting interpretation and insights. Embodiments 2 through 4 also
5 illustrate the use of metagene factors – multiple, aggregate measures of complex gene expression patterns – in a predictive modeling context. The fourth embodiment relates to the prediction of atherosclerotic phenotype determinative genes.

In the case of large numbers of candidate predictors, in particular, model
10 sensitivity to changes in selected subsets of predictors are ameliorated through the generation of multiple trees, and relevant, data-weighted averaging over multiple trees in prediction. The development of formal, simulation-based analyses of such models provides ways of dealing with the issues of high collinearity among multiple subsets of predictors, and challenging computational issues.

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BRIEF DESCRIPTION OF THE FIGURES

Figure 1: An example prediction tree for cookie fat outcomes. The root node splits on predictor/factor 92, followed by two subsequent splits on additional
20 predictors 330 and 305. The Π values are point estimates of the predictive probabilities of high fat versus low fat at each of the nodes, with suffixes simply indexing nodes. The labels $Z(0=1)$ indicate the numbers of low fat (0) and high fat (1) samples within each node, and the $F\#$ symbols indicate the thresholds that define the predictor based splits within each node.

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Figure 2: Two predictive factors in cookie dough analysis. All samples are represented by index numbers 1 through 78. Training data are denoted by blue (low fat) and red (high fat), and validation data by cyan (low fat) and magenta (high fat). The two full lines (black) demarcate the thresholds on the two predictors
30 in this example tree.

Figure 3: Scatter plot of cookie data on three factors in example tree. Samples are denoted by blue (low fat) and red (high fat), with training data represented by filled circles and validation data by open circles.

- 5 Figure 4: Three ER related metagenes in 49 primary breast tumors. Samples are denoted by blue (ER negative) and red (ER positive), with training data represented by filled circles and validation data by open circles.

- 10 Figure 5: Three ER related metagenes in 49 primary breast tumors. All samples are represented by index number in 1-78. Training data are denoted by blue (ER negative) and red (ER positive), and validation data by cyan (ER negative) and magenta (ER positive).

- 15 Figure 6: Honest predictions of ER status of breast tumors. Predictive probabilities are indicated, for each tumor, by the index number on the vertical probability scale, together with an approximate 90% uncertainty interval about the estimated probability. All probabilities are referenced to a notional initial probability (incidence rate) of 0.5 for comparison. Training data are denoted by blue (ER negative) and red (ER positive), and validation data by cyan (ER
20 negative) and magenta (ER positive).

Figure 7: Table of 491 ER metagenes in initial (random) order.

- 25 Figure 8: Table of 491 ER metagenes ordered in terms of nonlinear association with ER status.

- 30 Figure 9: Cross-validation probability predictions of lymph node status. Samples (tumors) are plotted by index number, and the plotted numbers are marked on the vertical scale at the estimated predictive probabilities of high risk (red) versus low risk (blue). Approximate 90% uncertainty(?confidence) intervals about these estimated probabilities are indicated by vertical dashed lines.

Figure 10: Gene expression patterns from the major metagene that predicts lymph node status. Samples are plotted by sample index number and by color (color coding as in Figure 9).

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Figure 11: Cross-validation probability predictions of 3-year recurrence. Samples (tumors) are plotted by index number, and the plotted numbers are marked on the vertical scale at the estimated predictive probabilities of 3 year recurrence (red) versus 3 year recurrence free survival (blue). Approximate 90% uncertainty intervals about these estimated probabilities are indicated by vertical dashed lines.

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Figure 12: Genes associated with metagene predictors of lymph node metastasis

15 Figure 13: Genes associated with metagene predictors of breast cancer recurrence.

DETAILED DESCRIPTION OF THE INVENTION

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Development of the Tree Clarification Model: Model Context and Methodology

Data $\{Z_i, \mathbf{x}_i\}$ ($i = 1, \dots, n$) are available on a binary response variable Z and a p – dimensional covariate vector \mathbf{x} : The 0/1 response totals are fixed by design. Each predictor variable x_j could be binary, discrete or continuous.

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1. Bayes' factor measures of association

30 At the heart of a classification tree is the assessment of association between each predictor and the response in subsamples, and we first consider this at a general

level in the full sample. For any chosen single predictor x ; a specified threshold τ on the levels of x organizes the data into the 2×2 table.

5

	$Z = 0$	$Z = 1$	
$x \leq \tau$	n_{00}	n_{01}	N_0
$x > \tau$	n_{10}	n_{11}	N_1
	M_0	M_1	

- With column totals fixed by design, the categorized data is properly viewed as two Bernoulli sequences within the two columns, hence sampling densities
- 10 With column totals fixed by design, the categorized data is properly viewed as two Bernoulli sequences within the two columns, hence sampling densities

$$p(n_{0z}, n_{1z} | M_z, \theta_{z,r}) = \theta_{0z}^{n_{0z}} (1 - \theta_{0z})^{n_{1z}}$$

- 15 for each column $z = 0, 1$. Here, of course $\theta_{0,r} = Pr(x \leq \tau | Z=0)$ and $\theta_{1,r} = Pr(x > \tau | Z=1)$. A test of association of the threshold predictor with the response will now be based on assessing the difference between the Bernoulli probabilities.

- The natural Bayesian approach is via the Bayes' factor B_r comparing the
- 20 null hypothesis $\theta_{0,r} = \theta_{1,r}$ to the full alternative $\theta_{0,r} \neq \theta_{1,r}$. We adopt the standard conjugate beta prior model and require that the

- null hypothesis be nested within the alternative. Thus, assuming $\theta_{0,r} \neq \theta_{1,r}$, we take $\theta_{0,r}$ and $\theta_{1,r}$ to be independent with common prior $Be(a_r, b_r)$ with mean $m_r =$
- 25 $a_r / (a_r + b_r)$. On the null hypothesis $\theta_{0,r} = \theta_{1,r}$, the common value has the same beta prior. The resulting Bayes' factor in favour of the alternative over the null hypothesis is then simply

$$\beta(n_{00} + a_r, n_{10} + b_r) \beta(n_{01} + a_r, n_{11} + b_r)$$

$$B_r = \frac{\beta(n_{00} + a_r, n_{10} + b_r) \beta(n_{01} + a_r, n_{11} + b_r)}{\beta(N_0 + a_r, N_1 + b_r) \beta(a_r, b_r)}$$

$$\beta(N_0 + a_r, N_1 + b_r) \beta(a_r, b_r)$$

- 5 As a Bayes' factor, this is calibrated to a likelihood ratio scale. In contrast to more traditional significance tests and also likelihood ratio approaches, the Bayes' factor will tend to provide more conservative assessments of significance, consistent with the general conservative properties of proper Bayesian tests of null hypotheses (see Sellke, T., Bayarri, M.J. and Berger, J.O., Calibration of
- 10 p-values for testing precise null hypotheses, *The American Statistician*, 55, 62-71, (2001) and references therein).

In the context of comparing predictors, the Bayes' factor B_τ may be evaluated for all predictors and, for each predictor, for any specified range of thresholds. As the threshold varies for a given predictor taking a range of (discrete or continuous)

15 values, the Bayes' factor maps out a function of τ and high values identify ranges of interest for thresholding that predictor. For a binary predictor, of course, the only relevant threshold to consider is $\tau = 0$.

2. Model consistency with respect to varying thresholds

20

A key question arises as to the consistency of this analysis as we vary the thresholds. By construction, each probability $\theta_{z\tau}$ is a non-decreasing function of τ , a constraint that must be formally represented in the model. The key point is that the beta prior specification must formally reflect this. To see how this is

25 achieved, note first that $\theta_{z\tau}$ is in fact the cumulative distribution function of the predictor values χ ; conditional on $Z = z$; ($z = 0; 1$); evaluated at the point $\chi = \tau$. Hence the sequence of beta priors, $Be(a_\tau, b_\tau)$ as τ varies, represents a set of marginal prior distributions for the corresponding set of values of the cdfs. It is immediate that the natural embedding is in a non-parametric Dirichlet process

30 model for the complete cdf. Thus the threshold-specific beta priors are consistent, and the resulting sets of Bayes' factors comparable as τ varies, under a Dirichlet

process prior with the betas as margins. The required constraint is that the prior mean values m_τ are themselves values of a cumulative distribution function on the range of χ , one that defines the prior mean of each θ_τ as a function. Thus, we simply rewrite the beta parameters (α_τ, b_τ) as $\alpha_\tau = \alpha m_\tau$ and $b_\tau = \alpha(1 - m_\tau)$ for a
 5 specified prior mean cdf m_τ , and where α is the prior precision (or “total mass”) of the underlying Dirichlet process model. Note that this specialises to a Dirichlet distribution when χ is discrete on a finite set of values, including special cases of ordered categories (such as arise if χ is truncated to a predefined set of bins), and also the extreme case of binary χ when the Dirichlet is a simple beta distribution.

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3. Generating a tree

The above development leads to a formal Bayes’ factor measure of association that may be used in the generation of trees in a forward-selection process as
 15 implemented in traditional classification tree approaches. Consider a single tree and the data in a node that is a candidate for a binary split. Given the data in this node, construct a binary split based on a chosen (predictor, threshold) pair (χ, τ) by (a) finding the (predictor, threshold) combination that maximizes the Bayes’ factor for a split, and (b) splitting if the resulting Bayes’ factor is sufficiently
 20 large. By reference to a posterior probability scale with respect to a notional 50:50 3 prior, Bayes’ factors of 2.2, 2.9, 3.7 and 5.3 correspond, approximately, to probabilities of .9, .95, .99 and .995, respectively. This guides the choice of threshold, which may be specified as a single value for each level of the tree. We have utilised Bayes’ factor thresholds of around 3 in a range of analyses, as
 25 exemplified below. Higher thresholds limit the growth of trees by ensuring a more stringent test for splits.

The Bayes’ factor measure will always generate less extreme values than corresponding generalized likelihood ratio tests (for example), and this can be especially marked when the sample sizes M_0 and M_1 are low. Thus the
 30 propensity to split nodes is always generally lower than with traditional testing methods, especially with lower samples sizes, and hence the approach tends to be

more conservative in extending existing trees. Post-generation pruning is therefore generally much less of an issue, and can in fact generally be ignored. Index the root node of any tree by zero, and consider the full data set of n observations, representing M_z outcomes with $Z = z$ in 0, 1. Label successive nodes sequentially: splitting the root node, the left branch terminates at node 1, the right branch at node 2; splitting node 1, the consequent left branch terminates at node 3, the right branch at node 4; splitting node 2, the consequent left branch terminates at node 5, and the right branch at node 6, and so forth. Any node in the tree is labelled numerically according to its “parent” node; that is, a node j splits into two children, namely the (left, right) children $(2j + 1; 2j + 2)$: At level m of the tree ($m = 0; 1; \dots$) the candidates nodes are, from left to right, as $2^m - 1; 2^m; \dots; 2^{m+1} - 2$.

Having generated a “current” tree, we run through each of the existing terminal nodes one at a time, and assess whether or not to create a further split at that node, stopping based on the above Bayes’ factor criterion. Unless samples are very large (thousands) typical trees will rarely extend to more than three or four levels.

4. Inference and prediction with a single tree

Suppose we have generated a tree with m levels; the tree has some number of terminal nodes up to the maximum possible of $L = 2^{m+1} - 2$. Inference and prediction involves computations for *branch probabilities* and the predictive probabilities for new cases that these underlie. We detail this for a specific path down the tree, i.e., a sequence of nodes from the root node to a specified terminal node.

First, consider a node j that is split based on a (predictor, threshold) pair labeled (χ_j, τ_j) , (note that we use the node index to label the chosen predictor, for clarity). Extend the notation of Section 2.1 to include the subscript j indexing this node. Then the data at this node involves M_{0j} cases with $Z = 0$ and M_{1j} cases with $Z = 1$. Based on the chosen (predictor, threshold) pair (χ_j, τ_j) these samples split

into cases n_{00j} , n_{01j} , n_{10j} , n_{11j} as in the table of Section 2.1, but now indexed by the node label j . The implied conditional probabilities $\theta_{z,\tau_j} = Pr(\chi_j \leq \tau_j | Z = z)$, for $z = 0, 1$ are the *branch probabilities* defined by such a split (note that these are also conditional on the tree and data subsample in this node, though the notation does not explicitly reflect this for clarity). These are uncertain parameters and, following the development of Section 2.1, have specified beta priors, now also indexed by parent node j , i.e., $Be(a_{\tau_j}, b_{\tau_j})$. Assuming the node is split, the two sample Bernoulli setup implies conditional posterior distributions for these branch probability parameters: they are independent with posterior beta

5 not explicitly reflect this for clarity). These are uncertain parameters and, following the development of Section 2.1, have specified beta priors, now also indexed by parent node j , i.e., $Be(a_{\tau_j}, b_{\tau_j})$. Assuming the node is split, the two sample Bernoulli setup implies conditional posterior distributions for these branch probability parameters: they are independent with posterior beta

10 distributions

$$\theta_{0,\tau_j} \sim Be(a_{\tau_j} + n_{00j}, b_{\tau_j} + n_{10j}) \text{ and } \theta_{1,\tau_j} \sim Be(a_{\tau_j} + n_{01j}, b_{\tau_j} + n_{11j}).$$

These distributions allow inference on branch probabilities, and feed into the predictive inference computations as follows.

15 Consider predicting the response Z^* of a new case based on the observed set of predictor values \mathbf{x}^* . The specified tree defines a unique path from the root to the terminal node for this new case. To predict requires that we compute the posterior predictive probability for $Z^* = 1/0$. We do this by following \mathbf{x}^* down the tree to the implied terminal node, and sequentially building up the relevant likelihood ratio defined by successive (predictor, threshold) pairs.

20 For example and specificity, suppose that the predictor profile of this new case is such that the implied path traverses nodes 0, 1, 4, 9, terminating at node 9. This path is based on a (predictor, threshold) pair (χ_0, τ_0) that defines the split of the root node, (χ_1, τ_1) that defines the split of node 1, and (χ_4, τ_4) that defines the split of node 4. The new case follows this path as a result of its predictor values, in sequence:

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$(x_0^* \leq \tau_0)$, $(x_1^* > \tau_1)$ and $(x_4^* \leq \tau_4)$. The implied likelihood ratio for $Z^* = 1$ relative to $Z^* = 0$ is then the product of the ratio of branch probabilities to this terminal node, namely

$$\lambda^* = \frac{\theta_{1,\tau_0,0}}{\theta_{0,\tau_0,0}} \times \frac{(1 - \theta_{1,\tau_1,1})}{(1 - \theta_{0,\tau_1,1})} \times \frac{\theta_{1,\tau_3,0}}{\theta_{0,\tau_3,0}}$$

Hence, for any specified prior probability $Pr(Z^* = 1)$, this single tree model implies that, as a function of the branch probabilities, the updated probability π^* is, on the odds scale, given by

$$\frac{\pi^*}{(1 - \pi^*)} = \lambda^* \frac{Pr(Z^* = 1)}{Pr(Z^* = 0)}.$$

Hence, for any specified prior probability π $Pr(Z^* = 1)$, this single tree model implies that, as a function the branch probabilities, the updated probability π^* is, on the odds scale, give by

$$\pi^* = \frac{\lambda^* \pi}{(1 - \pi^*) + \lambda^* \pi} = \frac{\lambda^* \pi}{1 - \pi^* + \lambda^* \pi}$$

10 The case-control design provides no information about $Pr(Z^* = 1)$ so it is up to the user to specify this or examine a range of values; one useful summary is obtained by simply taking a 50:50 prior odds as benchmark, whereupon the posterior probability is

$$15 \quad \pi^* = \lambda^* / (1 + \lambda^*).$$

Prediction follows by estimating π^* based on the sequence of conditionally independent posterior distributions for the branch probabilities that define it. For example, simply “plugging-in” the conditional posterior means of each θ . will lead to a plug-in estimate of λ^* and hence π^* . The full posterior for π^* is defined implicitly as it is a function of the θ .. Since the branch probabilities follow beta posteriors, it is trivial to draw Monte Carlo samples of the θ . and then simply compute the corresponding values of λ^* and hence π^* to generate a posterior sample for summarization. This way, we can evaluate simulation-based posterior

means and uncertainty intervals for π^* that represent predictions of the binary outcome for the new case.

5. Generating and weighting multiple trees

5

In considering potential (predictor, threshold) candidates at any node, there may be a number with high Bayes' factors, so that multiple possible trees with difference splits at this node are suggested. With continuous predictor variables, small variations in an "interesting" threshold will generally lead to small changes in the Bayes' factor – moving the threshold so that a single observation moves from one side of the threshold to the other, for example. This relates naturally to the need to consider thresholds as parameters to be inferred; for a given predictor χ , multiple candidate splits with various different threshold values τ reflects the inherent uncertainty about τ , and indicates the need to generate multiple trees to adequately represent that uncertainty. Hence, in such a situation, the tree generation can spawn multiple copies of the "current" tree, and then each will split the current node based on a different threshold for this predictor. Similarly, multiple trees may be spawned this way with the modification that they may involve different predictors.

20 In problems with many predictors, this naturally leads to the generation of many trees, often with small changes from one to the next, and the consequent need for careful development of tree-managing software to represent the multiple trees. In addition, there is then a need to develop inference and prediction in the context of multiple trees generated this way. The use of "forests of trees" has recently been urged by Breiman, L., Statistical Modeling: The two cultures (with discussion), *Statistical Science*, 16 199-225 (2001), and our perspective endorses this. The rationale here is quite simple: node splits are based on specific choices of what we regard as parameters of the overall predictive tree model, the (predictor, threshold) pairs. Inference based on any single tree chooses specific values for these parameters, whereas statistical learning about relevant trees requires that we

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explore aspects of the posterior distribution for the parameters (together with the resulting branch probabilities).

Within the current framework, the forward generation process allows easily for the computation of the resulting relative likelihood values for trees, and hence to relevant weighting of trees in prediction. For a given tree, identify the subset of nodes that are split to create branches. The overall marginal likelihood function for the tree is then the product of component marginal likelihoods, one component from each of these split nodes. Continue with the notation of Section 2.1 but now, again, indexed by any chosen node j : Conditional on splitting the node at the defined (predictor, threshold) pair (χ_j, τ_j) , the marginal likelihood component is

$$m_j = \int_0^1 \prod_{z=0,1} p(n_{0zj}, n_{1zj} | M_{zj}, \theta_{zj}, r_{j,j}) p(\theta_{zj}, r_{j,j}) d\theta_{zj}, r_{j,j}$$

where $p(\theta_{zj}, r_{j,j})$ is the $Be(a_{zj}, b_{r,j})$ prior to each $z=0,1$. This clearly reduces to

$$m_j = \prod_{z=0,1} \frac{B(n_{0zj} + a_{r,j}, n_{1zj} + b_{r,j})}{B(a_{r,j}, b_{r,j})}$$

The overall marginal likelihood value is the product of these terms over all nodes j that define branches in the tree. This provides the relative likelihood values for all trees within the set of trees generated. As a first reference analysis, we may simply normalise these values to provide relative posterior probabilities over trees based on an assumed uniform prior. This provides a reference weighting that can be used to both assess trees and as posterior probabilities with which to weight and average predictions for future cases.

DESCRIPTION OF THE SPECIFIC EMBODIMENTS

Before the subject invention is described further, it is to be understood that the invention is not limited to the particular embodiments of the invention described below, as variations of the particular embodiments may be made and still fall within the scope of the appended claims. It is also to be understood that the terminology employed is for the purpose of describing particular embodiments, and is not intended to be limiting. Instead, the scope of the present invention will be established by the appended claims.

In this specification and the appended claims, the singular forms “a,” “an” and “the” include plural reference unless the context clearly dictates otherwise.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs.

Where a range of values is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates otherwise, between the upper and lower limit of that range, and any other stated or intervening value in that stated range, is encompassed within the invention. The upper and lower limits of these smaller ranges may independently be included in the smaller ranges, and are also encompassed within the invention, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the invention.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs. Although any methods, devices and materials similar or equivalent to those described herein can be used in the practice or testing of the invention, the preferred methods, devices and materials are now described.

All publications mentioned herein are incorporated herein by reference for the purpose of describing and disclosing the subject components of the invention that are described in the publications, which components might be used in connection with the presently described invention.

Example 1: Analysis of Biscuit Dough Data

A first example concerns the application of biscuit dough data (publicly available at Osborne, B.G., Fearn, T., Miller, A.R. and Douglas, S., Applications of near
5 infrared reflectance spectroscopy to compositional analysis of biscuits and biscuit doughs, *J. Sci. Food Agric.*, **35**, 99-105 (1984); Brown, P.J., Fearn, T. and Vannucci, M., The choice of variables in multivariate regression: A non-conjugate Bayesian decision theory approach, *Biometrika*, **86**, 635-648 (1999)) in
10 which interest lies in relating aspects of near infrared ("NIR") spectra of dough to the fat content of the resulting biscuits. The data set provides 78 samples, of which 39 are taken as training data and the remaining 39 as validation cases to be predicted, precisely as in Brown *et al* (1999). The binary outcome is 0/1 according to whether the measured fat content exceeds a threshold, where the
15 threshold is the mean of the sample of fat values. As predictors, each x_i comprises 300 values of the spectrum of dough sample i , augmented by the set of singular factors (principal components) of the 78 sample spectra, so that $p = 378$; with singular factors indexed 301; : : : ; 378.

The analysis was developed repeatedly, exploring aspects of model fit and
20 prediction of the validation sample as the number of control parameters were varied. The particular parameters of key interest varied were the Bayes' factor thresholds that define splits, and controls on the number of such splits that may be made at any one node. It was determined that across ranges of these control parameters, that there was a good degree of robustness. The Bayes' factor
25 threshold was fixed at 3 on the log scale, after which and two-level trees were explored allowing at most 10 splits of the root node and then at most 4 splits of each of nodes 1 and 2. This allowed up to 160 trees, with this analysis generating 148 trees.

Many of the trees identified had one or two of the predictors in common, and
30 represent variation in the threshold values for those predictors. Figures 1-3 display some summaries. Figure 1 represents one of the 148 trees, split at the

root node by the spectral predictor labeled factor 92 (corresponding to a wavelength of 1566 nm). Multiple wavelength values appear in the 148 trees, with values close to this appearing commonly, reflecting the underlying continuity of the spectra. The key second level predictor is factor 305, one of the principal component predictors. The data are scatter plotted on these two predictors in Figure 2 with corresponding levels of the predictor-specific thresholds from this tree marked.

The data appears also against the three predictors in this tree in Figure 3. Evidently there is substantial overlap in predictor space between the 0/1 outcomes, and cases close to the boundaries defined by any single tree are hard to accurately predict. Nevertheless, in terms of posterior predictive probabilities for the 39 validation samples, accuracy is good. By simply establishing the predictive probability threshold at 0.5 it is determined that 18 of 20 (90%) low fat (blue) cases are “correctly” predicted, as are 19 of 20 (95%) high fat (red) cases. Predictive accuracy is high in this example with considerable overlap between predictor patterns among the two outcome groups. This is a positive example of the use of the predictive tree approach in a context where standard methods, such as logistic regression, would be less useful. Furthermore, the We end with a note that the 50:50 split of the 78 samples into training and validation sets followed the previous authors as references. Curious about this, we reran the analysis 500 times, each time randomly splitting the data 50:50 into training and validation samples. Predictive accuracy, as measured above, was generally not so good as reported for the initial sample split, varying from a little below 50% to 100% across this set of 500 analyses. The average accuracy for low fat (blue) cases was 80%, and that for high fat (red) cases 76%.

Example 2: Metagene Expression Profiling to Predict Estrogen Receptor Status of Breast Cancer Tumors

This example illustrates not only predictive utility but also exploratory use of the tree analysis framework in exploring data structure. Here, the tree analysis is used

to predict estrogen receptor ("ER") status of breast tumors using gene expression data. Prior analyses of such data involved binary regression models which utilized Bayesian generalized shrinkage approaches to factor regression. Specifically, prior statistical models involved the use of probit linear regression

5 linking principal components of selected subsets of genes to the binary (ER positive/negative) outcomes. See West, M., Blanchette, C., Dressman, H., Ishida, S., Spang, R., Zuzan, H., Marks, J.R. and Nevins, J.R. Utilization of gene expression profiles to predict the clinical status of human breast cancer. *Proc. Natl. Acad. Sci.*, **98**, 11462-11467 (2001). However, the tree model presents

10 some distinct advantages over Bayesian linear regression models in the analysis of large non-linear data sets such as these.

Primary breast tumors from the Duke Breast Cancer SPORE frozen tissue bank were selected for this study on the basis of several criteria. Tumors were either positive for both the estrogen and progesterone receptors or negative for both

15 receptors. Each tumor was diagnosed as invasive ductal carcinoma and was between 1.5 and 5 cm in maximal dimension. In each case, a diagnostic axillary lymph node dissection was performed. Each potential tumor was examined by hematoxylin/eosin staining and only those that were > 60% tumor (on a per-cell basis), with few infiltrating lymphocytes or necrotic tissue, were carried on for

20 RNA extraction. The final collection of tumors consisted of 13 estrogen receptor (ER)+ lymph node (LN)+ tumors, 12 ER LN+ tumors, 12 ER+ LN tumors, and 12 ER LN tumors

The RNA was derived from the tumors as follows: Approximately 30 mg of frozen breast tumor tissue was added to a chilled BioPulverizer H tube (Bio101)

25 (Q-Biogene, La Jolla, CA). Lysis buffer from the Qiagen (Chatsworth, CA) RNeasy Mini kit was added, and the tissue was homogenized for 20 sec in a MiniBeadbeater (Biospec Products, Bartlesville, OK). Tubes were spun briefly to pellet the garnet mixture and reduce foam. The lysate was transferred to a new 1.5-ml tube by using a syringe and 21-gauge needle, followed by passage through

30 the needle 10 times to shear genomic DNA. Total RNA was extracted by using the Qiagen RNeasy Mini kit. Two extractions were performed for each tumor,

and total RNA was pooled at the end of the RNeasy protocol, followed by a precipitation step to reduce volume. Quality of the RNA was checked by visualization of the 28S:18S ribosomal RNA ratio on a 1% agarose gel. After the RNA preparation, the samples were subject to Affymetrix GENECHIP analysis.

5 Affymetrix GENECHIP Analysis: The targets for Affymetrix DNA microarray analysis were prepared according to the manufacturer's instructions. All assays used the human HuGeneFL GENECHIP microarray. Arrays were hybridized with the targets at 45°C for 16 h and then washed and stained by using the GENECHIP Fluidics. DNA chips were scanned with the GENECHIP scanner,
10 and signals obtained by the scanning were processed by GENECHIP Expression Analysis algorithm (version 3.2) (Affymetrix, Santa Clara, CA).

The same set of $n = 49$ samples used in the binary regression analysis described in West et al (2001) is analyzed in this study, using predictors based on *metagene* summaries of the expression levels of many genes. Metagenes are useful
15 aggregate, summary measures of gene expression profiles. The evaluation and summarization of large-scale gene expression data in terms of lower dimensional factors of some form is utilized for two main purposes: first, to reduce dimension from typically several thousand, or tens of thousands of genes to a more practical dimension; second, to identify multiple underlying “patterns” of variation across
20 samples that small subsets of genes share, and that characterize the diversity of patterns evidenced in the full sample. Although, the analysis is conducive to the use of various factor model approaches known to those skilled in the art, a cluster-factor approach is used here to define empirical metagenes. This defines the predictor variables x utilized in the tree model.

25 Metagenes can be obtained by combining clustering with empirical factor methods. The metagene summaries used in the ER example in this disclosure, are based on the following steps.

Assume a sample of n profiles of p genes;

Screen genes to reduce the number by eliminating genes that show limited
30 variation across samples or that are evidently expressed at low levels that are not

- detectable at the resolution of the gene expression technology used to measure levels. This removes noise and reduces the dimension of the predictor variable; Cluster the genes using k_means, correlated-based clustering. Any standard statistical package may be used. This analysis uses the xcluster software created
5 by Gavin Sherlock (<http://genomewww.stanford.edu/sherlock/cluster.html>). A large number of clusters are targeted so as to capture multiple, correlated patterns of variation across samples, and generally small numbers of genes within clusters;
- Extract the dominant singular factor (principal component) from each of the
10 resulting clusters. Again, any standard statistical or numerical software package may be used for this; this analysis uses the efficient, reduced singular value decomposition function ("SVD") in the Matlab software environment (<http://www.mathworks.com/products/matlab>).
- 15 In the analysis of the ER data in this disclosure, the original data was developed using Affymetrix arrays with 7129 sequences, of which 7070 were used (following removal of Affymetrix controls from the data.). The expression estimates used were log₂ values of the signal intensity measures computed using the dChip software for post-processing Affymetrix output data (See Li, C. and
20 Wong, W.H. Model-based analysis of oligonucleotide arrays: Expression index computation and outlier detection. *Proc. Natl. Acad. Sci.*, **98**, 31-36 (2001), and the software site <http://www.biostat.harvard.edu/complab/dchip/>). With a target of 500 clusters, the xcluster software implementing the correlation-based k_means clustering produced p = 491 clusters. The corresponding p metagenes
25 were then evaluated as the dominant singular factors of each of these cluster, as referenced above. See Figures 7 – 8 that provide tables detailing the 491 metagenes.
- The data comprised 40 training samples and 9 validation cases. Among the latter,
3 were initial training samples that presented conflicting laboratory tests of the
30 ER protein levels, so casting into question their actual ER status; these were therefore placed in the validation sample to be predicted, along with an initial 6

validation cases selected at random. These three cases are numbers 14, 31 and 33. The color coding in the graphs is based on the first laboratory test (immunohistochemistry). Additional samples of interest are cases 7, 8 and 11, cases for which the DNA microarray hybridizations were of poor quality, with the resulting data exhibiting major patterns of differences relative to the rest. The metagene predictor has dimension $p = 491$: the analysis generated trees based on a Bayes' factor threshold of 3 on the log scale, allowing up to 10 splits of the root node and then up to 4 at each of nodes 1 and 2. Some pertinent summaries appear in the following figures. Figures 4 and 5 display 3-D and pairwise 2-D scatterplots of three of the key metagenes, all clearly strongly related to the ER status and also correlated. However, there are in fact five or six metagenes that quite strongly associate with ER status and it is evident that they reflect multiple aspects of this major biological pathway in breast tumors. In the study reported in West *et al* (2001), Bayesian probit regression models were utilized with singular factor predictors which identified a single major factor predictive of ER. That analysis identified ER negative tumors 16, 40 and 43 as difficult to predict based on the gene expression factor model; the predictive probabilities of ER positive versus negative for these cases were near or above 0.5, with very high uncertainties reflecting real ambiguity. In contrast to the more more traditional regression models, the current tree model identifies several metagene patterns that together combine to define an ER profile of tumors, and that when displayed as in Figures 4 and 5 isolate these three cases as quite clearly consistent with their designated ER negative status in some aspects, yet conflicting and much more in agreement with the ER positive patterns on others. Metagene 347 is the dominant ER signature; the genes involved in defining this metagene include two representations of the ER gene, and several other genes that are coregulated with, or regulated by, the ER gene. Many of these genes appeared in the dominant factor in the regression prediction. This metagene strongly discriminates the ER 11 negatives from positives, with several samples in the mid-range. Thus, it is no surprise that this metagene shows up as defining root node splits in many high-likelihood trees. This

metagene also clearly defines these three cases – 16, 40 and 43 – as appropriately ER negative. However, a second ER associated metagene, number 352, also defines a significant discrimination. In this dimension, however, it is clear that the three cases in question are very evidently much more consistent with ER

5 positives; a number of genes, including the ER regulated PS2 protein and androgen receptors, play roles in this metagene, as they did in the factor regression; it is this second genomic pattern that, when combined together with the first as is implicit in the factor regression model, breeds the conflicting information that fed through to ambivalent predictions with high uncertainty.

10 The tree model analysis here identifies multiple interacting patterns and allows easy access to displays such as those shown in Figures 4 to 6 that provide insights into the interactions, and hence to interpretation of individual cases. In the full tree analysis, predictions based on averaging multiple trees are in fact dominated by the root level splits on metagene 347, with all trees generated extending to two

15 levels where additional metagenes define subsidiary branches. Due to the dominance of metagene 347, the three interesting cases noted above are perfectly in accord with ER negative status, and so are well predicted, even though they exhibit additional, subsidiary patterns of ER associated behaviour identified in the figures. Figure 6 displays summary predictions. The 9 validation cases are

20 predicted based on the analysis of the full set of 40 training cases. Predictions are represented in terms of point predictions of ER positive status with accompanying, approximate 90% intervals from the average of multiple tree models. The training cases are each predicted in an honest, cross-validation sense: each tumor is removed from the data set, the tree model is then refitted

25 completely to the remaining 39 training cases only, and the hold-out case is predicted, *i.e.*, treated as a validation sample. Excellent predictive performance is observed for both these one-at-a-time honest predictions of training samples and for the out of sample predictions of the 9 validation cases. One ER negative, sample 31, is firmly predicted as having metagene expression patterns completely

30 consistent with ER positive status. This is in fact one of the three cases for which the two laboratory tests conflicted. The other two such cases, however agree with

the initial ER negative test result - number 33, for which the predictions firmly agree with the initial ER negative test result, and number 14, for which the predictions agree with the initial ER positive result though not quite so forcefully. The lack of conformity of expression patterns in some cases (Case 8, 11 and 7) are due to major distortions in the data on the DNA microarray due to hybridization problems.

Example 3: Prediction of Lymph Node Metastases and Cancer Recurrence

This study assesses complex, multivariate patterns in gene expression data from primary breast tumor samples that can accurately predict nodal metastatic states and relapse for the individual patient using the statistical tree model of the invention.

DNA microarray data on samples of primary breast tumors was generated to which non-linear statistical analyses embodied by the tree model of the invention was applied to evaluate multiple patterns of interactions of groups of genes that have true predictive value, at the individual patient level, with respect to lymph node metastasis and cancer recurrence. For both lymph node metastasis and cancer recurrence, patterns of gene expression (metagenes) were identified that associate with outcome. Much more importantly, these patterns were capable of honestly predicting outcomes in individual patients with about 90% accuracy, based on a simple threshold of 0.5 probability in each case. The metagenes that predict lymph node metastasis and recurrence identify distinct groups of genes, suggesting different biological processes underlying these two characteristics of breast cancer.

Patients and biopsy specimens: The analyses of gene expression phenotypes drew samples from 171 primary tumor biopsies at the Koo Foundation Sun Yat-Sen Cancer Center (KF-SYSCC) in Taipei, Taiwan, collected and banked from 1991 to 2001. Samples from eleven patients who received preoperative chemotherapy and one with *in-situ* carcinoma were excluded from analysis. These 159 samples represent a heterogeneous population, though patient

selection was enriched with cases of longer-term follow-up and observed recurrences. By September 2002, 62 patients developed recurrence whereas 97 remain disease free. The median follow-up was 49 months. Full details of clinical characteristics are shown in Table 1.

- 5 Microarray analysis: Tumor total RNA was extracted with Qiagen RNEasy kits, and assessed for quality with an Agilent Lab-on-a-Chip 2100 Bioanalyzer. Hybridization targets were prepared from total RNA according to Affymetrix protocols and hybridized to Affymetrix Human U95 GeneChip arrays See West M, Blanchette C, Dressman H, Huang E, Ishida S, Spang R et al. Predicting the
10 clinical status of human breast cancer by using gene expression profiles, *Proc Natl Acad Sci*, 98:11462-11467 (2001).

- Statistical analysis: This analysis used the predictive statistical tree model of this invention. The method of the invention first screens genes to reduce noise, applies k-means correlation-based clustering targeting a large number of clusters,
15 and then uses singular value decompositions ("SVD") to extract the single dominant factor (principal component) from each cluster. This generated 496 cluster-derived singular factors (metagenes) that characterize multiple patterns of expression of the genes across samples. The strategy aimed to extract multiple such patterns while reducing dimension and smoothing out gene-specific noise
20 through the aggregation within clusters. Formal predictive analysis then uses these metagenes in a Bayesian classification tree analysis. This generates multiple recursive partitions of the sample into subgroups (the "leaves" of the classification tree), and associates Bayesian predictive probabilities of outcomes with each subgroup. Overall predictions for an individual sample are then
25 generated by averaging predictions, with appropriate weights, across many such tree models. Iterative out-of-sample, cross-validation predictions are then performed leaving each tumor out of the data set one at a time, refitting the model from the remaining tumors and using it to predict the hold-out case. This rigorously tests the predictive value of a model and mirrors the real-world
30 prognostic context where prediction of new cases as they arise is the major goal.

Although, clinico-pathologic parameters such as the presence or absence of positive axillary nodes represent the best means available to classify patients into broad subgroups by recurrence and survival, such methods remain an imperfect tool. Among patients with no detectable lymph node involvement, a population
5 thought to be in a low risk category, between 22 and 33% develop recurrent disease after a 10-year follow-up. See Polychemotherapy for early breast cancer: an overview of the randomized trials, Early Breast Cancer Trialists' Collaborative Group, *Lancet*; 352:930-942 (2001). Thus, properly identifying individuals out of this group who are at risk for recurrence is beyond the current capabilities of
10 most predictive diagnostics.

The question of lymph node diagnosis is part of the broader issue of more accurately predicting breast cancer disease course and recurrence. Recently, genomic-scale measures of gene expression, using microarrays and other technologies have opened a new avenue for cancer diagnosis. They identify
15 patterns of gene activity that sub-classify tumors, and such patterns may correlate with the biological and clinical properties of the tumors. The utility of such data in improving prognosis will rely on analytical methods that accurately predict the behavior of the tumors based on expression patterns. Credible predictive evaluation is critical in establishing valid and reproducible results and implicating
20 expression patterns that do indeed reflect underlying biology. This predictive perspective is a key step towards integrating complex data into the process of prognosis for the individual patient, a step that can be accomplished through the practice of the present invention.

Furthermore, an ultimate goal is to integrate molecular and genomic information
25 with traditional clinical risk factors, including lymph node status, patient age, hormone receptor status, and tumor size, in comprehensive models for predicting disease outcomes. Rather than supplant traditional clinical appraisal, genomic data adds data to traditional risk factors, and assessing individuals based on combinations of relevant traditional risk factors with identified genomic factors
30 could potentially improve predictions. The present invention allows this goal to be realized by demonstrating the ability of genomic data to accurately predict

lymph node involvement and disease recurrence in defined patient subgroups. Most importantly, these predictions are relevant for the individual patient and can provide a quantitative measure of the probability for the clinical phenotype and outcome of disease. Such predictions may ultimately facilitate treating
5 patients as individuals rather than as unidentifiable members of a risk profile.

The present invention was applied to the analysis of gene expression patterns in primary breast tumors that predict lymph node metastasis, as well as tumor recurrence. The first study compares traditional “low-risk” versus “high-risk” patients, primarily based on age, primary tumor size, lymph node status, and
10 Estrogen receptor (“ER”) status. Among ER positive individuals, the “high-risk” clinical profile is represented by advanced lymph node metastases (10 or more positive nodes); the “low-risk profile” identifies node-negative women of age greater than 40 years with tumor size below 2cm. The number of samples in the tumor collection that met these criteria reduced down to 18 high-risk and 19 low-
15 risk cases. Expression data were generated and metagenes identified and used in the Bayesian statistical tree analysis. Figure 9 displays summary predictions from the resulting total of 37 cross-validation analyses. For each individual tumor, this graph illustrates the predicted probability for “high-risk” versus “low-risk” (red versus blue) together with an approximate 90% confidence interval,
20 based on analysis of the 36 remaining tumors performed successively 37 times as each tumor prediction is made. It is important to recognize that each sample in the data set, when assayed in this manner, constitutes a validation set that accurately assesses the robustness of the predictive model. The metagene model accurately predicts metastatic potential; about 90% of cases are accurately
25 predicted based on a simple threshold at 0.5 on the estimated probability in each case. Case number 7 is in the intermediate zone, exhibiting patterns of expression of the selected metagenes that relate equally well to those of “high-“ and “low-risk” cases, while case 22 is a clinical “high-risk” case with genomic expression patterns that relate more closely to “low-risk” cases. In contrast, node
30 negative patients 5 and 11 have gene expression patterns more strongly indicative

of “high-risk”, and are key cases for follow-up investigations. The details of clinical information in these apparently discordant cases are shown in Table 2. Clinical features of these “discordant” cases are illuminating, and suggestive of how a broader investigation of clinical data combined with molecular model-

5 based predictions may aid in the eventual decision-making process. Although case 22 did in fact recur, 6 years post-surgery; this patient’s clinical classification as high risk for recurrence based on purely clinical parameters was moderated by a lower risk based on metagenes, as demonstrated by this patient having survived recurrence-free for a longer time. Thus the lower probability prediction assigned

10 to patient 22 based on the gene expression profiles is reflected in the clinical behavior of her disease. The “low-risk” patient 7 recurred at 31 months, and patient 11 at 38 months, whereas case 5 is currently disease-free after only 12 months of follow-up. Again, case 7, and to some degree case 11, thus partly corroborate the predictions based on genomic criteria. data. With such

15 predictions as part of a prognostic model, more intensive or innovative post-surgical therapy should perhaps have been recommended for these two cases. A critical aspect of the analyses described here is allowing the complexity of distinct gene expression patterns to enter the predictive model. Tumors are graphed against metagene levels for three of the highest scoring metagene factors as shown in Figure 10. This analysis highlights the need to analyze multiple

20 aspects of gene expression patterns. For example, if the low-risk cases 1, 3 and 11 are assessed against metagene 146 alone, their levels are more consistent with high-risk cases. However, when additional dimensions are considered, the picture changes. The second frame (upper right) shows that low-risk is consistent

25 with low levels of metagene 130 or high levels of metagene 146; hence, cases 1 and 3 are not inconsistent in the overall pattern, though case 11 is consistent. An analysis that selects one set of genes, summarized here as one metagene, as a “predictor” would be potentially misleading, as it ignores the broader picture of multiple interlocked genomic patterns that together characterize a state. In the

30 predictions, these two metagenes play key roles: low levels of metagene 146 coupled with higher levels of metagene 130 are strongly predictive of high-risk

cases. Combined use of multiple metagenes, in the context of the tree selection model building process, ultimately yields a pattern that has the capacity to accurately predict the clinical outcome.

The second analysis concerns 3 year recurrence following primary surgery among
5 the challenging and varied subset of patients with 1-3 positive lymph nodes. Such patients typically receive adjuvant chemotherapy alone, but more than 20% suffer relapse within five years. Hence, improved prognosis for this heterogeneous group is of critical importance; patients identified with a high probability of relapse could be targeted for more intensive treatment. The dataset
10 provided 52 ER-positive cases in this lymph node category (34 non-recurrent, 18 recurrent). The aggregate predictions from the sets of generated statistical tree models defines a rather accurate picture; once again, there is an approximate 90% overall predictive accuracy in the 52 separate one-at-a-time, cross-validation prediction assessments as shown in Figure 11. Based on the gene expression
15 analysis, the 3 year non-recurrent cases 6 and 23, having profiles more akin to recurrent cases, would be candidates for intensive treatment. These patients did receive adjuvant chemotherapy based on additional clinical risk factors (especially tumor size). Thus traditional clinical risk factors other than lymph node status also indicate higher risk of recurrence for these two cases, consistent
20 with the molecular predictions. Each actually survived recurrence-free for over three years; case 6 recurred at 42 months and case 23 remains disease-free after over 6 years. Cases with low genomic criteria for recurrence would be 36, 38 and 42. They, however, experienced recurrence within three years. These are cases that, under prognosis informed by only the genomic model, would have been
25 indicated as more benign and not candidates for intensive treatment, whereas such a treatment might have proven to be more beneficial.

The tree model of the invention identified subsets of genes related to the metagene predictors of lymph node involvement. These are replete with those involved in cellular immunity, including a high proportion of genes that function
30 in the interferon pathway. They include genes that are induced by interferon such as various chemokines and chemokine receptors (Rantes, CXCL10, CCR2), other

interferon-induced genes (IFI30, IFI35, IFI27, IFIT1, IFIT4, IFITM3), as well as interferon effectors (2'-5' oligoA synthetase), and genes encoding proteins mediating the induction of these genes in response to interferon (STAT1 and IRF1). This connection is intriguing given the role of interferon as a mediator of the anti-tumor response and, together with the fact that many genes involved in T cell function (TCRA, CD3D, IL2R, MHC) are also included within the group that predict lymph node metastasis. This may reflect the distinct nature of these tumors that have acquired a metastatic potential that elicits an anti-tumor response that is ultimately unsuccessful or an aberration of the normal anti-tumor response.

Genes implicated in recurrence prediction as identified by the tree model of the invention do not exhibit such a striking functional clustering but do include many examples previously associated with breast cancer. Moreover, this group of genes is clearly distinct set from those that predict lymph node involvement.

They include genes associated with cell proliferation control, both cell cycle specific activities (CDKN2D, Cyclin F, E2F4, DNA primase, DNA ligase), more general cell growth and signaling activities (MK2, JAK3, MAPK8IP, and EF1 α), and a number of growth factor receptors and G-protein coupled receptors, some of which have been shown to facilitate breast tumor growth (EpoR). Possibly, the poor prognosis with respect to survival reflects a more vigorous proliferative capacity of the tumor.

Thus, the genes implicated in the prediction of lymph node metastasis and overall recurrence of disease, although clearly representing interrelated phenomena, nevertheless reflect the participation of distinct biological processes. The tree model is thus flexible in that regard as it only selects those metagenes that are most relevant to the prediction in hand. By contrast, traditional statistical testing perspectives that focus on significant differences at a population parameter level may say little of practical significance in terms of an individual patient's prognosis. Furthermore, the present invention takes into account the relevant multiple features of the complex patterns of gene expression, especially in a context such as breast cancer where multiple, interacting biological and

environmental processes define physiological states, and individual dimensions provide only partial information. The tree model of the present invention assesses the complex, multivariate patterns in gene expression data from primary tumor biopsies, exploring the value of such patterns in predicting lymph node
5 metastasis and relapse, two critically important aspects of breast cancer, at the individual patient level. The tree model identifies multivariate patterns of gene expression that, in this realistic context of substantial patient heterogeneity, deliver predictive accuracy of about 90%. The probabilistic models highlight cases where uncertainty is high, and generate subsets of implicated genes that
10 relate to the biology of metastasis and tumor evolution.

To ascertain the success of the tree model, an out-of-sample predictive assessment via cross-validation is always conducted. Any selection of gene, metagene or clinical variables must be part of each cross-validation analysis. The results of such "feature selection" will vary each time a tumor is analyzed, and
15 can dramatically impact on predictive accuracy. Analyses that select a set of predictors based on the entire dataset, including the individual to be predicted, in advance of predictive evaluation are inappropriate, and lead to misleadingly over-optimistic conclusions about predictive value. For breast cancer recurrence, the results provide evidence for gene expression profiles associated with recurrence
20 in a homogeneous cohort of low risk patients. There are, however, several distinctions. First is the evaluation of models on the basis of accuracy in prediction at the individual level, with predictions made in formal probabilistic terms. Second, multiple, related and interacting biological patterns, here represented as separate and distinct metagenes, together represent a clinical state.
25 Reducing high-dimensional genomic data to a single index may sacrifice opportunity for understanding complex interactions (see Figure 2) that are truly predictive. Thirdly, we believe that the integration of molecular profiles with clinical risk factors—rather than the replacement of clinical data with molecular data—will define the major step towards personalized prognosis utilizing
30 genomic data, hence the need for stratification using clinical variables.

<<< INSERT TABLES 1 & TABLE 2 from 7163557>>>

Example 4: Identifying Atherosclerotic Phenotype Determinative Genes related to Atherosclerosis Disease Progression and Susceptibility to Atherosclerosis.

5

Claims

What is claimed is:

- 5 1. The application of classification tree models incorporating Bayesian analysis to the statistical prediction of binary outcomes

-

Figure 1

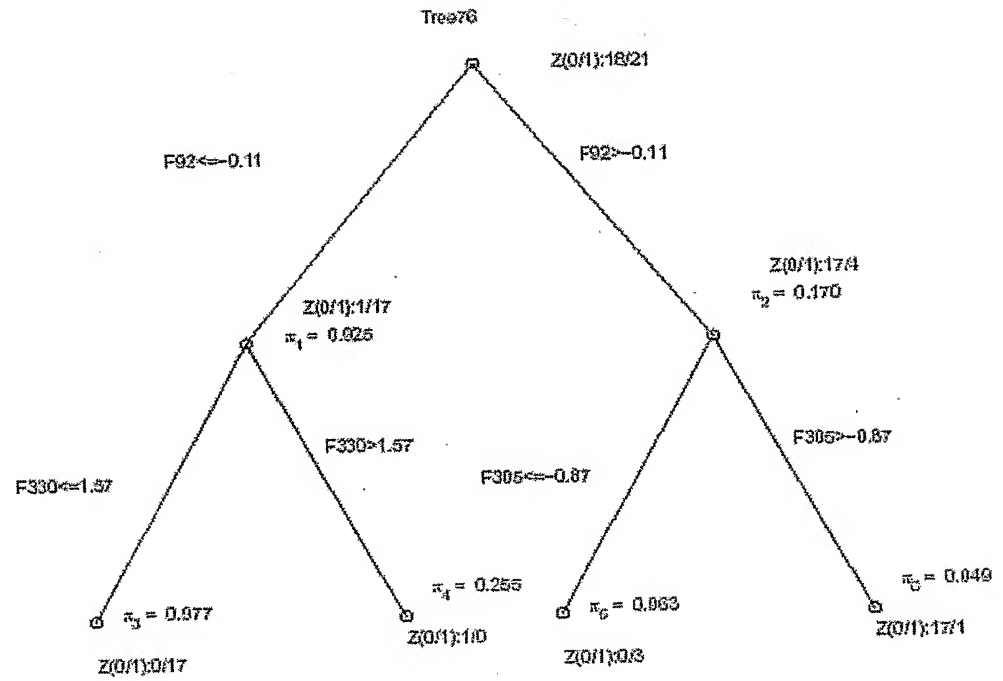


Figure 2

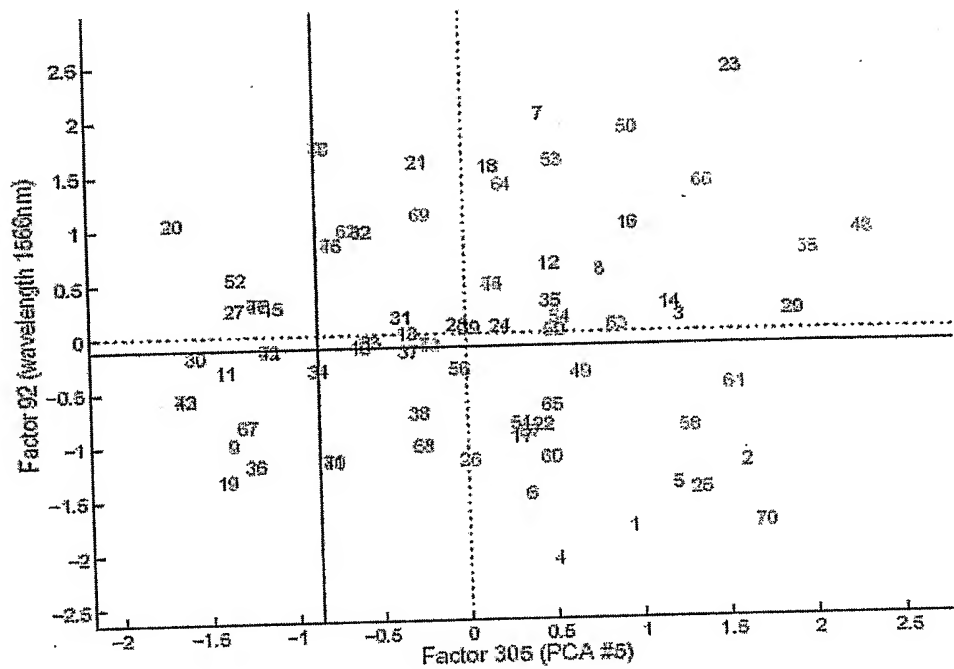


Figure 3

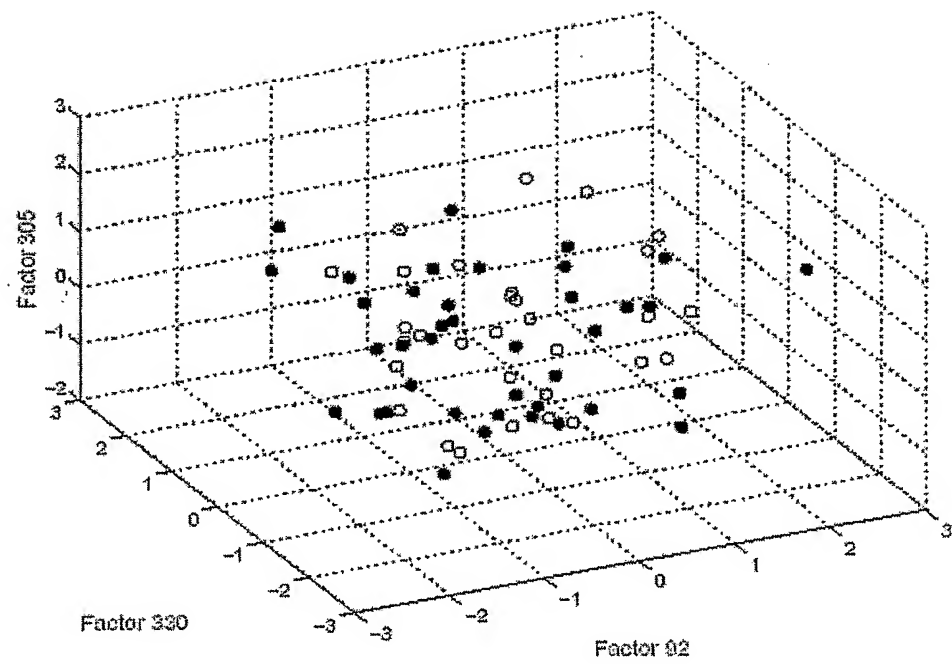


Figure 4

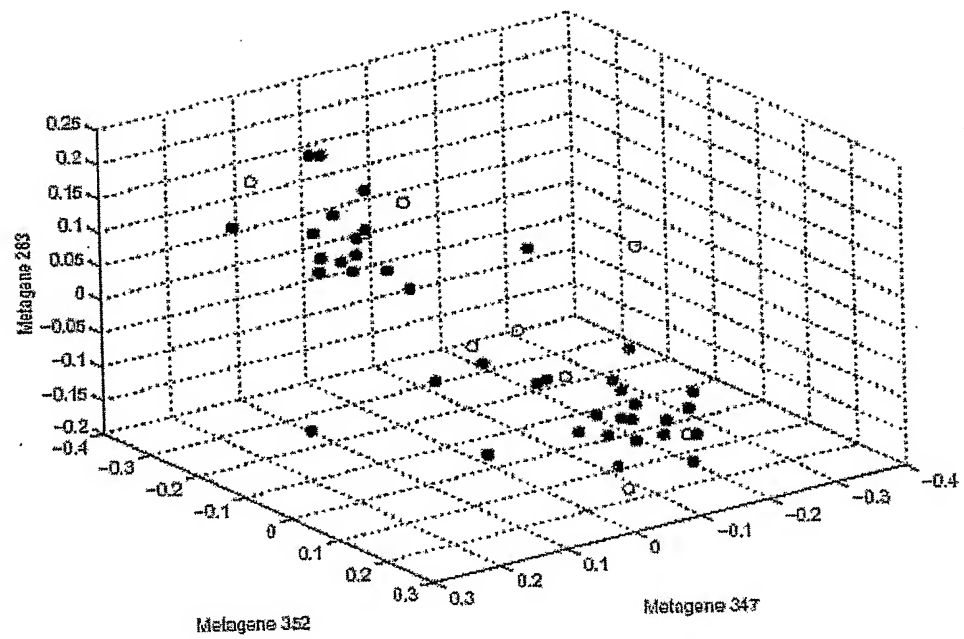


Figure 5

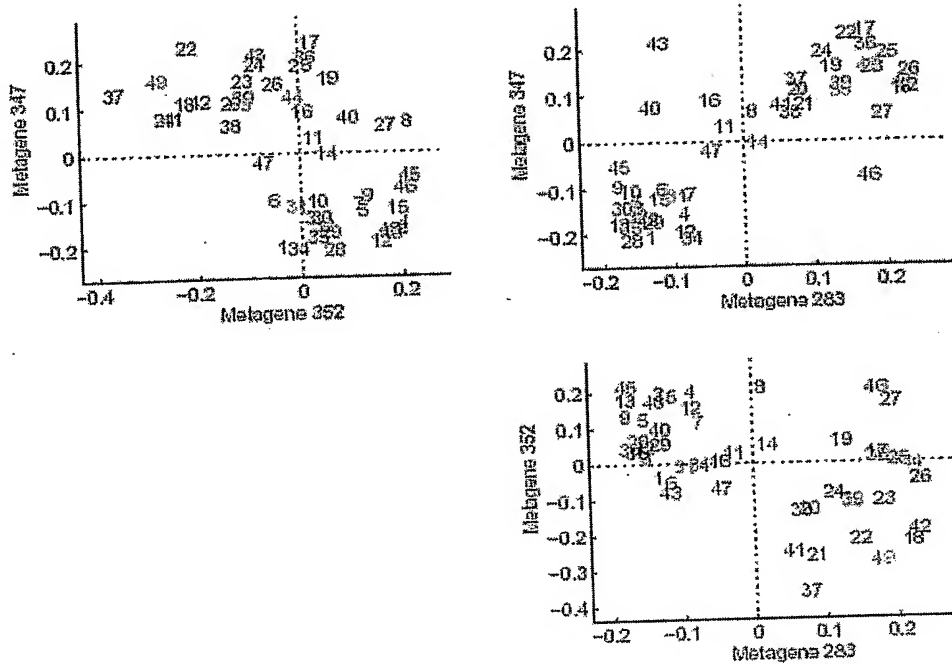


Figure 6

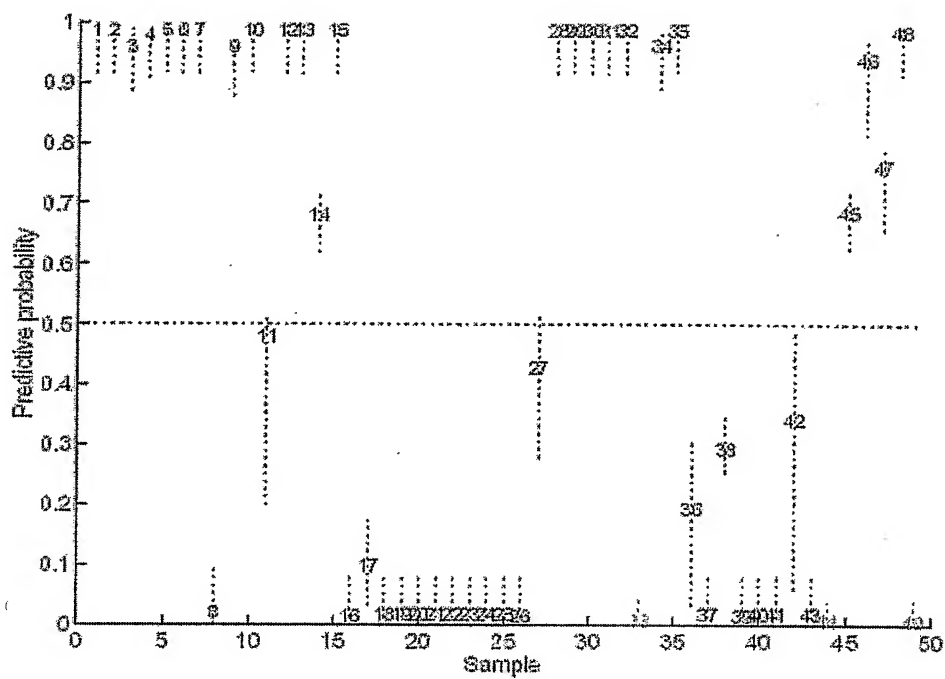
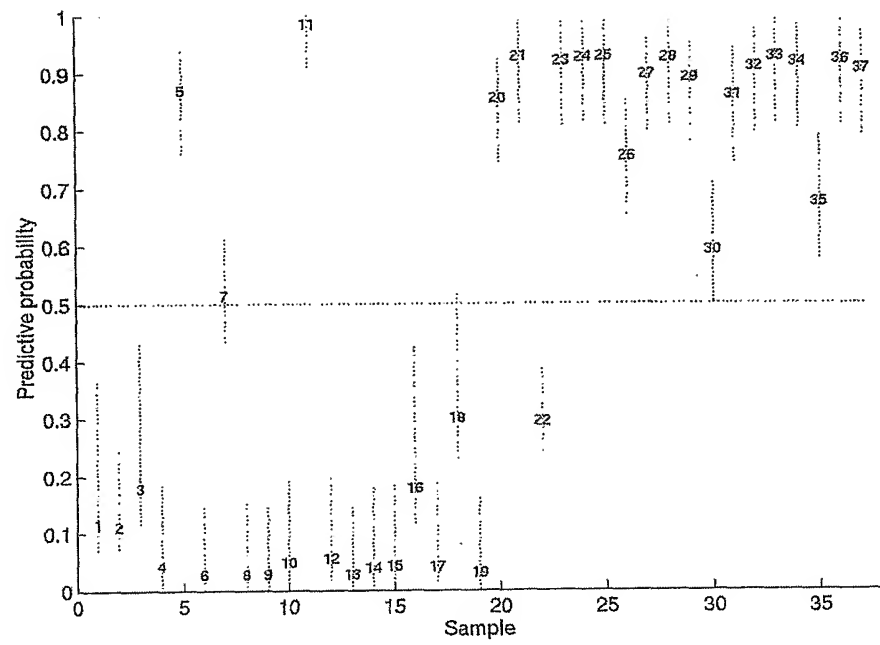


Figure 7

Figure 8

Figure
9



Figure

10

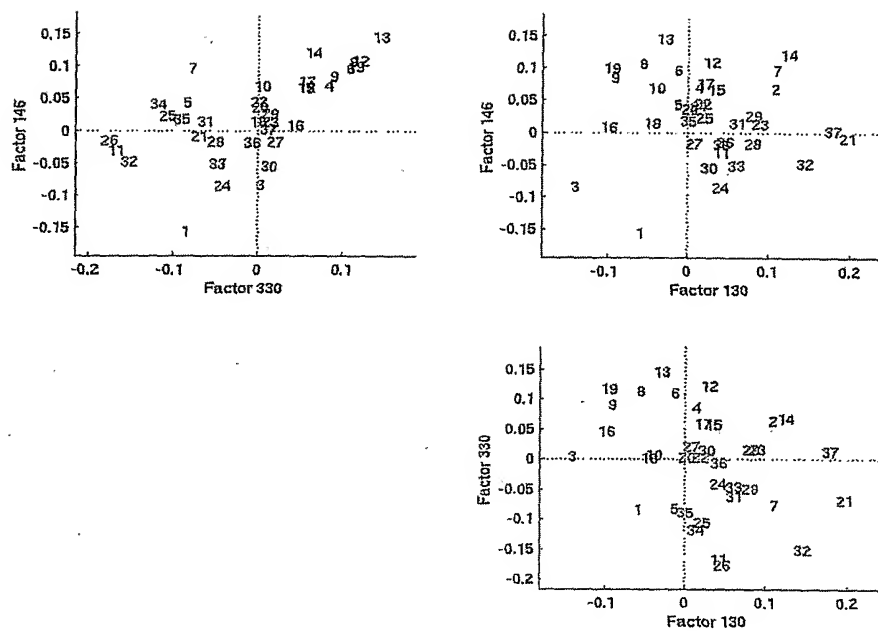


Figure
11

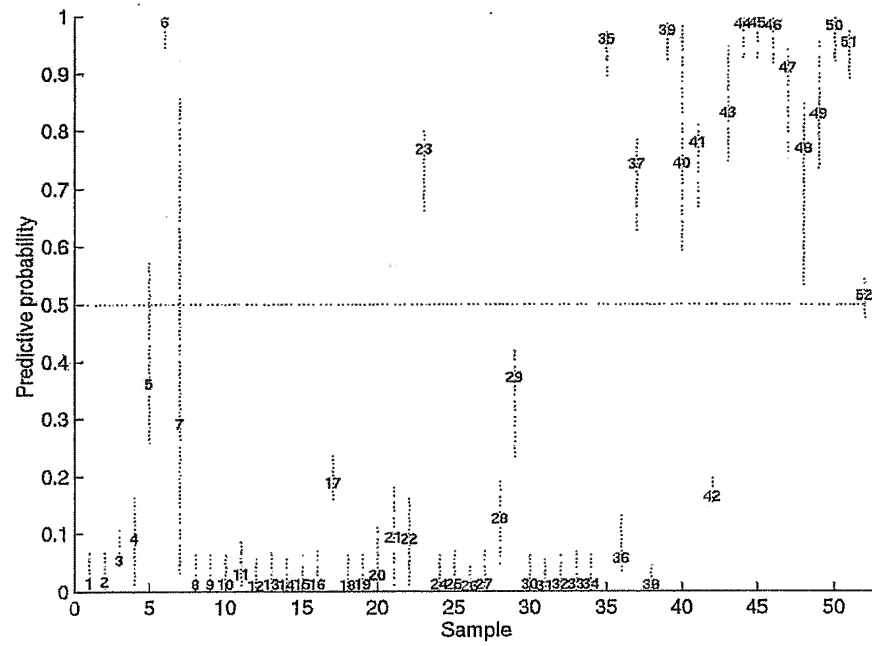


Figure 12

Genes associated with metagene predictors of lymph node metastasis

Acc. No.	Symbol	Gene name	GO Function
M12969	TCRA	T cell receptor alpha locus	G-protein linked receptor protein signalling pathway, developmental processes, cell-cell signaling, chemotaxis
M13755	ISG15	interferon-stimulated protein, 15 kDa	
D43707	CCL17	small inducible cytokine subfamily A (Cys-Cys), member 17	
D45248	PSME2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	FGF receptor signalling pathway
L03840	FGFR4	fibroblast growth factor receptor 4	
U22970		interferon, alpha-inducible protein (clone IFI-0-16)	
M21121	CCL5	small inducible cytokine A5 (RANTES)	
			exocytosis, oxidative stress response, cell motility, chemotaxis, inflammatory response, cellular defense response, cell-cell signalling, immune response, response to viruses, signal transduction, calcium ion homeostasis, cell adhesion
L05148	ZAP70	zeta-chain (TCR) associated protein kinase (70 kD)	deoxyribonucleoside monophosphate biosynthesis, nucleobase, nucleoside, nucleotide and nucleic acid metabolism
D00596	TYMS	thymidylate synthetase	
D11086	IL2RG	interleukin 2 receptor, gamma (severe combined immunodeficiency)	protein complex assembly, immune response, cell proliferation, signal transduction
J04086	TOP2A	topoisomerase (DNA) II alpha (170kD)	degradation of cyclin, ubiquitin-dependent protein degradation, protein modification, positive control of cell proliferation
U73376	UBE2C	ubiquitin-conjugating enzyme E2C	
U37352	PPP2R5C	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	anti-apoptosis, cell cycle control, developmental processes, transcription from Pol II promoter
M31393	STMN1	stathmin 1/oncoprotein 18	
X13293	MYBL2	v-myc myeloblastosis viral oncogene homolog (avian)-like 2	
M13194	ERCC1	exonin repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	DNA repair, nucleotide-excision repair, embryogenesis and morphogenesis
U09637	PLAUR	plasminogen activator, urokinase receptor	apoptosis, induction of apoptosis, proteolysis and peptidolysis
U29014	CASP4	caspase 4, apoptosis-related cysteine protease	
X73066	NME1	non-metastatic cells 1, protein (NM23A) expressed in	transcription from Pol II promoter protein biosynthesis
L40387	OASL	2'-5'-oligoadenylate synthetase-like	
J04162	TACSTD2	tumor-associated calcium signal transducer 2	
U58516	CH13L2	chitinase 3-like 2	
A1701049	FARF1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	
A8018280	KIAA0737	KIAA0737 gene product	transcription from Pol II promoter protein biosynthesis
X59280	BTF3	basic transcription factor 3	
X63527	RPL19	ribosomal protein L19	

AF026947	AKR7A2	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	aldehyde metabolism, carbohydrate metabolism, oncogenesis
Q37931	RNASE4	ribonuclease, RNase A family, 4	
AL080078	SSBP2	single-stranded DNA binding protein 2	
M55543	GBP2	guanylate binding protein 2, interferon-inducible	immune response
Q26070	ITPR1	inositol 1,4,5-bisphosphate receptor, type 1	small molecule transport, signal transduction
M24594	IFIT1	interferon-induced protein with tetrapeptide repeats 1	
M97925	STAT1	signal transducer and activator of transcription 1, 91kD	signal transduction, caspase activation, JAK-STAT cascade, NF- κ B/NF-kappaB cascade, STAT protein dimerization, STAT protein nuclear translocation, tyrosine phosphorylation of STAT protein, cell cycle control, response to pathogen/parasite, transcription from Pci II promoter
M97925	STAT1	signal transducer and activator of transcription 1, 91kD	
L13435		glycosyltransferase AD-017	
AF080228	RARRES3	retinoic acid receptor responder (tazarotene induced) 3	negative control of cell proliferation
U88964	ISG20	interferon stimulated gene (20kD)	cell proliferation
M97925	STAT1	signal transducer and activator of transcription 1, 91kD	
M97925	STAT1	signal transducer and activator of transcription 1, 91kD	
AL046977	CLDN8	claudin 8	
AB002320	LYSL1	lysosomal sputase-like 1	nucleobase, nucleoside, nucleotide and nucleic acid metabolism
A175157	KIAA1254	KIAA1254 protein	
D12485		ectonucleotide pyrophosphatase/phosphodiesterase 1	
AJ225089	OASL	2'-5'-oligoadenylate synthetase-like	
L07518	DLX2	distal-less homeo box 2	brain development
A1070793	MAP-1	modulator of apoptosis 1	
D14878	KNSL2	kinesin-like 2	
AL039459	LRIQ1	ortholog of mouse integral membrane glycoprotein LIG-1	
AL050127	DKFZP583D00623	DKFZP583D00623 protein	
AF011468	STK0	serine/threonine kinase 15	protein phosphorylation, oncogenesis, mitosis
AF010268	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	induction of apoptosis via death domain receptors, cell surface receptor linked signal transduction
Y13323	ADAMDEC1	ADAM-like, decysin 1	
AB002345	PER2	period homolog 2 (Drosophila)	circadian rhythm
X53281	BTF3	basic transcription factor 3	
AF030514	CXCL11	small inducible cytokine subfamily B (Cys-X-Cys), member 11	response to pathogenic fungi, cell-cell signaling, chemotaxis, inflammatory response, signal transduction
AF019225	APOL1	apolipoprotein L	lipid metabolism
AB011143	GAB2	GRB2-associated binding protein 2	
Z15008	LAMC2	laminin, gamma 2 (nicotin (100kD), kalinin (105kD), BM600 (100kD), Herlitz junctional epidermolysis bullosa)	epidermal differentiation
U54558	EIF3S7	eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67kD)	translational regulation, initiation
W28256	DKFZP585M1120		

XG9699 AB001451	HSXIAPAF1 SLI	XIAP associated factor-1 neuronal Shc adaptor homolog	central nervous system development, peripheral nervous system development, signal transduction
X87342 M55542 A1525393 D78139 AF004230	LLGL2 GBP1 ARPC3 SQLE LILRB1	lethal giant larvae homolog 2 (Drosophila) guanylate binding protein 1, interferon-inducible, 67kD actin related protein 2/3 complex, subunit 3 (21 kD) squalene epoxidase leukocyte immunoglobulin-like receptor, subfamily B (with TIR and ITIM domains), member 1	cell motility response to viruses
AF087036 AF006521 AB011064 AL080213 AJ000882 U26174 U52931 AJ131593	MSC C4orf1 ALEX2 NCOA1 GZMK IRF7 AKAP9	musculin (activated B-cell factor-1) chromosome 4 open reading frame 1 amedillo repeat protein ALEX2 nuclear receptor coactivator 1 granzyme K (serine protease, granzyme 3; tryptase II) interferon regulatory factor 7 A kinase (PRKA) anchor protein (yotiao) 9	transcription from Pol II promoter transcription synaptic transmission, signal transduction, small molecule transport
AL040446 X51965 M34455 M63193	OSBPL1A LAG3 INDO ECGF1	oxysterol-binding protein-related protein 1 lymphocyte activation gene 3 indoleamine-pyrole 2,3 dioxygenase endothelial cell growth factor 1 (platelet-derived)	tryptophan catabolism, pregnancy, defense response DNA replication, mitochondrial genome maintenance, pyrimidine nucleotide metabolism, cell-cell signaling, cell surface receptor linked signal transduction cell shape and cell size control
AF001691 AL022237 AB000115 U70063 M33962	PPL BIK C1orf29 ASAH1 MX1	periplakin BCL2-interacting killer (apoptosis-inducing) hypothetical protein, expressed in osteoblast N-acylsphingosine amidohydrolase (acid ceramidase) myxovirus (influenza) resistance 1, homolog of murine (interferon- inducible protein p78)	ceramide metabolism, fatty acid metabolism defense response, signal transduction, induction of apoptosis, pathogenesis
J02923 M62800 M17016 M85276 U95626 AB013924 X72755	LCP1 SSA1 GZMB GNLY LAMP3 CXCL9	lymphocyte cytosolic protein 1 (L-plasmin) Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS- A/Ro) granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) granulysin chemokine (C-C motif) receptor 2 lysosomal-associated membrane protein 3 monokine induced by gamma interferon	pathogenesis cellular defense response oncogenesis, cell proliferation defense response, immune response, inflammatory response, chemotaxis, cell-cell signaling, signal transduction, cellular defense response, G-protein linked receptor protein signalling pathway
D97071 X59536 AL022723	KIAA0233 HLA-C	KIAA0233 gene product major histocompatibility complex, class I, C major histocompatibility complex, class I, F	

AJ031634	CCL13	small inducible cytokine subfamily A (Cys-Cys), member 13	signal transduction, calcium ion homeostasis, cell-cell signaling, chemotaxis, immune response, inflammatory response
X39834	SALL2	sal-like 2 (Drosophila)	histogenesis and organogenesis
D29915		interferon-induced, hepatitis C-associated microtubular aggregate protein (44 kD)	
L13210	LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein	cellular defense response, signal transduction
AF072469	JRK	Jarky homolog (mouse)	
Z47553	FMOS	flavin containing monooxygenase 5	
AL082078			
U10523	GCH1	GTP cyclohydrolase 1 (dopa-responsive dystonia)	neurotransmitter synthesis and storage, nitric oxide biosynthesis
A436607	ATP5D	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit	
AL090942	ATIP1	AT2 receptor-interacting protein 1	
AL049367	LOC55970		
X59892	WARS	tryptophanyl-tRNA synthetase	tryptophanyl-tRNA biosynthesis, protein biosynthesis, negative control of cell proliferation
U00548	BTN3A3	butyrophilin, subfamily 3, member A3	
AA603061	PSMB9	prolensome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2)	proteolysis and peptidolysis
AA916102	CD3D	CD3D antigen, delta polypeptide (TTC complex)	cell surface receptor linked signal transduction, cellular defense response
M11810		2',5'-oligoadenylate synthetase 1 (40-46 kD)	
X04371	OAS1	2',5'-oligoadenylate synthetase 1 (40-46 kD)	
AA203213	ISG15	interferon-stimulated protein, 15 kDa	
M87503	ISGF3G	interferon-stimulated transcription factor 3, gamma (48 kD)	cell surface receptor linked signal transduction, transcription from Pci II promoter
AF026941	olg5		
AF026939	IFIT4	interferon-induced protein with tetratricopeptide repeats 4	
AL047566		capicua homolog (Drosophila)	
U97502			
U00546	BTN3A2	butyrophilin, subfamily 3, member A2	
AD001528	SMS	spermine synthase	methionine metabolism, polyamine metabolism
W20226	DJ171N18.2	hypothetical protein	
M11119			
AF007738	TNK1	tyrosine kinase, non-receptor, 1	
D44497	CORO1A	coronin, actin binding protein, 1A	phagosome formation, transport, mitosis, cell motility, cell shape and cell size control
AL031178			
D28137	BST2	bone marrow stromal cell antigen 2	humoral defense mechanism, cell proliferation, cell-cell signaling, developmental processes
M97434	OAS2	2',5'-oligoadenylate synthetase 2 (69-71 kD)	nucleobase, nucleoside, nucleotide and nucleic acid metabolism
M97284	OAS2	2',5'-oligoadenylate synthetase 2 (69-71 kD)	
AF070632			
AJ001902	MSC10558	thyroid hormone receptor interactor 6	
U03925	TRIM20	tripartite motif-containing 20	

U33267	GLRB	glycine receptor, beta	small molecule transport, cell surface receptor linked signal transduction
AI597018	MRPL33	mitochondrial ribosomal protein L33	
AA402538	MGC2749	hypothetical protein MGC2749	
D78124	CIRBP	cold inducible RNA binding protein	cold response
D21337	COL4A6	collagen, type IV, alpha 6	oncogenesis
AL031083		gamma-aminobutyric acid (GABA) B receptor, 1	
M74447	TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	cellular defense response, peptide transport, defense response
AB012017	KLK11	kallikrein 11	
AF020202	UNC13	unc-12-like (C. elegans)	excretion, induction of apoptosis, signal transduction, apoptosis
X57522	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	defense response, cellular defense response, peptide transport
D88153	HYA22	HYA22 protein	
U64197	COL20	small inducible cytokine subfamily A (Cys-Cys), member 20	antimicrobial humoral response, immune response, inflammatory response, chemotaxis, signal transduction, cell-cell signaling
Y03048		peroxisomal fatty-acylated protein	protein-peroxisome targeting, peroxisome organization and biogenesis
AA883502	UBE2L6	ubiquitin-conjugating enzyme E2 L 6	protein modification
Y00062	PTPRC	protein tyrosine phosphatase, receptor-type, C	cell surface receptor linked signal transduction
M01670	E2-EFF	ubiquitin carrier protein	protein modification
AL021683		SCO cytochrome oxidase deficient homolog 2 (yeast)	
M16336	CD2	CD2 antigen (p50), sheep red blood cell receptor	cell adhesion, signal transduction, antimicrobial humoral response
AB018289	RANBP10	RAN binding protein 10	
AL035494		hypothetical protein FLJ10097	
AI051806	CRIM1	cysteine-rich motor neuron 1	neurogenesis
U05975	IFNGR2	interferon gamma receptor 2 (interferon gamma transducer 1)	resistance to pathogenic bacteria, response to viruses, cell surface receptor linked signal transduction
D46248	PSME2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	
X87344		major histocompatibility complex, class II, DM alpha	
AL049417	DUSP3	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	protein dephosphorylation
D32129	HLA-A	major histocompatibility complex, class I, A	
AF035282	C1orf21	chromosome 1 open reading frame 21	
X57352	IFITM3	interferon induced transmembrane protein 3 (1-2U)	immune response
AB023194	KIAA0977	KIAA0977 protein	
AA149431	DKFZp781F2014	hypothetical protein DKFZp781F2014	
X67325	IFI27	interferon, alpha-inducible protein 27	
X02530	CXCL10	small inducible cytokine subfamily B (Cys-X-Cys), member 10	signal transduction, chemotaxis, cell motility, circulation, muscle development, positive control of cell proliferation, cell-cell signaling, inflammatory response, signal transduction, cell surface receptor linked signal transduction
U72882	IFI35	interferon-induced protein 35	
L78833		breast cancer 1, early onset	

L29874		dCMP deaminase		
LD5072		Interferon regulatory factor 1		pyrimidine nucleotide metabolism oncogenesis, transcription from Pol II promoter
JD4104	IFITM1	interferon induced transmembrane protein 1 (9-27)		negative control of cell proliferation, cell surface receptor linked signal transduction, cell cycle control
AB005782	LGALS9	lectin, galactoside-binding, soluble, 9 (galactin 9)		
D12435	PIGF	phosphatidylinositol glycan, class F		GPI anchor formation
M30318	MX2	myxovirus (influenza) resistance 2, homolog of murine		defense response
M01070	E2-EPF	ubiquitin carrier protein		
M91070	E2-EPF	ubiquitin carrier protein		
M24594	IFIT1	interferon-induced protein with tetrahydropeptide repeats 1		
JD2909	IFIT2	interferon, gamma-inducible protein 30		
Y10032	SGK	serum/glucocorticoid regulated kinase		sodium transport, stress response, protein phosphorylation

Figure 13

Acc. No.	Symbol	Gene name	GO Function
U50848	PRKR	protein kinase, interferon-inducible double stranded RNA dependent	Signal transduction, developmental processes, transcription regulation from Pol II promoter, oncogenesis, ectoderm development, histogenesis and organogenesis, embryogenesis and morphogenesis
U37055	MST1	macrophage stimulating 1 (hepatocyte growth factor-like)	
K03183	CGB7	chorionic gonadotropin, beta polypeptide 7	
J03069	MYCL2	v-myc myelocytomatosis viral oncogene homolog 2 (avian)	
M36711	TFAP2A	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	
X69699	PAX8	paired box gene 8	protein dephosphorylation, transmembrane receptor protein tyrosine phosphatase signalling, phosphate metabolism
L38929	PTPRD	protein tyrosine phosphatase, receptor type, D	
L76568	ERCC4	excision repair cross-complementing rodent repair deficiency, complementation group 4	
U11870	IL8RA	interleukin 8 receptor, alpha	
M36067	LIG1	ligase I, DNA, ATP-dependent	
D16105	LTK	leukocyte tyrosine kinase	DNA repair, embryogenesis and morphogenesis, DNA metabolism
U12779	MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	
L34059	CDH4	cadherin 4, type 1, R-cadherin (retinal)	Signal transduction, protein phosphorylation
U22028	CYP2A13	cytochrome P450, subfamily 11A (phenobarbital-inducible), polypeptide 13	
U27193	DUSP8	dual specificity phosphatase 8	protein dephosphorylation, inactivation of MAPK
L24559	POLA2	polymerase (DNA-directed), alpha (70kD)	
U40343	CDKN2D	cyclin-dependent kinase inhibitor 2D (p18, inhibits CDK4)	regulation of CDK activity, negative control of cell proliferation, cell cycle arrest, cell cycle control
Z36714	CCNF	cyclin F	
U18334	NOS2C	nitric oxide synthase 2C	
U31317	JAK3	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	protein phosphorylation, mesoderm development, cell growth and maintenance
U07375	ITGAV	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	
M64231	SRM	spermidine synthase	cell surface receptor linked signal transduction
AF023614	TNFRSF13B	tumor necrosis factor receptor superfamily, member 13B	
U34806	GPR15	G protein-coupled receptor 15	
U26209	SLC13A2	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2	
AL031983	GABBR1	gamma-aminobutyric acid (GABA) B receptor, 1	
AL031983	OR2H2	olfactory receptor, family 2, subfamily H, member 2	G-protein linked receptor protein signalling pathway
AL031983	OR2H5P	olfactory receptor, family 2, subfamily H, member 5 pseudogene	
AL031983	OR2J1P	olfactory receptor, family 2, subfamily J, member 1 pseudogene	small molecule transport

Y16768 AF047485	KRTHA3A LOC005886	keratin, hair, acidic, 3A amine oxidase pseudogene	cell shape and cell size control cell adhesion, inflammatory response, amine metabolism
X57282 AF027957	EPOR GPR35	erythropoietin receptor G protein-coupled receptor 35	Signal transduction G-protein linked receptor protein signalling pathway
AF007194 D86979 U92645 L14754	MUC3A KIAA0228 ELF4 IGHMBP2	mucin 3A, intestinal KIAA0228 gene product E74-like factor 4 (ets domain transcription factor) immunoglobulin mu binding protein 2	transcription from Pol II promoter DNA replication, DNA repair, single stranded DNA binding, DNA recombination
X63036 X74143 Z82180 AF017095	RHCE FOXG1A EAM57 PDPK1	Rhesus blood group, CcEe antigens forkhead box G1A hypothetical protein EAM57 3-phosphoinositide dependent protein kinase-1	brain development protein phosphorylation, insulin receptor signalling pathway, actin cytoskeleton reorganization
U06088 AB028950 AB000308 AB020703	GALNS TLN1 PSMD13 AP2A2	galactosamine (N-acetyl)-6-sulfate sulfatase (Morquio syndrome, mucopolysaccharidosis type IVA) talin 1 proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 adaptor-related protein complex 2, alpha 2 subunit	
L36318 D10704 X64118 U04810 X83127	GRM2 CHK PVR TROAP KCNA81	glutamate receptor, metabotropic 2 choline kinase poliovirus receptor trophinin associated protein (tastin) potassium voltage-gated channel, shaker-related subfamily, beta member 1	synaptic transmission, adenylate cyclase inhibition lipid metabolism, lipid transport cell adhesion potassium transport
L76703 AJ237872 M58378 AB007943 AF003837 AB023167 AF054185 AF052177 M03062 U48881	PPP2R5E MTHFR SYN1 RAP1GA1 JAG1 LFG PSMA7 KIAA1719 ATP4A CHRNA4	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform 5,10-methylenetetrahydrofolate reductase (NADPH) synapsin I RAP1, GTPase activating protein 1 Jagged 1 (Alagille syndrome) lifeguard proteasome (prosome, macropain) subunit, alpha type, 7 KIAA1719 protein ATPase, H ⁺ /K ⁺ exchanging, alpha polypeptide cholinergic receptor, nicotinic, beta polypeptide 4	circulation, amino acid metabolism Signal transduction, small molecule transport, synaptic transmission, cholinergic G-protein linked receptor protein signalling pathway, respiration, muscle contraction
D38081	TBXA2R	thromboxane A2 receptor	
AC004755 AC004756 AL080150	LOC148220 ONECUT3 GEMIN4	similar to GILP1 one cut domain, family member 3 gem (nuclear organelle) associated protein 4	
M31525 X73073 AJ012500 AB028953	HLA-DQA PIGR H6PD KIAA1030	major histocompatibility complex, class II, DQ alpha polymeric immunoglobulin receptor hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) KIAA1030 protein	ribosome biogenesis, rRNA processing protein secretion

S80071	SLC6A7	solute carrier family 6 (neurotransmitter transporter, L-proline), member small	molecule transport, synaptic transmission, proline transport
D84307	PCYT2	phosphate cytidylyltransferase 2, ethanolamine	
D49738	CKAP1	cytoskeleton-associated protein 1	
U33840	PCSK7	proprotein convertase subtilisin/kexin type 7	
U47827	USP5	ubiquitin specific protease 5 (isopeptidase T)	deubiquitylation
X84746	ABO	ABO blood group (transferase A, alpha 1-3-N-acetyl/galactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)	
U30186	OPRL1	opiate receptor-like 1	sensory perception, G-protein signalling, adenylate cyclase inhibiting pathway
X82634	KRTHA3B	keratin, hair, acidic, 3B	cell shape and cell size control
U14187	EFNA3	ephrin-A3	
D38587	FCN3	ficolin (collagen/fibrinogen domain containing) 3 (Hakata antigen)	
Z37028	RNASEH2A	ribonuclease H2, large subunit	DNA replication, RNA catabolism
M01592	ZNF78	zinc finger protein 78 (expressed in testis)	transcription regulation from Pci II and Pci III promoter
X17004	PACE	paired basic amino acid cleaving enzyme (furin, membrane associated receptor protein)	proteolysis and peptidolysis, cell-cell signaling
AC004523	CYP4F12	cytochrome P450, subfamily IVF, polypeptide 12	
X01832	GIPR	gastric inhibitory polypeptide receptor	
U30894	SGSH	N-sulfoglucosamine sulfohydrolase (sulfamidase)	proteoglycan metabolism
Z14900	RING1	ring finger protein 1	
Y00870	ACR	acrosin	acrosome reaction
AJ003147	MEFV	Mediterranean fever	
AJ003147	OR1F2	olfactory receptor, family 1, subfamily F, member 2	
AJ003147	MMPL1	olfactory receptor, family 1, subfamily F, member 2	
AJ003147	ZNF200	zinc finger protein 200	
AJ003147	OR1F1	olfactory receptor, family 1, subfamily F, member 1	
AJ010901	MUC4	mucin 4, tracheobronchial	
U90841	SSX4	synovial sarcoma, X breakpoint 4	
AF035531	STX10	syntaxin 10	
J05509	SPTB	spectrin, beta, erythrocytic (includes spherocytosis, clinical type 1)	cell shape and cell size control
AB020649	KIAA0842	KIAA0842 protein	
AB009693	SLC22A6	solute carrier family 22 (organic anion transporter), member 6	organic anion transport, alpha-ketoglutarate transport
X67734	CNTN2	contactin 2 (axonal)	cell adhesion
U40391	AANAT	arylalkylamine N-acetyltransferase	
X74814	ODF1	outer dense fibre of sperm tails 1	
AL050220	KLK13	kallikrein 13	
U29949	ELAVL2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	transcription regulation
U35647	SOLH	small optic lobes homolog (Drosophila)	
AB014590	KIAA0690	KIAA0690 protein	
U78521	AIP	aryl hydrocarbon receptor interacting protein	
M83751	ARMET	arginine-rich, mutated in early stage tumors	oncogenesis
X14640	KRT13	keratin 13	epidermal differentiation
M83458	MVK	mevalonate kinase (mevalonate acyluria)	protein phosphorylation, isoprenoid biosynthesis
D14720	MPZ	myelin protein zero (Charcot-Marie-Tooth neuropathy 1B)	
AB018352	KIAA0609	KIAA0609 protein	
D87463	PHYHIP	phytanoyl-CoA hydroxylase interacting protein	

XB0364	ALAS2	aminolevulinic acid, delta-, synthase 2 (sideroblastic/hypochromic anemia) heme biosynthesis	
AB018258	ATP10B	ATPase, Class V, type 10B	
U15131	ST5	suppression of tumorigenicity 5	
X53742	FBLN1	fibrillin 1	
X55446	G6PD	glucose-6-phosphate dehydrogenase	glucose 6-phosphate utilization
X55448	FAM3A	family with sequence similarity 3, member A	
D34110	RBPMS	RNA-binding protein gene with multiple splicing	RNA processing
Z22565	DPT	dermatopontin	
AF059252	DOM3Z	dom-3 homolog Z (C. elegans)	
AF112210	ESD	esterase D (formylglutathione hydrolase)	
X71874	PSMB10	proteasome (prosome, macropain) subunit, beta type, 10	proteolysis and peptidolysis, humoral defense mechanism
AB021833	APBA3	amyloid beta (A β) precursor protein-binding, family A, member 3 (X11-like 2)	
M29273	MAG	myelin associated glycoprotein	
AD001530	DXS028E	DNA segment on chromosome X (unique) 9928 expressed sequence	
AF027204	TMHSF5	transmembrane 4 superfamily member 5	N-linked glycosylation
S75174	E2F4	E2F transcription factor 4, p107/p130-binding	cell cycle control
AJ000730	SLC7A4	solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	small molecule transport, amino acid metabolism
AB023205	TBCD	tubulin-specific chaperone d	protein folding, beta tubulin folding
AF050145	IDS	iduronate 2-sulfatase (Hunter syndrome)	
AF045800	CKTSF1B1	cysteine knot superfamily 1, B1P antagonist 1	developmental processes, neurogenesis
X57871	EPOR	erythropoietin receptor	
AF033105	ARR3	arrestin 3, retinal (X-arrestin)	Signal transduction, vision
X07695	KRT4	keratin 4	cell shape and cell size control, epidermal differentiation
AB014522	CLASP1	cytoplasmic linker associated protein 1	
AF071748	CTSF	cathepsin F	proteolysis and peptidolysis
X03560	ARHGDI3	Rho GDP dissociation inhibitor (GDI) alpha	cell adhesion inhibition, RHO protein signal transduction
AB006288	CPNE6	copine VI (neuronal)	lipid metabolism, synaptic transmission, neurogenesis, vesicle transport
AF091890	RE2	G-protein coupled receptor	
AF091890	RE2	G-protein coupled receptor	
U57352	ACCN1	amilofide-sensitive cation channel 1, neuronal (degenerin)	synaptic transmission, peripheral nervous system development, monovalent inorganic cation transport, central nervous system development,
AL096740	UBE3B	ubiquitin protein ligase	
U10368	ALDH3B1	aldehyde dehydrogenase 3 family, member B1	lipid metabolism, alcohol metabolism
L41498	EEF1A1L14	eukaryotic translation elongation factor 1 alpha 14-like 14	
AL050903	PRPF31	PRP31 pre-mRNA processing factor 31 homolog (yeast)	
AB023202	RPH3A	likely ortholog of mouse rabphilin 3A	
AF087134	MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	
AJ000342	DMBT1	deleted in malignant brain tumors 1	
AF062529	NUOT3	nucleoside diphosphate linked moiety X)-type motif 3	cell-cell signaling, diadenosine polyphosphate catabolism
AB018274	KIAA0731	KIAA0731 protein	

X65633	MC2R	melanocortin 2 receptor (adrenocorticotrophic hormone)	G-protein linked receptor protein signalling pathway, G-protein signalling, linked to cyclic nucleotide second messenger
U20391	FOLR1	folate receptor 1 (adult)	
J04948	ALPPL2	alkaline phosphatase, placental-like 2	
J03071	GH1	growth hormone 1	
J03071	GH2	growth hormone 2	
J03071	CSH1	chorionic somatomammotropin hormone 1 (placental lactogen)	
J03071	CSH2	chorionic somatomammotropin hormone 2	
J03071	CSHL1	chorionic somatomammotropin hormone-like 1	
M55405	MUC3A	mucin 3A, intestinal	
M55405	MUC3A	mucin 3A, intestinal	
M55405	MUC3A	mucin 3A, intestinal	
M37435	CSF1	colony stimulating factor 1 (macrophage)	developmental processes, positive control of cell proliferation, cell proliferation, antitumor humoral response
M62302	LASS1	LAG1 longevity assurance homolog 1 (S. cerevisiae)	
M62302	GDF1	growth differentiation factor 1	

491 metagenes constructed (as described) in analysis of Duke breast cancer data with respect to ER status.

Metagene 1

100137cds#1_6-234:in_reversesequence,_8-
 134:not_in_gb_record,_ghrf_gene (growth_hormone_releasing_fa
 m33478mrna_653-1049,33-kda_phototransducing_protein_mrna,_complete_cds_
 all_m34344_114-364:in_m34344cds_3032-
 3069,platelet_glycoprotein_iib_(gpiib)_gene
 m62810_1350-1818,mitochondrial_transcription_factormrna,_complete_cds_
 m73239mrna_2114-
 2638,(clone_sf1)_hepatocyte_growth_factor_(hgf)_mrna,_complete_cds_
 m81758_7258-7798,skeletal_muscle_voltage-
 dependent_sodium_channel_alpha_subunit_(skm1)_mrna,_complet
 all_u51561_10617-28244:in_u51561cds_50,cosmid_n79e2,_complete_sequence
 u75309_1813-2376,tdp-associated_factor_(htafii100)_mrna,_partial_cds_
 u95090mrna_2166-2418:in_fullsequence,_36716-
 36854,chromosomecosmid_f19541,_complete_sequence
 all_x13766_14-551,beta-casein_mrna_3'-terminal_fragment_

Metagene 2

d13633_2141-2597,mrna_for_kiaa0008_gene,_complete_cds
 l19783_895-1351,gpi-h_mrna,_complete_cds_
 l33262_1751-
 2273,dna_repair_and_recombination_homologue_(rad52)_gene,_complete_cds
 m29927exon_229-703,ornithine_aminotransferase_gene_
 u09087_2090-2543,thymopoietin_beta_mrna,_complete_cds
 u67611_788-
 1130:not_in_gb_record,_mouse_transaldolase_gene_mrna,_complete_cds/gb=u67611_/n
 type=rna_
 u72936_9836-
 10377,putative_dna_dependent_atpase_and_helicase_(atrx)_mrna,_alternatively_spl
 iced_prod
 all_x67491_839-1137,gene_for_glutamate_dehydrogenase_
 x99586cds_12-223:in_reversesequence,_329,mrna_for_smt3c_protein_
 z46629mrna_3352-3730,sox9_mrna

Metagene 3

j00117mrna_9-428,chorionic_gonadotropin_(hcg)_beta_subunit_mrna,_complete_cds
 m12759cds_65-335:in_reversesequence,_1020-1260,ig_j_chain_gene
 all_m85220_15-
 201,heavy_chain_disease_iga_chain_gene,_ch3_region_with_a_369_bp_deletion,_3'_e
 nd

s71043mrna_442-
 970, _ig_alpha_2=immunoglobulin_a_heavy_chain_allotype{constant_region, _germ_line}
 e}_[hu
 u24152_1879-2215, p21-activated_protein_kinase_(pak1)_gene, _complete_cds
 all_x60992_2450-3021, cd6_mrna_for_t_cell_glycoprotein_cd6

Metagene 4

ac002477cds_444-988, pac_clone_dj327a19_from_xq25-
 q26, _complete_sequence/gb=ac002477/_ntype=dna/_anno
 hg4243-ht4513_at_hg4243-ht4513_zinc_finger_protein_znf155
 j00129mrna#1_1282-1552: not_in_gb_record, fibrinogen_beta-
 chain_mrna, _partial_cds_
 all_m58026_831-1240, nb-1_mrna, _complete_cds
 u30255_977-1493, phosphogluconate_dehydrogenase_(hpgdh)_gene, _complete_cds
 u37022mrna_860-1322, cyclin-dependent_kinase_(cdk4)_gene, _complete_cds_
 u67191_3391-3967, multiple_exostosis-like_protein_(extl)_mrna, _complete_cds_
 u67369_2300-2720, growth_factor_independence-1_(gfi-1)_mrna, _complete_cds_
 u85245_3310-3718, phosphatidylinositol-4-phosphate_5-
 kinase_type_ii_beta_mrna, _complete_cds.
 u97018_3439-3853, echinoderm_microtubule-
 associated_protein_homolog_huemap_mrna, _complete_cds
 x13461cds_88-422: in_reversesequence, _1502-1737, intronless_calmodulin-
 like_gene_(clp_gene)_for_calmod
 all_x72632_1746-2326, mrna_encoding_rev-erbaalpha_(internal_fragment).
 z48314cds_2683-3086: in_reversesequence, _3110-3249, mrna_for_apomucin

Metagene 5

m20030_68-612, small_proline_rich_protein_(sprii)_mrna, _clone_930_

Metagene 6

hg1139-ht4910_at_hg1139-ht4910_fk506-binding_protein, _altsplice_2
 m14123cds#4_3521-3935, _pol_fromendogenous_retrovirus_herv-
 k10/gb=m14123/_ntype=dna/_annot=cds, _pol_f
 m27396mrna_1389-1842, asparagine_synthetase_mrna, _complete_cds
 m89470_2855-3271, paired-box_protein_(pax2)_mrna, _complete_cds
 s73885_1537-2082, _ap-4=basic_helix-loop-helix_dna-
 binding_protein_[human, _cervical_carcinoma, _hela_c
 u35005_764-1278, jnk1_beta2_protein_kinase_(jnk1b2)_mrna, _complete_cds
 u51333_2437-3005, hexokinase_iii_(hk3)_mrna, _complete_cds_
 u73738_74-107, calcium/calmodulin-
 dependent_protein_kinase_ii_delta_e_mrna, _partial_cds/gb=u73738/_nt

Metagene 7

j00207mrna#2_661-1075, _ifna_gene_(interferon_alpha-
 a)_extracted_fromleukocyte_interferon_(leif)_alph

j05016mrna_2252-
 2824,(clone_pa3)_protein_disulfide_isomerase_related_protein_(erp72)_mrna,_complete
 141268_f_at_141268_141268,_4040_in_141268mrna_1043-1571,natural_killer-
 associated_transcript(nkat2)_
 m31776cds_35-365,brain_natriuretic_protein_(bnp)_gene,_complete_cds
 u82311_39-112,unknown_protein_mrna,_partial_cds/gb=u82311_/ntype=rna_
 all_x06661_1817-2340,mrna_for_27-kda_calbindin_
 x13100cds_3130-3466:in_reversesequence,_3496-
 3592,mrna_fragment_for_myosin_heavy_chain
 x64994cds_642-912:in_reversesequence,_1279-
 1471,hgmp07i_gene_for_olfactory_receptor_

Metagene 8

all_d00003_1681-1721,liver_cytochrome_p-
 450_mrna,_complete_cds,liver_cytochrome_p-450_mrna,_complete
 d17408_906-1481,mrna_for_calponin,_complete_cds
 d49490_1092-1644,mrna_for_protein_disulfide_isomerase-
 related_protein_(pdir),_complete_cds_
 d64053_3337-3467,mrna_for_protein-tyrosine_phosphatase_
 d70830_1610-2018,mrna_for_doc2_beta,_complete_cds
 hg174-ht174_at_hg174-ht174_desmoplakin_i_
 hg2147-ht2217_at_hg2147-ht2217_mucin_3,_intestinal_
 hg3502-ht3696_at_hg3502-ht3696_homeotic_protein_hox5.4_
 hg363-ht363_at_hg363-ht363_epidermal_growth_factor_receptor-related_protein
 hg37-ht37_at_hg37-ht37_iron-responsive_element-binding_protein_
 j05158mrna_2315-2825,carboxypeptidase_n_mrna,_3'_end_
 all_j05412_3866-4062:in_j05412cds_411-
 439,regenerating_protein_(reg)_gene,_complete_cds_
 k03207mrna_286-748:in_reversesequence,_772-848,prb4_locus_salivary_proline-
 rich_protein_mrna,_comple
 l02648_1312-1852,(clone_v6)_transcobalamin_ii_(tcn2)_mrna,_complete_cds_
 l10377_879-1441,(clone_ctg-b37)_mrna_sequence
 l13266_4056-4630,n-methyl-d-aspartate_receptor_(nr1-1)_mrna,_complete_cds_
 l16464_440-752,ets_oncogene_(pep1)_mrna,_complete_cds
 l28175_1375-1933,prostaglandin_e2_receptor_ep2_subtype_mrna,_complete_cds_
 l31584exon_1488-1986,g_protein-coupled_receptor_(ebi_1)_gene_
 m19878cds_3-
 125:in_reversesequence,_1964,calbindin_27_gene,_exonsand_2,_and_alu_repeat/gb=m
 19878_/nt
 m23197_848-1388,differentiation_antigen_(cd33)_mrna,_complete_cds
 m26657_1861-2430,testicular_angiotensin_converting_enzyme_mrna,_complete_cds_
 m27318_365-878,interferon_(ifn-alpha-m1)_mrna,_complete_cds
 all_m28439_261-360,keratin_typegene
 m30625_1154-1554,dopamine_d2_receptor,_mrna,_complete_cds
 m35531_2832-3318,gdp-1-fucose:beta-d-galactoside_2-alpha-1-
 fucosyltransferase_mrna,_complete_cds_
 m55621_2074-2452,n-acetylglucosaminyltransferase_i_(glcnac-
 ti)_mrna,_complete_cds
 m58600mrna_1634-2168,heparin_cofactor_ii_(hcf2)_gene,_exonsthrough_5_
 all_m60331_669-1094:in_m60331cds_116,protaminegene,_complete_cds_
 m62783_3069-3453,alpha-n-acetylgalactosaminidase_mrna,_complete_cds
 m64930_2982-3366,protein_phosphatase_2a_beta_subunit_mrna,_complete_cds
 m68907_2-187,tachykinin-a_(gamma-ppt-a)_gene,_partial_cds/gb=m68907_/ntype=rna_

m83181cds_918-1206:in_reversesequence,_1639-
 1867,serotonin_receptor_gene,_complete_cds_
 s78723mrna#1_565-991,_5-ht2ar=serotonin_5-
 ht2a_receptor_{promoter}_[human,_genomic,_1678_nt]_
 s80905_f_at_s80905_s80905,_4040_in_s80905cds_17-
 1067,_prb2_(prb2l_con1+)=con1_{exon_3}_[human,_perip
 s82075_115-283,_pa4=candidate_oncogene_{3'_region}_[human,_hen-16,_hen-
 16t_transformed_endocervical_
 s83308_920-1400,_sox5=sry-
 related_hmg_box_gene_{alternatively_spliced}_[human,_testis,_mrna,_1473_nt
 u02566_2456-2990,receptor_tyrosine_kinase_tif_mrna,_partial_cds
 u09117_2164-2536,phospholipase_c_deltamrna,_complete_cds
 u10099_938-1435,pom-zp3_mrna,_complete_cds_
 u11791_662-1160,cyclin_h_mrna,_complete_cds
 u25041_at_u25041_u25041,not_in_gb_record,5c5_mrna,_putative_complete_cds
 u27699_2929-3349,pephbgt-1_betaine-gaba_transporter_mrna,_complete_cds_
 u31216_3168-
 3641,metabotropic_glutamate_receptorbeta_(mglur1beta)_mrna,_complete_cds
 all_u33447_1311-1888,putative_g-protein-
 coupled_receptor_(gpr17)_gene,_complete_cds
 u40279cds_70-574,beta-2_integrin_alphad_subunit_(itgad)_gene,_exons_25-
 30,_and_partial_cds/gb=u40279
 u46752_1476-1872,phosphotyrosine_independent_ligand_p62b_b-
 cell_isoform_for_the_lck_sh2_domain_mrna,
 u47334_7-307,gamma_aminobutyric_acid_receptor_beta4_subunit-
 like_mrna,_partial_cds/gb=u47334_/ntype=
 u57650_4714-5224,sh2-containing_inositol_5-
 phosphatase_(hship)_mrna,_complete_cds
 u77975_1042-1420,hepatocyte_nuclear_factor(hnf-6)_mrna,_partial_cds_
 u79725_2240-2744,a33_antigen_precursor_mrna,_complete_cds
 all_x02958_1064-1245,interferon_alpha_gene_ifn-alpha_6_
 all_x13444_852-1357,mrna_for_cd8_beta-chain_glycoprotein_(cd8_beta.1)
 x56687cds_1698-2154:in_reversesequence,_2348,mrna_for_autoantigen_nor-90
 x57110mrna_2510-2998,mrna_for_c-cbl_proto-oncogene.
 all_x60299_3486-4065,kalig-1_mrna_for_neural_cell_adhesion_and_axonal_path-
 finding_molecule_homologu
 x70083mrna_166-460,abp-280-like_mrna_for_filamin_(695_bps)/gb=x70083_/ntype=rna
 x76132mrna_4097-4583,dcc_mrna
 x79510cds_3165-3459:in_reversesequence,_3839-3971,mrna_for_protein-tyrosine-
 phosphatase_d1
 all_x80026_1785-2363,b-cam_mrna
 all_x81882_2153-
 2682,mrna_for_for_vasopressin_activated_calcium_mobilizing_receptor-
 like_protein_
 x82324cds_866-1055:in_reversesequence,_1096-1450,brainmrna_
 x82877cds_1533-1809:in_reversesequence,_3974-4118,na+-d-
 glucose_cotransport_regulator_gene
 x86371cds_2629-3129,mrna_for_tumour_suppressor_protein,_hugl_
 x91348mrna_893-1211,predicted_non_coding_cdna_(dgcr5)
 y10936_637-1027,mrna_for_hypothetical_protein_downstream_of_dmpk_and_dmahp_
 y13153_1404-1950,mrna_for_kynurenine_3-monooxygenase/gb=y13153_/ntype=rna_
 all_z80787_563-700,h4/j_gene.

Metagene 9

hg371-ht26388_at_hg371-ht26388_mucin_1,_epithelial,_altsplice_9
 j05582mrna_3910-4100,pancreatic_mucin_mrna,_complete_cds_
 l24893cds_218-679,myelin_protein_zero_(po)_gene
 all_m30838_4028-4631,pulmonary_surfactant_apoprotein_(psap)_gene,_complete_cds_
 z48633mrna_1624-2020,mrna_for_retrotransposon

Metagene 10

d78333_1188-1734,mrna_for_testis-specific_tcp20,_complete_cds
 m86707_1190-1580,myristoyl_coa:protein_n-myristoyltransferase_mrna
 s77410_1805-2225,_typeangiotensin_ii_receptor_[human,_liver,_mrna,_2268_nt]
 u25997_3311-3824,stanniocalcin_precursor_(stc)_mrna,_complete_cds
 u40490_3673-
 4177,nicotinamide_nucleotide_transhydrogenase_mrna,_nuclear_gene_encoding_mitoc
 hondrial_
 u50078_14603-15101,guanine_nucleotide_exchange_factor_p532_mrna,_complete_cds
 u65932_1244-1634,extracellular_matrix_protein(ecm1)_mrna,_complete_cds
 all_x84373_6655-7208,mrna_for_nuclear_factor_rip140

Metagene 11

hg2662-ht2758_at_hg2662-ht2758_homeotic_protein_emx1_
 l09753_1377-1827,cd30_ligand_mrna,_complete_cds_
 s71018_282-798,cyclophilin_c_[human,_kidney,_mrna,_883_nt]_
 s76473_2563-3079,_trkb_[human,_brain,_mrna,_3194_nt]

Metagene 12

d14823_851-
 1343,chimeric_mrna_derived_from_aml1_gene_and_mtg8(eto)_gene,_partial_sequence
 d38076_322-700,mrna_for_ranbp1_(ran-binding_protein_1),_complete_cds_
 d80004_6550-6898,mrna_for_kiaa0182_gene,_partial_cds_
 d87075_5013-5469,mrna_for_kiaa0238_gene,_partial_cds_
 d87673_960-1434,mrna_for_heat_shock_transcription_factor_4,_complete_cds_
 d87716_2447-2942,mrna_for_kiaa0007_gene,_partial_cds_
 hg2271-ht2367_at_hg2271-ht2367_profilaggrin
 hg3039-ht3200_at_hg3039-ht3200_adp-ribosylation-like_factor
 hg3636-ht3846_at_hg3636-ht3846_myosin,_heavy_polypeptide_9,_non-muscle_
 hg3884-ht4154_at_hg3884-ht4154_homeotic_protein_hpx-42_
 j02783mrna_2075-2465,thyroid_hormone_binding_protein_(p55)_mrna,_complete_cds
 j03824_756-1230,uroporphyrinogen_iii_synthase_mrna,_complete_cds_
 l16782_1994-2522,putative_m_phase_phosphoprotein(mpp1)_mrna,_partial_cds
 l18972cds_1821-2019:in_reversesequence,_2065-2305,anonymous_gene,_complete_cds
 l19711_4952-5414,dystroglycan_(dag1)_mrna,_complete_cds
 l34587_109-
 403,rna_polymerase_ii_elongation_factor_siii,_p15_subunit_mrna,_complete_cds_
 l37936_439-961,nuclear-encoded_mitochondrial_elongation_factor_ts_(ef-
 ts)_mrna,_3'_end_of_cds
 l40407cds_696-882:in_reversesequence,_1060-
 1264,thyroid_receptor_interactor_(trip9)_gene,_complete_c
 l41067_3380-3884,nf-at4c_mrna,_complete_cds_

176191mrna_3005-3521,interleukin-1_receptor-associated_kinase_(irak)_mrna,_complete_cds_
 177730exon_529-1009,a3_adenosine_receptor_(adora3)_gene_
 all_m14158_1529-1794,_t-cell_receptor_beta-chain_j1.3_gene_extracted_fromt-cell_receptor_germline_be
 m19961_55-469,cytochrome_c_oxidase_subunit_vb_(coxvb)_mrna,_complete_cds_
 m34338_626-1197,spermidine_synthase_mrna,_complete_cds_
 m60047_641-1097,heparin_binding_protein_(hbp17)_mrna,_complete_cds_
 m65199_735-1101,endothelin(et2)_mrna,_complete_cds_
 m86752_1512-2046,transformation-sensitive_protein_(ief_ssp_3521)_mrna,_complete_cds_
 s40719_2440-2964,_glial_fibrillary_acidic_protein_[human,_glioma_cell_line_u-251_mg,_mrna,_3033_nt]
 s66793_697-1219,_x-arrestin=s-antigen_homolog_[human,_retina,_mrna,_1314_nt]
 u05340_1103-1571,p55cdc_mrna,_complete_cds_
 u07424_1266-1764,putative_trna_synthetase-like_protein_mrna,_complete_cds_
 u47621_1758-2286,nucleolar_autoantigen_no55_mrna,_complete_cds_
 u55206_790-1222:not_in_gb_record,gamma-glutamyl_hydrolase_(hgh)_mrna,_complete_cds_
 u61263_1603-2077,acetolactate_synthase_homolog_mrna,_complete_cds_
 u62962_927-1347,int-6_mrna,_complete_cds_
 u68566_638-1124,hs1_binding_protein_hax-1_mrna,_nuclear_gene_encoding_mitochondrial_protein,_complet
 u70735_507-1005,34_kda_mov34_isologue_mrna,_complete_cds/gb=u70735_/ntype=rna
 u79270_774-1176,clone_23707_mrna,_partial_cds
 u85943_1527-1680,mrna-associated_protein_mrnnp41_mrna,_complete_cds/gb=u85943_/ntype=rna
 x00368mrna_7-52,_exonfromprolactin_gene_5'_region/gb=x00368_/ntype=dna_/annot=mrna_
 x12794cds_864-1176:in_reversesequence,_1905-2139,v-erba_related_ear-2_gene_
 x13482cds_490-712:in_reversesequence,_870-942,mrna_for_u2_snrnp-specific_a'_protein_
 x79781cds_276-546:in_reversesequence,_675-681,ray_mrna
 x92744cds_6-174:in_reversesequence,_61-271,mrna_for_hbd-1_protein_
 all_y00285_8502-8980,mrna_for_insuline-like_growth_factor_ii_receptor

Metagene 13

all_d32001_61-294,husaalg_gene_for_serum_amyloid_a1_gamma,_exonand_intron_3_
 hg2059-ht2114_at_hg2059-ht2114_arrestin,_beta_2
 hg2480-ht2576_at_hg2480-ht2576_fm1p-related_receptor_i_
 hg2809-ht2920_s_at_hg2809-ht2920_lung_surfactant_protein_d_
 hg3107-ht3283_s_at_hg3107-ht3283_plasma_membrane_calcium_pump_hpmca2a
 hg759-ht759_s_at_hg759-ht759_adrenergic_receptor,_beta_1_
 j05036mrna_1546-2119,cathepsin_e_mrna,_complete_cds_
 j05073cds_239-641,phosphoglycerate_mutase_(pgam-m)_gene,_complete_cds_
 k02766_2028-2436,complement_component_c9_mrna,_complete_cds_
 l29008_2014-2464,l-iditol-2_dehydrogenase_mrna,_complete_cds_
 l33477_3692-4142,(clone_8b1)_br-cadherin_mrna,_complete_cds_
 l35592mrna#1_1633-2107,germline_mrna_sequence_
 l37112mrna_1710-1816,vasopressin_v3_receptor_mrna,_complete_cds_
 l40933cds_1218-1470:in_reversesequence,_1639-1819,phosphoglucomutase-related_protein_(pgmrp)_gene,_c
 all_m80333_1628-2079,m5_muscarinic_acetylcholine_receptor_gene,_complete_cds_
 m85217_2529-2955,k+_channel_protein_(h1k3)_mrna,_complete_cds

m89473_1394-1706,neurokininreceptor_(nk3r)_mrna,_complete_cds_
 m96859_3150-3630,dipeptidyl_aminopeptidase_like_protein_mrna,_complete_cds_
 u09609_2198-2708,p80ht_(p80ht/nkfb-2)_mrna,_complete_cds_
 u13737_2046-2556,cysteine_protease_cpp32_isoform_alpha_mrna,_complete_cds_
 u14910_910-1360,rpe-retinal_g_protein-coupled_receptor_(rgr)_mrna,_complete_cds_
 u18671mrna_2702-3266,stat2_gene,_complete_cds_
 u29615_1098-1530,chitotriosidase_precursor_mrna,_complete_cds_
 u31929cds_1063-1361:in_reversesequence,_6372-
 6576,orphan_nuclear_receptor_(dax1)_gene,_complete_cds_
 u63336_1666-2062,mhc_i_region_proline_rich_protein_mrna,_complete_cds_
 u65404_1140-1530,erythroid-
 specific_transcription_factor_eklf_mrna,_complete_cds.
 u78180_3340-
 3880,sodium_channel(hbnac2)_mrna,_alternatively_spliced,_complete_cds_
 u85992_1236-1596,clone_image:35527_unknown_protein_mrna,_partial_cds_
 all_u87408_1441-1952,clone_image:74593_unknown_protein_mrna,_partial_cds_
 v00535mrna#1_253-
 692,_interferon_betagene_extracted_from_gene_forfibroblast_interferon_beta_1
 all_x04729_2-263,mrna_for_plasminogen_activator_inhibitor_typen-
 terminus/gb=x04729_/ntype=rna_
 x54816_at_x54816_x54816,not_in_gb_record,gene_for_alpha-1-microglobulin-
 bikunin,_exons_5-jan_(encodi
 all_x54938_1175-1752,mrna_for_inositol_1,4,5-triphosphate_3-kinase_
 x55889cds_264-
 546:not_in_gb_record,gene_for_ciliary_neurotrophic_factor,_exon_1_
 x55990mrna_163-489,ecp_gene_for_eosinophil_cationic_protein_
 all_x66141_261-784,mrna_for_cardiac_ventricular_myosin_light_chain-2_
 x97748mrna_59-189,ptx3_gene_promotor_region/gb=x97748_/ntype=dna_/annot=mrna_
 all_x99140_1407-1822,mrna_for_hair_keratin,_hnb5_
 y10376cds_888-1158:in_reversesequence,_1222-1408,mrna_for_sirp-beta1_
 y13115cds_2477-
 2879:in_reversesequence,_3061,mrna_for_serine/threonine_protein_kinase_sak
 z24680mrna_3558-4044,garp_gene_mrna,_complete_cds
 all_z31357_967-1502,mrna_for_cysteine_dioxygenase_type_1_

Metagene 14

d16532exon_123-
 561,gene_for_very_low_density_lipoprotein_receptor,_5'_flanking_and_
 d49354_769-1293,mrna_for_enhancer_protein_in_hsp70_gene,_partial_cds_
 d79984_5275-5836,mrna_for_kiaa0162_gene,_complete_cds_
 d79999_4526-4922,mrna_for_kiaa0177_gene,_partial_cds_
 d82346_944-1316,mrna_for_hnspc,_complete_cds_
 d83597_2108-2612,mrna_for_rp105,_complete_cds_
 d84361_1601-2135,mrna_for_p52_and_p64_isoforms_of_n-shc,_complete_cds_
 d87435_5153-5591,mrna_for_kiaa0248_gene,_partial_cds_
 d87454_4950-5490,mrna_for_kiaa0265_gene,_partial_cds_
 d87455_4996-5542,mrna_for_kiaa0266_gene,_complete_cds_
 d87957cds_549-825:in_reversesequence,_1148-
 1256,male_foreskin_fibroblast_dna_for_protein_involved_in
 hg1699-ht1704_s_at_hg1699-ht1704_epimorphin
 hg1751-ht1768_at_hg1751-ht1768_chorionic_somatotropin_hormone_cs-5
 hg2228-ht2305_at_hg2228-ht2305_crystallin,_beta_b
 hg2936-ht3080_at_hg2936-ht3080_immunoglobulin_heavy_chain,_enhancer_element
 hg3132-ht3308_at_hg3132-ht3308_cea_family,_bi-like_domain

hg3227-ht3404_at_hg3227-ht3404_guanine_nucleotide-binding_protein_hsr1_
 hg3286-ht3463_at_hg3286-ht3463_crystallin_alpha_a_
 hg721-ht4828_s_at_hg721-
 ht4828_placental_protein_14_endometrial_alphaglobulin_altsplice_3_
 hg907-ht907_at_hg907-ht907_mg44
 hg921-ht3995_at_hg921-ht3995_serine/threonine_kinase_receptor_2-2_altsplice_3_
 all_j00301_342-715_parathyroid_pth_gene_3'_end
 j03910mrna_31-319_clone_14vs_metallothionein-ig_mt1g_gene_complete_cds_
 j04809mrna_1742-2216_cytosolic_adenylate_kinase_ak1_gene_complete_cds_
 l05624_910-1418_map_kinase_kinase_mrna_complete_cds_
 l10386_2036-2498_transglutaminase_e3_tgase3_mrna_complete_cds_
 l11238_2922-3445_platelet_membrane_glycoprotein_v_mrna_complete_cds_
 l18920exon#4_970-1461_mage-2_gene_exons_1-4_complete_cds_
 l19267_2335-2755_59_protein_mrna_3'_end
 l22005_797-1349_ubiquitin_conjugating_enzyme_mrna_partial_cds_
 l39874exon#5_778-1198_deoxycytidylate_deaminase_gene_complete_cds_
 m17754_1298-1838_bn51_mrna_complete_cds_
 m19684cds_912-1212:in_reversesequence_3443-3539_alpha-1-antitrypsin-related_protein_gene_
 m19720mrna#2_2659-3217_l-myc_gene_l-myc_protein_extracted_froml-myc_protein_gene_complete_cds_l
 m19722_1843-2245_fgr_proto-oncogene_encoded_p55-c-fgr_protein_complete_cds_
 m21142cds#1_889-1109:in_reversesequence_1884-2122_guanine_nucleotide-binding_protein_g-s-alpha-3_g
 m24594mrna_1077-1593_interferon-inducible_56_kd_protein_mrna_complete_cds_
 m25393_1686-2253_protein_tyrosine_phosphatase_ptpase_mrna_complete_cds_
 m30607mrna_2131-2301:in_reversesequence_2607_zinc_finger_protein_y-linked_zfy_mrna_complete_cds_
 m36542mrna_1437-1832_lymphoid-specific_transcription_factor_mrna_complete_cds_
 m37457cds_2823-2990_na+k+_#name?_catalytic_subunit_alpha-iii_isoform_gene_na+k+_#name?_catalytic_s
 m58597_2260-2806_elam-1_ligand_fucosyltransferase_elft_mrna_complete_cds_
 m63391mrna_1637-2189_desmin_gene_complete_cds_
 m64752_2904-3150_glutamate_receptor_subunit_gluh1_mrna_complete_cds_
 m67439cds_941-1355_d5_dopamine_receptor_drd5_gene_complete_cds_
 m76665mrna_792-1332_11-beta-hydroxysteroid_dehydrogenase_hsd11_gene
 m77836_1239-1749_pyrroline_5-carboxylate_reductase_mrna_complete_cds_
 m81780cds#4_49-265:in_fullsequence_3676-3940_smpd1_gene_acid_sphingomyelinase_extracted_fromacid
 m83667mrna_713-1143_nf-il6-beta_protein_mrna_complete_cds_
 m88579_1225-1615_zinc_finger_protein_sre-zbp_mrna_3'_end
 m89796mrna_3128-3671_high_affinity_ige_receptor_beta_chain_gene_complete_cds_
 m94065_1051-1417_dihydroorotate_dehydrogenase_mrna_3'_end_
 m94856_163-619_fatty_acid_binding_protein_homologue_pa-fabp_mrna_complete_cds_
 m97796_88-595_helix-loop-helix_protein_id-2_mrna_complete_cds_
 m97936_2354-2564_transcription_factor_isgf-3_mrna_sequence_
 s45630_108-612_alpha_b-crystallin=rosenthal_fiber_component_human_glioma_cell_line_mrna_691_nt]
 s62696_39-119_ebv/c3d_receptor_alternatively_spliced_exons_8a,9,10_human_jurkat_t_cells_mrna_
 s79639_2588-3068_ext1=putative_tumour_suppressor/hereditary_multiple_exostoses_candidate_gene_huma
 s82597mrna_9-507_description:udp-galnac:polypeptide_n-acetylgalactosaminyltransferase_gene_extract

u00946_1382-1916,clone_a9a2brb5_(cac)n/(gtg)n_repeat-containing_mrna_
 all_u01317_19502-63478:in_u01317cds#1_82-113,_epsilon-
 globin_gene_extracted_frombeta_globin_region_o
 u05572_2563-3028,lysosomal_alpha-mannosidase_(manb)_mrna,_complete_cds_
 u09366_2042-2540,zinc_finger_protein_znf133
 u10689exon#3_939-1505,mage-5a_antigen_(mage5a)_gene,_complete_cds
 u16126_2216-2684,glutamate/kainate_receptor_subunit_(eaa4)_mrna,_complete_cds
 u23435_832-1319,abl_interactor(abi-2)_mrna,_complete_cds
 u28811_3404-3866,cysteine-rich_fibroblast_growth_factor_receptor_(cfr-
 1)_mrna,_complete_cds
 u36922_19-136:in_reversesequence,_205-
 220,fork_head_domain_protein_(fkhr)_mrna,_3'_end/gb=u36922_/nt
 u37055mrna_1680-2195,hepatocyte_growth_factor-like_protein_gene,_complete_cds_
 u37139mrna#1_596-998,beta_3-
 endonexin_mrna,_long_form_and_short_form,_complete_cds_
 u38175_719-1205,hur_rna_binding_protein_(hur)_mrna,_complete_cds_
 u42408_1997-2393,ladinin_(lad)_mrna,_complete_cds
 u43030_1121-1484,cardiotrophin-1_(ctf1)_mrna,_complete_cds_
 all_u44429_1151-1626,d53_(hd53)_mrna,_partial_cds
 u49082_1830-2370,transporter_protein_(g17)_mrna,_complete_cds
 u49188_1187-1685,placenta_(diff33)_mrna,_complete_cds
 u53442_1615-2131,p38beta_map_kinase_mrna,_complete_cds_
 u59111_892-1444,dermatan_sulfate_proteoglycan(dspg3)_mrna,_complete_cds_
 all_u63842_423-1018,neurogenic_basic-helix-loop-
 helix_protein_(neurod3)_gene,_complete_cds_
 u70732mrna_1335-1899,glutamate_pyruvate_transaminase_(gpt)_gene,_complete_cds_
 u72512_4-196,b-
 cell_receptor_associated_protein_(hbap)_alternatively_spliced_mrna,_partial_3'_
 utr/gb
 u79259_1214-1610,clone_23945_mrna,_complete_cds
 u82169_1613-2135,frizzled_homolog_(fzd3)_mrna,_complete_cds
 u83601mrna_58-
 136,calpastatin_gene,_exonsand_15,_partial_cds/gb=u83601_/ntype=dna_/annot=mrna
 v01514mrna_1440-1986,mrna_encoding_alpha-
 fetoprotein_(afp)afp_is_a_major_serum_protein_(mg:_70000)_s
 x12517cds_261-441:in_reversesequence,_480-660,mrna_for_u1_small_nuclear_rnp-
 specific_c_protein
 x15875cds_1176-1476:in_reversesequence,_1604-
 1622,mrna_for_camp_response_element_(cre-bp1)_binding_p
 all_x52889_24339-24440,gene_for_cardiac_beta_myosin_heavy_chain
 all_x53390_2839-3093,mrna_for_upstream_binding_factor_(hubf)_
 x53795mrna_1868-2003,r2_mrna_for_an_inducible_membrane_protein_
 all_x60487_686-948,h4/h_gene_for_h4_histone
 all_x63131_1996-2179,myl_(pml)_mrna
 all_x64037_1887-2200,mrna_for_rna_polymerase_ii_associated_protein_rap74_
 x72879cds_3-52:in_reversesequence,_76-208,14a2ak_dna_sequence_
 all_x73874_3675-4156,phkamrna_
 x79067utr#1_1631-2165,erf-1_mrna_3'_end
 all_x82434_589-1112,mrna_for_emerin
 all_x86401_1686-2217,mrna_for_l-arginine:glycine_amidinotransferase
 x90976_26-185,mrna_for_an_acute_myeloid_leukaemia_protein_(3917bp)_
 x92098cds_368-560:in_reversesequence,_635-
 737,mrna_for_transmembrane_protein_rnp24
 x92972cds_585-885:in_reversesequence,_968-1148,mrna_for_protein_phosphatase_6_
 x93499cds_285-591:in_reversesequence,_1241-1451,mrna_for_rab7_protein_
 all_x93920_1520-2031,mrna_for_protein-tyrosine-
 phosphatase_(tissue_type:_foreskin)_

all_x95876_1330-1415,mrna_for_g-protein_coupled_receptor_
x99699cds_603-855:in_reversesequence,_939-1131,mrna_for_xiap_associated_factor-
1
y08837_275-473:not_in_gb_record,mrna_for_rad51-
like_protein/gb=y08837_/ntype=rna
y10210mrna_55-433,mrna_for_cd22_protein/gb=y10210_/ntype=rna_
z23090cds_277-589:in_reversesequence,_1086-
1098,mrna_for_28_kda_heat_shock_protein
all_z35307_2215-2636,mrna_for_endothelin-converting-enzyme_1_
z83806_25-283,mrna_for_axonemal_dynein_heavy_chain_(partial,_id_hdhc9) .

Metagene 15

l29306_723-
1116,tryptophan_hydroxylase_(tph)_mrna,_complete_cds/gb=l29306_/ntype=rna
all_m14159_1264-1482,_t-cell_receptor_beta-chain_j2.1_gene_extracted_fromt-
cell_receptor_germline_be
m20566mrna_2745-3180,interleukinreceptor_mrna,_complete_cds_
s69232_1584-1992,_electron_transfer_flavoprotein-
ubiquinone_oxidoreductase_[human,_fetal_liver,_mrna
u09851_44-254,zinc_finger_protein_(znf148)_mrna,_partial_cds_
y07512_3211-3715,mrna_for_type_i_beta_cgmp-
dependent_protein_kinase_(ec_2.7.1.37)
all_z80779_563-822,h2b/g_gene

Metagene 16

k01396mrna_769-1201,alpha-1-antitrypsin_mrna,_complete_cds_
m80482_3922-4324,subtilisin-like_protein_(pace4)_mrna,_complete_cds
all_x15422_3003-3550,mrna_for_mannose-binding_protein_c
all_x64810_4454-5019,encoding_pc1/pc3
all_x81438_2665-3206,mrna_for_amphiphysin
z12830cds_344-764:in_reversesequence,_943,mrna_for_ssr_alpha_subunit
all_z22534_2132-2637,alk-2_mrna

Metagene 17

d50931_2527-2971,mrna_for_kiaa0141_gene,_complete_cds
m97016_1231-1803,osteogenic_protein-2_(op-2)_mrna,_complete_cds.
s58544_1884-2382,_75_kda_infertility-
related_sperm_protein_[human,_testis,_mrna_partial,_2427_nt]_
s81737_1159-1681,_alphasyntrophin_[human,_mrna_partial,_1771_nt]_
u06233_2545-3055,pou_domain_protein_(brn-3b)_mrna,_complete_cds
u07681_2075-2585,nad(h) -
specific_isocitrate_dehydrogenase_alpha_subunit_precursor_mrna,_complete_cds
u68385_1259-1643,meis1-related_protein(mrg2),_mrna,_partial_cds.
u69108_2155-2632,tnf_receptor_associated_factor_mrna,_partial_cds_
all_x79066_390-973,_hsapiens_erf-1_mrna_5'_end
x91653exon_5-125,dna_for_exon_encoding_for_n-
acetylglucosaminyltransferase_v_(340_bp)/gb=x91653_/nty

y00083cds_902-1201:in_reversesequence,_1416-1641,mrna_for_glioblastoma-derived_t-cell_suppressor_fac

Metagene 18

u39231_1739-1979,gip_receptor_(gipr)_mrna,_complete_cds
all_v00503_2330-2452,mrna_encoding_pro-alpha-
2_chain_of_type_i_procollagen(major_part)_
all_x79200_380-600,mrna_for_syt-
ssx,_synovial_sarcoma_translocation_junction/gb=x79200_/ntype=rna,mr

Metagene 19

hg721-ht4827_s_at_hg721-
ht4827_placental_protein_14,_endometrial_alphaglobulin,_altssplice_2_
l19593mrna_2261-2747:in_reversesequence,_2765-
2771,interleukinreceptor_beta_(il8rb)_mrna,_complete_c
s34389_1166-1586,_heme_oxygenase-2_[human,_kidney,_mrna,_1627_nt]_
u19523_2299-2851,gtp_cyclohydrolase_i_mrna,_complete_cds_
all_x05232_1530-1771,mrna_for_stromelysin
x12662mrna_936-
1398,arginase_gene_exonand_flanking_regions_(ec_3.5.3.1)_(and_joined_cds)_
all_x57809_309-
474,rearranged_immunoglobulin_lambda_light_chain_mrna,rearranged_immunoglobulin
_lambd
x72308_419-842,mcp-3_mrna_for_monocyte_chemotactic_protein-3_
y00081cds_293-588:in_reversesequence,_5486-5706,(bsf-
2/il6)_gene_for_b_cell_stimulatory_factor-2
y11306mrna_1993-2395,_htcf-4_gene_extracted_frommrna_for_beta_catenin/tcf-4_

Metagene 20

af008937_508-916,syntaxin-16c_mrna,_complete_cds/gb=af008937_/ntype=rna_
d90282_4830-5136,carbaryl_phosphate_synthetase_i_(ec_6.3.4.16)_mrna
hg2846-ht2983_at_hg2846-ht2983_dihydrofolate_reductase,_altssplice_6
l19161_1001-1385,translation_initiation_factor_eif-
2_gamma_subunit_mrna,_complete_cds
l24804_223-721,(p23)_mrna,_complete_cds
l36463_2081-2627,ras_inhibitor_(rin1)_mrna,_complete_cds
l77701mrna_43-337,cox17_mrna,_complete_cds
m90356cds_222-618:in_reversesequence,_1194-
1281,btf3_protein_homologue_gene,_complete_cds_
u34301mrna_2-
35,nonmuscle_myosin_heavy_chain_iib_gene,_promoter_region_and_exon/gb=u34301_/n
type=dna
u47025_3462-3994,fetal_brain_glycogen_phosphorylase_b_mrna,_complete_cds_
u55936_367-757,snap-23_mrna,_complete_cds
u70322_2456-3014,transportin_(trn)_mrna,_complete_cds
x68836cds_653-1139,mrna_for_s-adenosylmethionine_synthetase

z18859mrna_933-
1461,cone_transducin_alpha_subunit_gene_extracted_fromgene_for_cone_transducin_alpha_

Metagene 21

af012270_815-1325,peropsin_(rrh)_mrna,_complete_cds/gb=af012270_/ntype=rna
140411mrna_43-511,thyroid_receptor_interactor_(trip8)_mrna,_3'_end_of_cds_
all_x64877_494-529,mrna_for_serum_protein,mrna_for_serum_protein

Metagene 22

af001787_990-1150,uncoupling_proteinmrna,_complete_cds/gb=af001787_/ntype=rna
s81957mrna#1_40-112,_bmp-5=bone_morphogenic_protein-
5_{promoter}_[human,_genomic,_1116_nt]/gb=s81957
all_x55777_1833-
2326,_putorf_gene_extracted_frommahlavu_hepatocellular_carcinoma_hhc(m)_dna_

Metagene 23

all_x77748_2815-3296,mrna_for_metabotropic_glutamate_receptor_type_3_
x84003cds_140-305:in_reversesequence,_373-
379,tafi118_mrna_for_transcription_factor_tfiid_
y10510mrna_13-268,mrna_for_cd67s_protein/gb=y10510_/ntype=rna

Metagene 24

l34357_1655-2165,gata-4_mrna,_complete_cds
u09860_3095-3653,enterokinase_mrna,_complete_cds_
u33448cds_773-1108:in_reversesequence,_1666-1883,putative_g-protein-
coupled_receptor_(gpr16)_gene,_c
u40370_1443-
1929,3',5'_cyclic_nucleotide_phosphodiesterase_(hspde1a3a)_mrna,_complete_cds_
all_x02750_1332-1729,liver_mrna_for_protein_c
z47727cds_6-150:in_reversesequence,_28-313,mrna_for_rna_polymerase_ii_subunit
z80780cds_2-339,h2b/h_gene.

Metagene 25

af001294_285-735,ipl_(ipl)_mrna,_complete_cds.
d16227_589-943,mrna_for_bdp-
1_protein_(a_member_of_the_recoverin_family),_complete_cds_
d50930_4876-5368,mrna_for_kiaa0140_gene,_complete_cds
d78012_2289-2793,mrna_for_dihydropyrimidinase_related_protein-1,_complete_cds
d79985_3997-4393,mrna_for_kiaa0163_gene,_complete_cds
d90359_5384-5912,ccg1_mrna_

hg2566-ht4792_r_at_hg2566-ht4792_microtubule-associated_protein_tau,_altsplice_3,_exon_8_j03930exon#11_638-1118,intestinal_alkaline_phosphatase_(alpi)_gene,_complete_cds_j04469exon#9_11-173:not_in_gb_record,mitochondrial_creatine_kinase_(ckmt)_gene,_complete_cds_j05249_941-1409,replication_protein_a_32-kda_subunit_mrna,_complete_cds_114856cds_746-1100:in_reversesequence,_1324-1393,somatostatin_receptor_gene,_complete_cds_118983mrna_3114-3588,tyrosine_phosphatase_(ia-2/ptp)_mrna,_complete_cds_127479_797-1307,x123_mrna,_3'_end_147345_2141-2609,elongin_a_mrna,_complete_cds_m36430_321-753,transducin_beta-1_subunit_mrna,_3'_end_m57732mrna_2643-3165,hepatic_nuclear_factor(tcf1)_mrna,_complete_cds,_clones_hcl10,_hcl12,_hcl17,_an_reverse_m81780_4000-4487:in_m81780cds#3_175-296,_smpd1_gene_(acid_sphingomyelinase)_extracted_fromac_m88468_1378-1906,mevalonate_kinase_mrna,_complete_cds_u01147mrna_4659-5211,guanine_nucleotide_regulatory_protein_(abr)_mrna,_complete_cds_u09584_1382-1835,pl6_protein_(pl6)_mrna,_complete_cds_u47742_7360-7810,monocytic_leukaemia_zinc_finger_protein_(moz)_mrna,_complete_cds_u47928_2047-2491,protein_a_alternatively_spliced_form(a-2)_mrna,_complete_cds_u53786_6024-6432:not_in_gb_record,envoplakin_(evpl)_mrna,_complete_cds

Metagene 26

d14134_1646-2192,mrna_for_rad51,_complete_cds_j03778_520-1075,microtubule-associated_protein_tau_mrna,_complete_cds_108096_314-794,cd27_ligand_mrna,_complete_cds_u17977_79-379,hsul7977cdna_u39196_2616-3084,clone_hgirk1_g-protein_coupled_inwardly_rectifying_potassium_channel_mrna,_complete_u58090_1035-1605,hs-cul-4a_mrna,_partial_cds_u94320_828-1392,neuropeptide_y5_receptor_(npyy5)_mrna,_complete_cds_x00949cds_65-487,mrna_for_prepro-relaxin_h1/gb=x00949/_ntype=rna_x58822mrna_905-1422,ifn-omegagene_for_interferon-omega_1_x59841mrna_2006-2444,pbx3_mrna_x97230cds_782-1274:in_reversesequence,_1290-1353,mrna_for_nk_receptor,_clone_library_4m1#6_x98001cds_572-932:in_reversesequence,_998-1064,mrna_for_geranylgeranyl_transferase_ii_

Metagene 27

ac002073cds#1_507-759:in_reversesequence,_23812-24010,_wugsc:dj515n1.2_gene_extracted_frompac_clone_hg3345-ht3522_at_hg3345-ht3522_pou_domain-containing_protein_137036exon#2_29-92:in_reversesequence,_1754-1971,neutrophil-activating_peptide_78_(ena-78)_gene,_com

m15169mrna#1_1704-1950:in_reversesequence,_3390-3408,beta-2-
 adrenergic_receptor_mrna,_complete_cds
 m25756_1777-2287,secretogranin_ii_gene,_complete_cds_
 m28983_1823-2369,interleukinalpha_(il_1)_mrna,_complete_cds
 m33317mrna_1158-1693,cytochrome_p450iia4_(cyp2a4)_mrna,_complete_cds_
 m62486exon_17-359:not_in_gb_record,c4b-binding_protein_gene_
 u66580cds_510-1026:in_reversesequence,_1075-1081,putative_g_protein-
 coupled_receptor_(gpr21)_gene,_c
 u79242_1043-1589,clone_23560_mrna_sequence_
 all_x02404_227-
 750,mrna_fragment_for_second_calcitonin_gene_related_peptide_(cgrp)_from_medull
 ary_th
 x55005mrna_2002-2230,c-erba-1_mrna_for_thyroid_hormone_receptor_alpha_
 x77533cds_982-1390:in_reversesequence,_1532-
 1544,mrna_for_activin_type_ii_receptor
 all_z11933_1730-1942,mrna_for_n-oct_3,_n-oct5a,_and_n-oct_5b_proteins

Metagene 28

d14822_570-
 717,chimeric_mrna_derived_from_aml1_gene_and_mtg8(eto)_gene,_partial_sequence.
 d87743_3861-4323,mrna_for_kiaa0267_gene,_partial_cds_
 hg3942-ht4212_at_hg3942-ht4212_interferon
 l14787_1203-1641,dna-binding_protein_mrna,_3'_end
 l15388_1992-2478,g_protein-coupled_receptor_kinase_(grk5)_mrna,_complete_cds_
 l24564_854-1400,rad_mrna,_complete_cds_
 all_m61853_1735-2240,cytochrome_p4502c18_(cyp2c18)_mrna,_clone_6b
 m76482_2855-3251,130-kd_pemphigus_vulgaris_antigen_mrna,_complete_cds
 s74683_848-1268,_adp-
 ribosyltransferase_[human,_skeletal_muscle,_mrna,_1334_nt]_
 u13369cds_1792-
 2248,ribosomal_dna_complete_repeating_unit/gb=u13369_/ntype=dna_/annot=cds
 all_x96584_1444-1961,mrna_for_nov_protein

Metagene 29

d78014_4608-4998,mrna_for_dihydropyrimidinase_related_protein-3,_complete_cds
 hg2614-ht2710_at_hg2614-ht2710_collagen,_type_viii,_alpha_1
 m61906_2813-3326,p13-kinase_associated_p85_mrna_sequence_
 u29953mrna_1150-1468,pigment_epithelium-derived_factor_gene,_complete_cds_
 u40572_1105-1627,beta2-syntrophin_(snt_b2)_mrna,_complete_cds_
 u79294_831-1371,clone_23748_mrna,_complete_cds.
 x15525mrna_1670-
 2084,lysosomal_acid_phosphatase_gene_(ec_3.1.3.2)_exon(and_joined_cds)_
 all_x68742_2942-3423,mrna_for_integrin,_alpha_subunit
 x96719cds_86-398:in_reversesequence,_674-710,mrna_for_aicl_(activation-
 induced_c-type_lectin)_

Metagene 30

j04132_919-1417,t_cell_receptor_zeta-chain_mrna,_complete_cds

m76559_3065-3521,neuronal_dhp-sensitive,_voltage-
 dependent,_calcium_channel_alpha-2b_subunit_mrna,_c
 m81882mrna_1835-2261,glutamate_decarboxylase_(gad65)_mrna,_complete_cds
 s68874_113-469,_ep3_prostanoid_receptor_ep3-
 i_{3'_region,_alternatively_spliced}_[human,_mrna_partia
 u0092lexon#3_273-313:not_in_gb_record,lst-1_gene,_complete_cds_
 u01828_5837-5942,microtubule-associated_protein(map2)_mrna,_complete_cds
 u20759_3683-3758,parathyroid_cell_calcium-sensing_receptor_mrna,_complete_cds
 u29943_1609-2065,elav-like_neuronal_protein-2_hel-n2_mrna,_complete_cds
 u31628_1015-1507,interleukin-
 15_receptor_alpha_chain_precursor_(il15ra)_mrna,_complete_cds_
 x02883exon#4_568-736,gene_for_t-
 cell_receptor_alpha_chain_c_region/gb=x02883_/ntype=dna_/annot=exon
 all_x70811_2067-2566,mrna_for_betaadrenergic_receptor_
 all_x81832_1592-2163,mrna_for_glucose-
 dependant_insulinotropic_polypeptide_receptor_gene_
 x86570_1208-1532,mrna_for_acidic_hair_keratin_1
 y07683_951-1413,mrna_for_p2x3_purinoreceptor/gb=y07683_/ntype=rna

Metagene 31

d26155_4647-5214,mrna_for_transcriptional_activator_hsnf2a,_complete_cds_
 hg3412-ht3593_s_at_hg3412-ht3593_blue_cone_photoreceptor_pigment_
 j02758exon#3_568-980:in_reversesequence,_3307-3464,apolipoprotein_a-
 iv_gene,_complete_cds_
 m13982mrna_7-508,interleukin(il-4)_mrna,_complete_cds_
 m26901cds_808-1187:in_reversesequence,_218-293,renin_gene_
 u03056_1988-2468,tumor_suppressor_(luca-1)_mrna,_complete_cds
 u16120_2267-2833,placental_taurine_transporter_mrna,_complete_cds
 x68285cds_886-976,mrna_for_glycerol_kinase_

Metagene 32

d85376exon_2003-2453,dna_for_thyrotropin-releasing_hormon_receptor_
 hg1034-ht1034_f_at_hg1034-ht1034_atpase,_na+/k+_transporting,_alphapolypeptide
 hg1471-ht3923_s_at_hg1471-ht3923_transcription_factor_oct-
 1a/1b,_altsplice_2,_oct-1b_
 hg2147-ht2217_r_at_hg2147-ht2217_mucin_3,_intestinal_
 hg3565-ht3768_at_hg3565-ht3768_zinc_finger_protein_
 all_k03431_5910-6163:not_in_gb_record,_hpr_gene_(haptoglobin-
 related_protein)_extracted_fromhaptoglo
 103840_2419-2970,fibroblast_growth_factor_receptor(fgfr4)_mrna,_complete_cds
 107590_4754-
 5138,protein_phosphatase_2a_130_kda_regulatory_subunit_mrna,_complete_cds
 l11708_761-1205,_humanbeta_hydroxysteroid_dehydrogenase_typemrna,_complete_cds_
 l13197_1853-2099,(clone_d21s418e)_pregnancy-associated_plasma_protein_a_(papp-
 a)_gene,_5'_utr
 l27943mrna_291-867,cytidine_deaminase_(cda)_mrna,_complete_cds
 l28821_4394-4838,alpha_mannosidase_ii_isozyme_mrna,_complete_cds
 l40992mrna_906-1368,(clone_pebp2aa1)_core-
 binding_factor,_runt_domain,_alpha_subunit(cbfa1)_mrna,_3'
 l49169mrna_3270-3612,g0s3_mrna,_complete_cds_
 m14016mrna_644-947,uroporphyrinogen_decarboxylase_mrna,_complete_cds_

m14660exon_1123-1363:in_reversesequence,_1460-1646, isg-
 54k_gene_(interferon_stimulated_gene)_encodin
 m23892mrna_2101-2549,15-lipoxygenase_mrna,_complete_cds
 m27288exon_225-555:in_reversesequence,_567-768,oncostatin_m_gene
 m27783_2-433,neutrophil_elastase_mrna,_3'_end
 m28213_94-627,gtp-binding_protein_(rab2)_mrna,_complete_cds_
 m31525mrna_517-1081,mhc_ii_lymphocyte_antigen_(hla-dna)_gene,_complete_cds_
 m55131mrna_5636-
 6134,cystic_fibrosis_transmembrane_conductance_regulator_(cftr)_gene_
 m55172_6712-
 7102,large_aggregating_cartilage_proteoglycan_core_protein_mrna,_complete_cds
 m63896cds_927-1197:in_reversesequence,_1866-
 2022,transcriptional_enhancer_factor_(tef1)_dna,_complet
 m63967exon#2_1319-
 1625,mitochondrial_aldehyde_dehydrogenase_x_gene,_complete_cds_
 m80478exon#3_119-
 635,platelet_glycoprotein_ix_precursor_(gpix)_gene,_complete_cds
 m96995_497-1025,epidermal_growth_factor_receptor-binding_protein_grb2_(egfrbp-
 grb2)_mrna_sequence_
 s50017cds_904-1241:in_reversesequence,_444-505,_2'_3'-cyclic_nucleotide_3'_-
 phosphodiesterase_[hum
 u07563_cds1_at_u07563_u07563,not_in_gb_record,abl_gene,_exon_1b_and_intron_1b,_
 and_putative_m8604_me
 u11861_511-949,g10_homolog_(edg-2)_mrna,_complete_cds
 u33841_8844-9294,ataxia_telangiectasia_(atm)_mrna,_complete_cds
 u34605_3365-3851,retinoic_acid-_and_interferon-
 inducible_58k_protein_ri58_mrna,_complete_cds_
 u35246_1518-1962,vacuolar_protein_sorting_homolog_h-vps45_mrna,_complete_cds_
 u38980_841-972,pms2_related_(hpmsr6)_mrna,_complete_cds
 u43586_1531-2101,kinase_suppressor_of_ras-1_(ksr1)_mrna,_partial_cds_
 u43747_993-1425,frataxin_(frda)_mrna,_complete_cds_
 u50839_1969-2413:not_in_gb_record,g16_protein_(g16)_mrna,_partial_cds.
 u52513_1318-1642,rig-g_mrna,_complete_cds
 u65533_3076-
 3620,regulator_of_nonsense_transcript_stability_(rent1)_mrna,_complete_cds_
 u66828_2341-2500,carnitine_palmitoyltransferase_i_(cpti)_mrna,_complete_cds
 u70867_3444-3936,prostaglandin_transporter_hpgt_mrna,_complete_cds_
 u75362_2155-2557,isopeptidase_t-3_(isot-3)_mrna,_complete_cds
 u92971_1235-1805,protease-activated_receptor(par3)_mrna,_complete_cds.
 u93049_1841-2375,slp-76_associated_protein_mrna,_complete_cds
 x01038mrna_285-824,fetal_gene_for_apolipoprotein_ai_precursor_
 x14445exon#3_240-702,int-2_proto-oncogene
 all_x14789_1204-1793,alpha-a_crystallin_gene_exon_1,2_and_pseudoexon_
 x15357cds_2853-3135:in_reversesequence,_3262-
 3454,mrna_for_natriuretic_peptide_receptor_(anp-a_recep
 x71874cds#1_268-739:in_reversesequence,_4531-4534,_proteasome-
 like_subunit_mecl1-1_gene_extracted_fro
 x84746cds_544-1012,histo-blood_group_ab0_gene,_exon_1
 all_x85137_3131-3726,mrna_for_kinesin-related_protein
 x98833mrna_3475-3937,mrna_for_zinc_finger_protein,_hsall1
 all_y10260_1483-2048,eyal_gene_
 z30643cds_1860-1921,mrna_for_chloride_channel_(putative)_2139bp
 z46967cds_1216-1714,mrna_for_calicin_(partial)_

Metagene 33

hg1728-ht1734_at_hg1728-ht1734_non-specific_cross_reacting_antigen,_altsplice_form_2_
 j04046mrna_1559-2089,calmodulin_mrna,_complete_cds_
 s77835_88-380,_il-2=interleukin-2_[human,_brain,_mrna,_418_nt]/gb=s77835_/ntype=rna_
 s83362mrna_10-109,_differentiation-stimulating_factor/leukemia_inhibitory_factor_receptor_{5'_region
 u65581_958-1420,ribosomal_protein_l3-like_mrna,_complete_cds.
 x58234mrna_31-253,mrna_for_anti-lectin_antibody_epitope_(clone_p36/8-5)

Metagene 34

hg3992-ht4262_at_hg3992-ht4262_cpg-enriched_dna,_clone_e35_
 j02843cds_1103-1451:in_reversesequence,_14089-14119,cytochrome_p450iie1_(ethanol-inducible)_gene,_co
 m54927mrna_2349-2907,myelin_proteolipid_protein_mrna,_complete_cds_
 u38480_1008-1521,retinoid_x_receptor-gamma_mrna,_complete_cds
 x05608exon#4_172-406:not_in_gb_record,gene_for_neurofilament_subunit_nf-1_

Metagene 35

af012024_658-1175,integrin_cytoplasmic_domain_associated_protein_(icap-1b)_mrna,_complete_cds/gb=af0
 d23660_889-1369,mrna_for_ribosomal_protein,_complete_cds_
 d31883_6153-6711,mrna_for_kiaa0059_gene,_complete_cds
 d78361_504-942,mrna_for_ornithine_decarboxylase_antizyme,_orfand_orf_2
 d86331_1281-1777,mt2-mmp_gene_for_matrix_metalloprotein,_complete_cds
 hg1103-ht1103_at_hg1103-ht1103_guanine_nucleotide-binding_protein_ral,_ras-oncogene_related
 hg180-ht180_at_hg180-ht180_ahnak-a_nucleoprotein_ahnak-a_
 hg2873-ht3017_at_hg2873-ht3017_ribosomal_protein_l30_homolog_
 hg3362-ht3539_s_at_hg3362-ht3539_chromosomal-translocation_associated_gene_ltg19/enl_
 hg3395-ht3573_s_at_hg3395-ht3573_dnaj_homolog,_altsplice_form_2
 hg3549-ht3751_at_hg3549-ht3751_wilm_tumor-related_protein
 hg4319-ht4589_at_hg4319-ht4589_ribosomal_protein_l5
 hg821-ht821_at_hg821-ht821_ribosomal_protein_s13_
 j03592_707-1085,adp/atp_translocase_mrna,_3'_end,_clone_phat8
 j04617cds_1069-1364:in_reversesequence,_3823-4030,elongation_factor_ef-1-alpha_gene,_complete_cds_
 l04483_39-272,ribosomal_protein_s21_(rps21)_mrna,_complete_cds_
 l06499mrna_4-301,ribosomal_protein_l37a_(rpl37a)_mrna,_complete_cds_
 l06505mrna_259-553,ribosomal_protein_l12_mrna,_complete_cds
 l07868_4919-5429,receptor_tyrosine_kinase_(erbb4)_gene,_complete_cds
 l11566_77-521,ribosomal_protein_l18_(rpl18)_mrna,_complete_cds
 all_m10277_3236-3578,cytoplasmic_beta-actin_gene,_complete_cds_
 m17886mrna_7-475,acidic_ribosomal_phosphoprotein_p1_mrna,_complete_cds_
 m18000cds_78-360,ribosomal_protein_s17_gene,_complete_cds
 m19828exon#8_1305-1576:in_reversesequence,_14367-14518,apolipoprotein_b-100_(apob)_gene_
 m24194mrna_504-1023,mhc_protein_homologous_to_chicken_b_complex_protein_mrna,_complete_cds_

all_m31520_25-
 590,ribosomal_protein_s24_mrna,ribosomal_protein_s24_mrna,ribosomal_protein_s24_mrna
 m31520mrna_2-
 106,ribosomal_protein_s24_mrna,ribosomal_protein_s24_mrna,ribosomal_protein_s24_mrna
 m36072_368-770,ribosomal_protein_l7a_(surf_3)_large_subunit_mrna,_complete_cds_
 m55409_556-1069,pancreatic_tumor-related_protein_mrna,_3'_end
 m58603_3120-3600,nuclear_factor_kappa-b_dna_binding_subunit_(nf-kappa-b)_mrna,_complete_cds
 m60854_19-373,ribosomal_protein_s16_mrna,_complete_cds_
 m64098_3873-
 4305,high_density_lipoprotein_binding_protein_(hbp)_mrna,_complete_cds_
 m64716mrna_31-451,ribosomal_protein_s25_mrna,_complete_cds_
 m81757_49-421,s19_ribosomal_protein_mrna,_complete_cds_
 s79522_19-481,_ubiquitin_carboxyl_extension_protein_[human,_mrna,_540_nt]_
 u07804_1857-2384,dna_topoisomerase_i_mrna,_partial_cds_
 u07806_2865-
 3382,camptothecin_resistant_clone_cem/c2_dna_topoisomerase_i_mrna,_partial_cds_
 u09953_153-621,ribosomal_protein_l9_mrna,_complete_cds_
 u14968_133-451,ribosomal_protein_l27a_mrna,_complete_cds_
 u14969_43-451,ribosomal_protein_l28_mrna,_complete_cds_
 u14971_91-661,ribosomal_protein_s9_mrna,_complete_cds_
 u14973_13-235,ribosomal_protein_s29_mrna,_complete_cds_
 u25789_19-481,ribosomal_protein_l21_mrna,_complete_cds_
 u49352_548-1106,liver_2,4-dienoyl-coa_reductase_mrna,_complete_cds_
 u49785_311-641,d-dopachrome_tautomerase_mrna,_complete_cds.
 u78027mrna#3_3-350,_l44l_gene_(l44-like_ribosomal_protein)_extracted_frombruton_tyrosine_kinase_(btk
 u79273_851-1127,clone_23933_mrna_sequence
 u83461_1235-
 1619,putative_copper_uptake_protein_(hctr2)_mrna,_complete_cds/gb=u83461_/ntype=rna
 x01677cds_629-983:in_reversesequence,_1109-1229,liver_mrna_for_glyceraldehyde-3-phosphate_dehydrogen
 x03342cds_51-375:in_reversesequence,_439-445,mrna_for_ribosomal_protein_l32_
 x06617mrna_31-475,mrna_for_ribosomal_protein_s11_
 x16064cds_147-483:in_reversesequence,_625-745,mrna_for_translationally_controlled_tumor_protein_
 x17206cds_111-585:in_reversesequence,_885,mrna_for_llrep3_
 x52966cds_11-299:in_reversesequence,_19-373,mrna_for_ribosomal_protein_l35a_
 x55715cds_228-618:in_reversesequence,_748-784,hums3_mrna_for_40s_ribosomal_protein_s3_
 x56932cds_114-576:in_reversesequence,_611-623,mrna_for_23_kd_highly_basic_protein_
 x56997mrna#1_19-475:not_in_gb_record,uba52_gene_coding_for_ubiquitin-52_amino_acid_fusion_protein
 all_x64707_401-888,bbc1_mrna_
 x67247mrna_116-662,rps8_gene_for_ribosomal_protein_s8_
 x69150mrna_25-403,_l06432mrna_for_ribosomal_protein_s18
 x79234cds_115-511,mrna_for_ribosomal_protein_l11_
 z26876_43-328,gene_for_ribosomal_protein_l38_
 z28407cds_220-703:in_reversesequence,_809-818,mrna_for_ribosomal_protein_l8_
 z49148cds_2-418:in_reversesequence,_18-589,mrna_for_ribosomal_protein_l29_
 z69043cds_66-489:in_reversesequence,_30-598,mrna_translocon-associated_protein_delta_subunit_precurs
 all_z70759_4-251,mitochondrial_16s_rrna_gene_(partial).

Metagene 36

hg2538-ht2634_at_hg2538-ht2634_heterogeneous_nuclear_ribonucleoprotein_c_
u43653_2816-3155,obese_protein_(ob)_mrna,_complete_cds_
v00532mrna_387-911,_ifna_gene_(interferon_alpha-
i)_extracted_fromgene_for_leukocyte_(alpha)_interfer
all_z46632_2953-3206,hspde4c1_gene_for_3',5'-
cyclic_amp_phosphodiesterase,hspde4c1_gene_for_3',5'

Metagene 37

j04076mrna_2171-2651,early_growth_responseprotein_(egr2)_mrna,_complete_cds_
m31659mrna_1130-
1640,gt_mitochondrial_solute_carrier_protein_homologue_mrna,_complete_cds
all_x95677_1773-2368,mrna_for_argbpib_protein/gb=x95677_/ntype=rna_

Metagene 38

d21267mrna_1481-1979,mrna_for_highly_expressed_protein_
d83781_4231-4729,mrna_for_kiaa0197_gene,_partial_cds_
hg3930-ht4200_at_hg3930-ht4200_stearoyl-coenzyme_a_desaturase_
l42176_844-1384,(clone_35.3)_dral_mrna,_complete_cds
l49054_587-1067,t(3;5)(q25.1;p34)_fusion_gene_npm-mlf1_mrna,_complete_cds.
m95167mrna_3333-3897,dopamine_transporter_(slc6a3)_mrna,_complete_cds_
u32376_2548-3028,channel_associated_protein_of_synapse_(chapsyn-
110)_mrna,_complete_cds
x78712cds_1319-1637:in_reversesequence,_1691-
1823,mrna_for_glycerol_kinase_testis_specific_2
x82209_7019-7511,mn1_mrna
y10505mrna_94-658,mrna_for_cd104_protein/gb=y10505_/ntype=rna

Metagene 39

d26579_2683-3205,mrna_for_transmembrane_protein,_complete_cds
hg2663-ht2759_at_hg2663-ht2759_homeotic_protein_emx2_
l06797_1041-1599,(clone_15)_orphan_g_protein-
coupled_receptor_mrna,_complete_cds_
l08177_1042-1606,ebv_induced_g-
protein_coupled_receptor_(ebi2)_mrna,_complete_cds
m30773_1983-2499,calcineurin_b_mrna,_complete_cds
u20758mrna_885-1437,osteopontin_gene,_complete_cds
all_x17042_689-1158,mrna_for_hematopoietic_proteoglycan_core_protein

Metagene 40

d49487_32-512,mrna_for_obese_gene,_complete_cds

hg2148-ht2218_f_at_hg2148-ht2218_mucin_3,_intestinal_
 hg2239-ht2324_r_at_hg2239-ht2324_potassium_channel_protein_
 hg3725-ht3981_s_at_hg3725-ht3981_insulin-like_leydig_hormone_
 hg406-ht406_at_hg406-ht406_p97_antigen,_melanoma-specific
 hg4113-ht4383_s_at_hg4113-ht4383_olfactory_receptor_or17-201_
 hg4593-ht4998_at_hg4593-ht4998_sodium_channel_
 hg960-ht960_at_hg960-ht960_guanine_nucleotide_exchange_factor_
 k03498cds#1_2-163,_pol_protein_fromendogenous_retrovirus_herv-
 k22_pol_and_envelope_orf_region/gb=k03
 l10615mrna_502-528,beta_casein_(csn2)_gene,_complete_cds
 l38490mrna_785-1319,adp-ribosylation_factor_mrna,_complete_cds
 all_m13485_188-243:in_m13485cds_47:not_in_gb_record,metallothionein_i-b_gene_
 all_m55418_2452-2650,amelogenin_(amelx)_gene,_3'_end_of_cds
 m84820_1155-1709,retinoid_x_receptor_beta_(rxr-beta)_mrna,_complete_cds
 all_m86406_3670-4169,skeletal_muscle_alphaactinin_(actn20_mrna,_complete_cds_
 m92424_1822-2209,p53-associated_mrna,_complete_cds_
 s57212_1561-2027,_hmef2c=myocyte_enhancer-
 binding_factor[human,_skeletal_muscles,_mrna,_2161_nt]_
 s72493_617-
 819,_keratin=keratinhomolog_[human,_tracheobronchial_epithelial_cells,_mrna_par-
 tial,_976_
 s77893_121-
 203,_gpsat=glycophorin_sat_[human,_peripheral_bloods,_mrna_partial,_407_nt]
 all_s78653_1782-2347,_mrg=mas-related_[human,_genomic,_2416_nt]_
 u14577_974-1504,microtubule-associated_protein_1a_(map1a)_mrna,_complete_cds_
 u16296_4938-5478,t-
 lymphoma_invasion_and_metastasis_inducing_tiam1_protein_(tiam1)_mrna,_complete_
 cd
 u23852_1523-2066,t-
 lymphocyte_specific_protein_tyrosine_kinase_p56lck_(lck)_abberant_mrna,_complet
 e_
 all_u28055_2678-3165,hepatocyte_growth_factor-
 like_protein_homolog_(dlf15s1a)_mrna,_partial_cds
 u40002_3192-3701,hormone-sensitive_lipase_testicular_isoform_mrna,_complete_cds
 u48865cds_400-
 807:in_reversesequence,_3499,c/ebp_epsilon_(cebpe)_gene,_complete_cds_
 u52077cds_428-
 982,mariner1_transposase_gene,_complete_consensus_sequence/gb=u52077_/ntype=dna
 /annot
 u57971_3646-4130,calcium_atpase_isoform_3x/a_mrna,_complete_cds
 u59058_8-508,beta-a3/a1_crystallin_(cyrba3/a1)_mrna,_partial_cds_
 u74667_1599-2067,tat_interactive_protein_(tip60)_mrna,_complete_cds
 u79275_509-989,clone_23947_mrna,_partial_cds.
 u80226_1440-1476,gamma-
 aminobutyric_acid_transaminase_mrna,_partial_cds/gb=u80226_/ntype=rna_
 u82467_2667-3213,tub_homolog_(tub)_mrna,_complete_cds
 u89336exon#54_51-
 369:not_in_gb_record,_unknown_gene_extracted_fromhla_iii_region_containing_notc
 h4_g
 u89336exon#65_12-282:in_reversesequence,_54136-
 54166:not_in_gb_record,_unknown_gene_extracted_fromhl
 u92436_2591-
 3077,mutated_in_multiple_advanced_cancers_protein_(mmac1)_mrna,_complete_cds.
 x03072cds_765-1089:in_reversesequence,_3505-3649,int-1_mammary_oncogene_
 x04707cds_815-1343:in_reversesequence,_1649-1673,c-erb-
 a_mrna_for_thyroid_hormone_receptor
 all_x07203_1419-1576,mrna_for_cd20_receptor_(s7)_

all_x16866_688-1280,mrna_for_cytochrome_p-450iid_(clone_pmp33)_
 all_x51823_2-51,mrna_for_b-
 subunit_of_coagulation_factor_xiii_(fxiiib)_(partial)/gb=x51823_/ntype=rn
 x52008cds_899-1325:in_reversesequence,_1748-1814,alpha-
 2_strychnine_binding_subunit_of_inhibitory_gl
 x58431mrna#1_1781-
 2299,_hox_2.2_gene_extracted_fromhox2.2_gene_for_a_homeobox_protein_
 x61072mrna_43-325,mrna_for_t_cell_receptor,_clone_igra17.
 all_x62466_25-410,mrna_for_campath-1_(cdw52)_antigen_
 all_x68314_466-923,mrna_for_glutathione_peroxidase-gi
 x80923mrna_31-361,nov_gene/gb=x80923_/ntype=dna_/annot=mrna
 all_x89059_722-1203,mrna_for_unknown_protein_expressed_in_macrophages
 x90763_1272-1632,mrna_for_type_i_keratin,_hha5_
 x91103cds_587-965:in_reversesequence,_1055-
 1097,mrna_for_hr44_protein/gb=x91103_/ntype=rna
 all_z11737_1537-2120,mrna_for_flavin-containing_monooxygenase_4
 z15114cds_1319-1589:in_reversesequence,_1595-
 1805,mrna_for_protein_kinase_c_gamma_(partial)_
 all_z48482_2998-3401,mrna_for_membrane-type_matrix_metalloproteinase_2_
 all_z80783_510-565,h2b/l_gene
 all_z83336_618-702,hh2b/d_gene.
 z83821cds#2_1428-1668:in_reversesequence,_39964-
 40156,dna_sequence_from_pac_296k21_on_chromosome_x_c

Metagene 41

hg2441-ht2537_s_at_hg2441-ht2537_retinoblastoma_protein,_mutated_
 m16282cds_25-133:in_reversesequence,_283-
 469,fragile_x_locus_m2c_containing_an_unidentified_open_rea
 all_m17254_1366-1889,erg2_gene_encoding_erg2_protein,_complete_cds_
 u84540mrna_1083-1341,dystrobrevin_isoform_dtn-
 3_(dtn)_gene,_exon_11b_and_complete_cds/gb=u84540_/nty
 y10202mrna_169-529,mrna_for_cd207_protein/gb=y10202_/ntype=rna_

Metagene 42

ab000462_6801-7227,mrna_for_sh3_binding_protein,_clone_res4-23a,_complete_cds
 m65062_1233-1527,insulin-like_growth_factor_binding_protein(igfbp-
 5)_mrna,_complete_cds_
 m93221mrna_4618-5110,macrophage_mannose_receptor_(mrc1)_gene_
 u25801_225-675,tax1_binding_protein_mrna,_partial_cds
 all_x16699_2053-2130,mrna_for_cytochrome_p-450hp_
 x72177mrna_2964-3510,c6_gene,_exon_1

Metagene 43

d11086_976-1408,mrna_for_interleukinreceptor_gamma_chain
 hg2090-ht2152_s_at_hg2090-ht2152_external_membrane_protein,_130_kda
 hg2639-ht2735_s_at_hg2639-ht2735_single-stranded_dna-binding_protein_mssp-1
 m30257_2214-2709,vascular_cell_adhesion_moleculemrna,_complete_cds
 m33600_581-1109,mhc_ii_hla-dr-beta-1_(hla-drb1)_mrna,_complete_cds

m37033_915-1395,cd53_glycoprotein_mrna,_complete_cds_
 m60830exon_1480-2020,evi2b3p_gene,_exon_and_complete_cds_
 m83221_1788-2262,i-rel_mrna,_complete_cds_
 s73813_1337-
 1775,_cd39=lymphoid_cell_activation_antigen_[human,_b_lymphoblastoid_cell_line,
 _mp-1,_mr
 u95626mrna#3_2792-
 3278,_ccr2_gene_(ccr2a)_extracted_fromccr2b_(ccr2),_ccr2a_(ccr2),_ccr5_(ccr5)_a
 nd_
 x04500exon#7_244-778,gene_for_prointerleukinbeta
 x56841mrna_1269-1713,hla-e_gene
 all_x57522_2229-2788,ring4_cdna
 x64072cds_1948-2281:not_in_gb_record,_hsapiens_cd18_exon_2_
 all_x99687_221-732,mrna_for_methyl-cpg-
 binding_protein_2,_intron/gb=x99687/_ntype=rna_
 all_y00062_3996-4597,mrna_for_t200_leukocyte_common_antigen_(cd45,_lc-a)_
 y09561cds_1238-1676:in_reversesequence,_1798,mrna_for_p2x7_receptor_
 z14982mrna#1_616-1150,_mhc-encoded_proteasome_subunit_gene_lamp7-
 e1_gene_(proteasome_subunit_lmp7)_e

Metagene 44

hg3733-ht4003_at_hg3733-ht4003_epiligrin,_alpha_3
 m65291_715-
 1189,natural_killer_cell_stimulatory_factor_(nksf)_mrna,_complete_cds,_clone_p3
 5
 u15422cds#2_17-269:in_reversesequence,_20347-
 20563,_prm2_gene_(protamine_2)_extracted_fromprotamine(
 u18297_1298-1805,mst1_(mst1)_mrna,_complete_cds

Metagene 45

d38163_3117-3661,mrna_for_a1(xix)_collagen_chain,_complete_cds_
 all_x03066_787-1268,mrna_for_hla-d_ii_antigen_do_beta_chain
 x14766mrna_1363-1711,mrna_for_gaba-a_receptor,_alphasubunit_
 x76104cds_4113-4257:in_reversesequence,_4629-4827,dap-kinase_mrna_
 z34974cds_1816-2144:in_reversesequence,_2439-
 2515,mrna_for_plakophilin_(partial)

Metagene 46

af000424_214-610,lst1_mrna,_clst1/c_splice_variant,_complete_cds
 d30036_1743-2283,mrna_for_phosphatidylinositol_transfer_protein_(pi-
 tpalpha),_complete_cds_
 d64109_642-1152,mrna_for_tob_family,_complete_cds
 l11672_3266-
 3562,kruppel_related_zinc_finger_protein_(htf10)_mrna,_complete_cds,kruppel_rel
 ated_zinc
 l15326_2760-3323,endoperoxide_synthase_type_ii_mrna,_complete_cds
 m27543mrna_2548-3070,guanine_nucleotide-
 binding_protein_(gi)_alpha_subunit_mrna,_complete_cds

m29335_2-180,mhc_ii_do-alpha_mrna,_partial_cds,mhc_ii_do-
 alpha_mrna,_partial_cds
 m95178_2567-2996,non-muscle_alpha-actinin_mrna,_complete_cds_
 u37248_848-1304,alpha-mannosidase_(6a8)_mrna,_complete_cds_
 u42387_1180-1642,pancreatic_polypeptide_receptor_mrna,_complete_cds_
 u49957_5044-5581,lim_protein_(lpp)_mrna,_partial_cds_
 u66661_2656-3082,gaba-a_receptor_epsilon_subunit_mrna,_complete_cds_
 u77665_393-873, rnasep_protein_p30_(rpp30)_mrna,_complete_cds.
 u78524_1571-1967,gu_binding_protein_mrna,_partial_cds
 u90904_1102-1342,clone_23773_mrna_sequence_
 x01630cds_883-1213:in_reversesequence,_1312-
 1468,mrna_for_argininosuccinate_synthetase
 x04143cds_49-265:in_reversesequence,_1430-1592, gene_for_bone_gla_protein_(bpg)
 all_x16832_840-1381,mrna_for_cathepsin_h_(ec_3.4.22.16)
 all_x54936_1140-1627,mrna_for_placenta_growth_factor_(plgf)
 all_x70683_2322-2752,mrna_for_sox-4_protein
 all_x85545_1122-1591,mrna_for_protein_kinase,_pkx1_
 all_x90392_2058-2545,mrna_for_dnase_x_gene_
 z32765exon_79-159,cd36_gene_exon/gb=z32765_/ntype=dna_/annot=exon

Metagene 47

m30496_321-759,ubiquitin_carboxyl-terminal_hydrolase_(pgp_9.5,_uch-
 l3)_isozyme_l3_mrna,_complete_cds
 s62539_5366-5756,_insulin_receptor_substrate-
 1_[human,_skeletal_muscle,_mrna,_5828_nt]
 s77393_43-
 205,_transcript_ch138_[human,_rf1,rf48_stomach_cancer_cell_lines,_mrna,_235_nt]
 /gb=s77393_
 u17886mrna_507-981,succinate_dehydrogenase_iron-protein_subunit_(sdhb)_gene
 x82068cds_2293-2647:in_reversesequence,_3019-
 3103,mrna_for_glutamate_receptor_subunit_glurc_
 all_x86163_2233-2564,mrna_for_b2-bradykinin_receptor,_3'_
 x93511cds_2-312,mrna_for_telomeric_dna_binding_protein_(orf1)

Metagene 48

d26561cds#2_153-435:in_reversesequence,_3711-
 3717,_orf_for_l1_protein_gene_extracted_frompapillomavi
 hg3703-ht3915_s_at_hg3703-ht3915_udp-
 glucuronosyltransferasefamily,_polypeptide_1,_altssplice_1
 all_l37868_3521-4088,pou-domain_transcription_factor_(n-oct-3),_complete_cds
 x74819cds_509-809:in_reversesequence,_913-1015,mrna_for_cardiac_troponin_t

Metagene 49

hg4316-ht4586_at_hg4316-ht4586_transketolase-like_protein

Metagene 50

d10667_2830-3307,mrna_for_smooth_muscle_myosin_heavy_chain_
 m72885mrna_207-750,_g0s2_gene_extracted_fromgos2_gene,_5'_flank_and_cds_
 all_u22028_8029-
 8330,cytochrome_p450_(cyp2a13)_gene,_complete_cds,cytochrome_p450_(cyp2a13)_gen
 e,_co
 u92459_2702-3194,metabotropic_glutamate_receptormrna,_complete_cds

Metagene 51

d13988_897-1353,rab_gdi_mrna,_complete_cds_
 d31763_5458-5968,mrna_for_kiaa0065_gene,_partial_cds_
 hg1747-ht1764_s_at_hg1747-ht1764_proto-oncogene_met,_altsplise_form_2
 hg4074-ht4344_at_hg4074-ht4344_rad2
 j05614mrna_4-
 41,proliferating_cell_nuclear_antigen_(pcna)_gene,_promoter_region/gb=j05614/_n
 type=dna
 l23959_971-1415,e2f-related_transcription_factor_(dp-1)_mrna,_complete_cds
 l40386mrna_657-1122,dp-2_mrna,_complete_cds
 l40403mrna_1725-2277,(clone_zap3)_mrna,_3'_end_of_cds_
 m28209_158-680,gtp-binding_protein_(rab1)_mrna,_complete_cds
 m37104_13-
 421,mitochondrial_atpase_coupling_factorsubunit_(atp5a)_mrna,_complete_cds
 m37583mrna_368-824,histone_(h2a.z)_mrna,_complete_cds
 m58525_603-933,catechol-o-methyltransferase_(comt)_mrna,_complete_cds_
 m81118exon#2_669-1149,alcohol_dehydrogenase_chi_polypeptide_(adh5)_gene
 m83738_3328-3883,protein-tyrosine_phosphatase_(ptpase_meg2)_mrna,_complete_cds_
 m86737_2236-2776,high_mobility_group_box_(ssrp1)_mrna,_complete_cds
 m92439_4255-4633,leucine-rich_protein_mrna,_complete_cds_
 m94630_832-1027,hnrnp-c_like_protein_mrna,_complete_cds_
 s83364_19-325,_putative_rab5-interacting_protein_{clone_l1-
 57}_[human,hela_cells,mrna_partial,_366
 s85655_435-969,_prohibitin_[human,mrna,_1043_nt]_
 u25182_350-860,antioxidant_enzyme_aoe37-2_mrna,_complete_cds_
 u41387_2693-3263,gu_protein_mrna,_partial_cds
 u56833_940-1468,vhl_binding_protein-1_(vbp-1)_mrna,_partial_cds
 u57627_4598-
 5078,fetal_brain_oculocerebrorenal_syndrome_(ocrl1)_mrna,_complete_cds_
 u65410_961-1459,mad2_(hsmad2)_mrna,_complete_cds_
 u83843_725-1145,hiv-1_nef_interacting_protein_(nip7-
 1)_mrna,_partial_cds/gb=u83843/_ntype=rna
 all_x92396_1999-2480,mrna_for_novel_gene_in_xq28_region
 x94754cds_2213-2645:in_reversesequence,_2712-2730,mrna_for_yeast_methionyl-
 trna_synthetase_homologue
 all_x99585_193-608,mrna_for_smt3b_protein

Metagene 52

hg2841-ht2969_s_at_hg2841-
 ht2969_albumin,_altsplise_3,_missplicing_in_alloalbumin_venezia
 hg3417-ht3600_s_at_hg3417-ht3600_gtp_cyclohydrolase_i,_altsplise_1_
 j05008exon#5_637-1183,endothelin-1_(edn1)_gene,_complete_cds
 u44105_314-574,rab9_expressed_pseudogene_mrna,_complete_cds

all_x04602_920-1086,mrna_for_interleukin_bsf-2_(b-cell_differentiation_factor)_

Metagene 53

k01160mrna_1077-1232,ii_histocompatibility_antigen_dc-alpha_chain_mrna_
m26041_1273-1405,mhc_ii_dq_alpha_mrna,_complete_cds
m63379mrna_1190-1646,trpm-2_protein_gene_
u38810_2191-2659,mab-21_cell_fate-
determining_protein_homolog_(cagr1)_mrna,_complete_cds_

Metagene 54

127213cds_2481-2749:in_reversesequence,_2815-
3030,anion_exchange_protein_mrna,_complete_cds
m29874_2457-2977,cytochrome_p450-iiib_(hiib1)_mrna,_complete_cds
z36714mrna_3697-4135,mrna_for_cyclin_f_

Metagene 55

d13626_1857-2373,mrna_for_kiaa0001_gene,_complete_cds

Metagene 56

ab000467_1590-2118,_clone_res4-25,_partial_cds
d16181exon_1310-1712,pmp2_gene_for_peripheral_myelin_protein_2_
hg4165-ht4435_at_hg4165-ht4435_hpc-1_
l17328_1400-1868,pre-t/nk_cell_associated_protein_(3cl)_mrna,_complete_cds_
l22650_84-636,early_lymphoid_activation_protein_(epag)_mrna_sequence_
m24902mrna_2694-3018,prostatic_acid_phosphatase_mrna,_complete_cds_
m82882_3023-3503,cis-acting_sequence_
s76617_2203-
2569,_blk=protein_tyrosine_kinase_[human,_b_lymphocytes,_mrna,_2608_nt]_
s78467_987-1384,_pig-a-
ii=glycoinositol_phospholipid_anchor_synthetic_element_[human,_paroxysmal_noc
u20350_2697-3045,g_protein-coupled_receptor_v28_mrna,_complete_cds_
u46194_1466-1997,renal_cell_carcinoma_antigen_rage-
4_mrna,_complete_putative_cds_
u66726_2378-
2846,testis_specific_rna_binding_protein_(spgyla)_mrna,_complete_cds,testis_spe
cific_rna
u85265_7-
63,down_syndrome_critical_region(dscr1)_gene,_alternative_exon/gb=u85265_/ntype
=rna_

Metagene 57

all_141913_305-
 502,retinoblastoma_susceptibility_protein_(rb1)_gene,_exon_26,_bases_174145-
 174668_in
 all_x75958_1683-2170,trkb_mrna_for_protein-tyrosine_kinase_

Metagene 58

x02544cds_256-544:in_reversesequence,_688-772,mrna_for_alpha1-
 acid_glycoprotein_(orosomuroid)_
 all_x78932_421-976,hzf9_mrna_for_zinc_finger_protein_

Metagene 59

af001548mrna_6079-
 6385,_815a9.1_gene_(myosin_heavy_chain)_extracted_fromchromosomebac_clone_cit98
 7sk
 d15049_3317-3845,mrna_for_protein_tyrosine_phosphatase_
 l36531mrna_2573-3059,integrin_alphasubunit_mrna,_3'_end
 l41680_1371-1869,alpha-2,8-polysialyltransferase_(pst)_gene,_complete_cds_
 m17316exon_3-249:in_reversesequence,_260-338:not_in_gb_record,gamma-a-
 crystallin_gene_(gamma-g5)_
 m26061mrna_2449-
 2890:not_in_gb_record,cgmp_phosphodiesterase_alpha_subunit_(cgpr-
 a)_mrna,_complete_c
 m73482mrna_757-1279,neuromedin_b_receptor_(nmb-r)_mrna,_complete_cds_
 u43916_147-698,tumor-
 associated_membrane_protein_homolog_(tmp)_mrna,_complete_cds
 u46744_2358-2493,dystrobrevin-alpha_mrna,_complete_cds_
 u94747_838-1276,wd_repeat_protein_han11_mrna,_complete_cds/gb=u94747_/ntype=rna
 all_x74142_1952-2535,hbf-1_mrna_for_transcription_factor_
 y09445cds_1175-1517:in_reversesequence,_2206-
 2368,mrna_for_transcription_factor_tbx5_

Metagene 60

u31382_69-621,g_protein_gamma-4_subunit_mrna,_complete_cds_
 x07820cds_1252-1378:in_reversesequence,_1430-
 1694,mrna_for_metalloproteinase_stromelysin-2
 x14329cds_1050-1350:in_reversesequence,_1569-
 1641,mrna_for_carboxypeptidase_n_small_subunit_(ec_3.4.
 z47043cds_540-
 1080,partial_cdna_sequence,_clone_x529,_unknown_open_reading_frame;/gb=z47043_
 ntype=d

Metagene 61

m31166mrna_1286-1784,tumor_necrosis_factor-inducible_(tsg-
 14)_mrna,_complete_cds_
 u60415_2126-2570,bhlh-pas_protein_jap3_mrna,_complete_cds

u70981_749-1283,interleukin-13_receptor_mrna,_complete_cds_
z83803_7-259,mrna_for_axonemal_dynein_heavy_chain_(partial,_id_hdhc4)

Metagene 62

u07132_1415-1961,steroid_hormone_receptor_ner-i_mrna,_complete_cds_
x99374cds_1846-2174:in_reversesequence,_2211-2318,mrna_for_fertilin_beta

Metagene 63

d55638_227-659,b-cell_pabl_(pseudoautosomal_boundary-
like_sequence)_mrna,_clone_bc4/gb=d55638/_ntype
d78261_1293-
1433,icsat_transcription_factor_mrna,_partial_cds,_similar_to_mouse_pip/lisrf_(
_irf-4)_s
hg1437-ht1437_s_at_hg1437-ht1437_proto-oncogene_trk
hg2825-ht2949_at_hg2825-ht2949_ret_transforming_gene_
hg3570-ht3773_at_hg3570-ht3773_protein_phosphatase_inhibitor_homolog_
hg668-ht4793_at_hg668-ht4793_t-cell_factor_1,_a/b/c,_altsplice_1,_a
j04430mrna_794-1350,tartrate-resistant_acid_phosphatase_typemrna,_complete_cds
l08187_551-1079,cytokine_receptor_(ebi3)_mrna,_complete_cds
l34059_2447-3017,cadherin-4_mrna,_complete_cds
m37984mrna_97-
589,slow_twitch_skeletal_muscle/cardiac_muscle_troponin_c_gene,_complete_cds
m57506mrna_25-481,_scya1_gene_(secreted_protein_i-
309)_extracted_fromsecreted_protein_(i-309)_gene,_
m74089_1911-2271,tb1_gene_mrna,_3'_end_
s77094_1075-
1621,_nicotinic_acetylcholine_receptor_alpha_subunit|achr_alpha_subunit_[human,
_thymic_c
s80050mrna_653-1133,_udp-n-acetylglucosamine:_alpha-6-d-mannoside_beta-1,6-n-
acetylglucosaminyltrans
s82185_419-905,_brag-1=brain-related_apoptosis_gene/bcl-2_homolog_[human,_mg-
107_glioma,_mrna_partia
u00928_611-1151,clone_ce29_4.1_(cac)n/(gtg)n_repeat-containing_mrna
u09412_1619-2045,zinc_finger_protein_znf134_mrna,_complete_cds_
u11878_4-169,interleukin-
8_receptor_type_b_(il8rb)_mrna,_splice_variant_il8rb10,_partial_cds/gb=u118
u12775exon_156-342:not_in_gb_record,agouti_gene
u13022_1572-2124,negative_regulator_of_programmed_cell_death_ich-1s_(ich-
1)_mrna,_complete_cds_
u15306_3076-3466,cysteine-rich_sequence-specific_dna-
binding_protein_nfxl_mrna,_complete_cds_
u18259_6077-6647,clone_ciita-8_mhc_ii_transactivator_ciita_mrna,_complete_cds
u22178_3-
321,prostatic_secretory_protein_57_mrna,_complete_cds/gb=u22178/_ntype=rna
u28488_1344-1847,putative_g_protein-coupled_receptor_(az3b)_mrna,_complete_cds_
u34877_511-997,biliverdin-ixalpha_reductase_mrna,_complete_cds_
u43959_758-815,betaadducin_mrna,_alternatively_spliced_partial_cds
u77129_2447-2975,sps1/ste20_homolog_khs1_mrna,_complete_cds
u79247_1157-1559,clone_23599_mrna_sequence_
u83115_6327-6753,non-lens_beta_gamma-
crystallin_like_protein_(aim1)_mrna,_partial_cds

u85430_3114-3279,transcription_factor_nfatx4_mrna,_complete_cds
 x04327mrna_1084-1564,erythrocyte_2,3-bisphosphoglycerate_mutase_mrna_ec_2.7.5.4
 all_x13255_2280-2725,mrna_for_dopamine_beta-hydroxylase_type_a_(ec_1.14.17.1)
 x15393mrna_19-541,motilin_gene_exon(and_joined_cds)
 x59711cds_626-998:in_reversesequence,_1244-1280,mrna_for_caat-
 box_dna_binding_protein_subunit_a_
 x67337_2825-3365,hpbrii-4_mrna_
 all_x69636_1268-1951,mrna_sequence_(15q11-13)
 all_x78933_1420-1970,hzf10_mrna_for_zinc_finger_protein
 x83441mrna_2724-3102,mrna_for_dna_ligase_iv
 all_x90568_81371-81864,mrna_for_titin_protein_(clone_hh1-hh54)_
 all_x91868_915-1378,mrna_for_six1_protein
 all_x96754_846-1051,gene_encoding_kappa_light_chain_constant_region
 x98206mrna_55-277:in_reversesequence,_307,mrna_for_uv-
 b_repressed_sequence,_hur/gb=x98206_/ntype=rna

Metagene 64

hg2702-ht2798_r_at_hg2702-ht2798_serine/threonine_kinase_
 s79781mrna_31-
 169,_wt1_{antisense_promoter,_intron_1}_[human,_kidney,_genomic,_780_nt]/gb=s79
 781_/nt
 x54162mrna_3362-
 3818,mrna_for_a_64_kd_autoantigen_expressed_in_thyroid_and_extra-ocular_muscle_
 x61118mrna_1457-1955,_ttg-2a_gene_extracted_fromttg-
 2_mrna_for_a_cysteine_rich_protein_with_lim_moti
 y13896_4-
 179,skeletal_muscle_alternate_5'_end_of_gene_kir4.2_5'_utr/gb=y13896_/ntype=rna

Metagene 65

d29642_2294-2582,mrna_for_kiaa0053_gene,_complete_cds
 hg1155-ht4822_at_hg1155-ht4822_colony-
 stimulating_factor_1,_macrophage,_altsplice_3
 hg1996-ht2044_at_hg1996-ht2044_guanine_nucleotide-binding_protein_rap2,_ras-
 oncogene_related_
 hg243-ht243_s_at_hg243-ht243_lowe_oculocerebrorenal_syndrome_protein_
 hg2797-ht2905_at_hg2797-ht2905_clathrin,_light_polypeptide_altsplice_1
 hg4011-ht4804_s_at_hg4011-ht4804_dystrophin-
 associated_glycoprotein,_50_kda,_altsplice_2_
 hg4757-ht5207_s_at_hg4757-ht5207_oncogene_mll-af4,_fusion_activated
 j00268gene_270-1415,insulin_gene_
 l78440mrna_2089-2509,stat4_mrna,_complete_cds_
 m10321mrna_5749-6321,von_willebrand_factor_mrna,_3'_end
 m34455_1427-1889,interferon-gamma-inducible_indoleamine_2,3-
 dioxygenase_(ido)_mrna,_complete_cds_
 m61827mrna_1289-1850,leukosialin_(cd43)_gene,_complete_cds
 m74542_1131-1611,aldehyde_dehydrogenase_type_iii_(aldhiii)_mrna,_complete_cds
 all_u24683_219-474,anti-b_cell_autoantibody_igm_heavy_chain_variable_v-d-
 j_region_(vh4)_gene,_clone_
 u34587_1545-2061,corticotropin-releasing_factor_receptormrna,_complete_cds
 u48861_1914-
 2430,betanicotinic_acetylcholine_receptor_subunit_mrna,_complete_cds

u51096_1240-1720,homeobox_protein_cdx2_mrna,_complete_cds
 all_u58675_25626-39844,_or17-
 228_gene_extracted_fromolfactory_receptor_gene_cluster_on_chromosome_17
 u64315_2269-2832,dna_repair_endonuclease_subunit_(xpf)_mrna,_complete_cds
 u81600_368-734,paired-like_homeodomain_protein_prx-2_mrna,_partial_cds.
 u82010mrna_2432-
 2930,_homo_sapiensheme_a:_farnesyltransferase_(cox10)_gene_promoter_region_and
 x58399mrna_491-903,12-
 9_transcript_of_unrearranged_immunoglobulin_v(h)5_pseudogene.
 x60003mrna_543-965,delta_creb_mrna_for_camp-
 responsive_element_(cre)_binding_protein_
 all_x63359_2216-2781,ugt2bio_mrna_for_udp_glucuronosyltransferase
 x68985cds_482-656,mrna_for_hepatic_leukemia_factor_
 x72882cds_19-103:in_reversesequence,_144-186,14a6ck_dna_sequence
 x74764cds_2202-2538:in_reversesequence,_2903-
 3041,mrna_for_receptor_protein_tyrosine_kinase_
 x75342cds_1407-1767:in_reversesequence,_2095-2239,shb_mrna
 all_x84213_1094-1357,bak_mrna_for_bcl-2_homologue
 x89416cds_1386-1440:in_reversesequence,_1533-
 1932,mrna_for_protein_phosphatase_5_
 x91911cds_321-711:in_reversesequence,_912-950,mrna_for_rtvpr-1_protein_
 x97267mrna_321-861,lpap_gene
 all_x98085_4149-4642,mrna_for_tenascin-r_
 all_x99664_723-1276,mrna_for_protein_containing_sh3_domain,_sh3gl3_
 all_y00796_4559-5109,mrna_for_leukocyte-associated_molecule-
 1_alpha_subunit_(lfa-1_alpha_subunit)
 y08409cds_4-385:in_reversesequence,_431,spot14_gene_
 y08639cds_837-1353:in_reversesequence,_1953-
 2001,mrna_for_transcription_factor_rzrbeta
 y09216_214-736,mrna_for_protein_kinase,_dyrk2
 all_z11697_1190-1701,mrna_for_hb15
 z23115cds_197-677:in_reversesequence,_817-835,bcl-xl_mrna_
 z67743cds_1792-2320:in_reversesequence,_2350,mrna_for_clc-
 7_chloride_channel_protein

Metagene 66

d49824_945-1110,hla-b_null_allele_mrna,hla-b_null_allele_mrna_
 hg862-ht862_s_at_hg862-ht862_transition_protein_
 j04040mrna_563-1016,glucagon_mrna,_complete_cds
 m15881_1752-2310,uromodulin_(tamm-horsfall_glycoprotein)_mrna,_complete_cds
 u77970_2339-2855,neuronal_pas2_(npas2)_mrna,_complete_cds
 x67318cds_851-1229:in_reversesequence,_1260,mrna_for_procarboxypeptidase_a1_

Metagene 67

hg2171-ht2241_at_hg2171-ht2241_12-lipoxygenase_
 m97347_1499-2060,beta-1,6-n-acetylglucosaminyltransferase_mrna,_complete_cds_
 u46116mrna_5907-6477,receptor_tyrosine_phosphatase_gamma_(ptprg)_gene
 all_u83600_202-
 527,death_domain_receptor(DDR3)_mrna,_alternatively_spliced_form_2,_partial_cds
 /gb=u8
 all_x95715_1306-1901,mrna_for_anthracycline_resistance_associated_protein

Metagene 68

d63875_3762-4200,mrna_for_kiaa0155_gene,_complete_cds
 d87002cds#2_4-201:not_in_gb_record,_pom121-
 likegene_extracted_from(lambda)_dna_for_immunoglobulin_ligh
 all_j00277_3607-3724,(genomic_clones_lambda-[sk2-t2,_hs578t]);_cdna_clones_rs-
 [3,4,_6])_c-ha-ras1_pro
 j04810_2923-3414,msh3_gene,_complete_cds_
 m13232mrna_1850-
 2405,factor_vii_serine_protease_precursor_mrna,_complete_cds,_clone_lambda-
 hvii2463
 m34376mrna_2-238,(clone_lambda_msp131)_beta-microseminoprotein_(msp)_gene_
 all_m76732_736-1273,hox7_gene
 s67325_1328-
 1712,_propionyl_coa_carboxylase_beta_subunit_[human,_liver,_placenta,_hl1008,_m
 rna,_1791
 u09196mrna_725-1169,1.1_kb_mrna_upregulated_in_retinoic_acid_treated_hl-
 60_neutrophilic_cells
 u21858_704-1064,transcriptional_activation_factor_tafii32_mrna,_complete_cds_
 u26266_490-1046,deoxyhypusine_synthase_mrna,_complete_cds/gb=u26266_/ntype=rna_
 u31176_1677-2217,herv1_mrna,_complete_cds
 u37221_1537-1981,cyclophilin-like_protein_mrna,_partial_cds
 u43408_2308-2668,tyrosine_kinase_(tnk1)_mrna,_complete_cds_
 u50383_2015-2441,retinoic_acid-responsive_protein_(nn8-4ag)_mrna,_complete_cds_
 u61981_3743-
 3819,putative_mismatch_repair/binding_protein_hmsh3_(hmsh3)_mrna,_complete_cds_
 u66702_4190-4616,phogrin_mrna,_complete_cds
 u83239_323-877,cc_chemokine_stcp-1_mrna,_complete_cds
 all_x52426_1139-1665,mrna_for_cytokeratin_13_
 all_x64643_1944-2407,c6.1a_mrna
 x68733mrna_1056-1488,gene_for_alpha1-antichymotrypsin,_exon_1_
 all_x81836_812-1414,mrna_for_dents_disease_candidate_gene
 x89984cds_465-573:in_reversesequence,_1646-1820,mrna_for_bcl7a_protein
 all_x91648_1082-1611,mrna_for_pur_alpha_extended_3'_untranslated_region
 all_x92106_1361-1932,mrna_for_bleomycin_hydrolase
 x93036cds_88-163:in_reversesequence,_34-37,mrna_for_mat8_protein
 all_x96484_497-1056,mrna_for_dgcr6_protein_
 x97444cds_2-405,mrna_for_transmembrane_protein_tmp21-iiex/gb=x97444_/ntype=rna_
 x98834mrna_4116-
 4620,_zinc_finger_protein_hsal2_gene_extracted_frommrna_for_zinc_finger_protein
 ,_hsa
 z78289_35-153,mrna_(clone_1d2).

Metagene 69

d85759_2398-2701,fetuses,_20-
 26_weeks_brain_mrna_for_mnb_protein_kinase,_complete_cds
 hg2479-ht2575_s_at_hg2479-ht2575_helix-loop-helix_protein_sef2-1d
 l76528exon_146-615,presenilin(ps1;_s182)_gene
 m29551_2520-3054,calcineurin_a2_mrna,_complete_cds_
 m83941_2764-3124,receptor_tyrosine_kinase_(hek)_mrna,_complete_cds_

s77154_1862-2362,_tinur=ngfi-b/nur77_beta-
 type_transcription_factor_homolog_[human,_t_lymphoid_cell
 u17989_3352-3796,nuclear_autoantigen_gs2na_mrna,_complete_cds
 u56244_at_u56244_u56244,not_in_gb_record,hig-1_mrna,_complete_cds_
 u58091_427-883,hs-cul-4b_mrna,_partial_cds_
 u69611_2905-2985,tnf-alpha_converting_enzyme_mrna,_complete_cds
 u72648cds_1037-1354:in_reversesequence,_4177-4210,alpha2-c4-
 adrenergic_receptor_gene,_complete_cds
 u80456_3416-3788,transcription_factor_sim2_long_form_mrna,_complete_cds
 u86755_2390-2735,tnf-alpha_converting_enzyme_mrna,_complete_cds
 all_x79204_10002-10585,sca1_mrna_for_ataxin
 x83573_1377-1803,arse_mrna_
 x84194cds_61-271:in_reversesequence,_501-
 555,mrna_for_acylphosphatase,_erythrocyte_(ct)_isoenzyme_
 x91196mrna#2_3588-4161,mrna_for_e14_and_a-t_proteins/gb=x91196_/ntype=rna

Metagene 70

u02687_2874-3312,growth_factor_receptor_tyrosine_kinase_(stk-
 1)_mrna,_complete_cds_
 u79271_596-1130,clones_23920_and_23921_mrna_sequence_

Metagene 71

ab000220_4588-5134,mrna_for_semaphorin_e,_complete_cds_
 l09749_1019-1463,(clone_f4)_transmembrane_protein_mrna_sequence_
 m87313_793-1335,myotonin_protein_kinase_(dm)_mrna_
 u04520mrna_6221-6641,type_iv_collagen_a5_chain_(col4a5)_gene_
 all_x87904_4159-4670,mrna_for_sep_protein
 z78285_3-137,mrna_(clone_1a7)

Metagene 72

j02986exon#3_1617-
 1983,_fgf4_gene_(transforming_protein)_extracted_fromtransforming_protein_(hst)
 _ge
 m22489_1036-1504,bone_morphogenetic_protein_2a_(bmp-2a)_mrna_
 u63289_1548-2010,rna-binding_protein_cug-bp/hnab50_(nab50)_mrna,_complete_cds

Metagene 73

ab000466_2465-2963,_clone_res4-24c,_exon_1,_2,_3
 aj001487_25-265,mrna_for_transformation-
 sensitive_protein,_3'_utr/gb=aj001487_/ntype=rna
 hg4755-ht5203_s_at_hg4755-ht5203_spinal_muscular_atrophy
 j03260mrna_2076-2576,transducin_alpha-subunit_(gnaz)_mrna,_complete_cds
 all_m20530_85-212,pancreatic_secretory_trypsin_inhibitor_(psti)_gene_
 m59911_4048-4612,integrin_alpha-3_chain_mrna,_complete_cds_

m62400_1400-1928,gamma-aminobutyric_acid_receptor_type_a_rho-1_subunit_(gaba-a_rho-1)_mrna,_complete
 m74826_1928-2396,glutamate_decarboxylase_(gad-2)_mrna,_complete_cds
 all_u01317_19502-63478,_epsilon-globin_gene_extracted_frombeta_globin_region_on_chromosome_11,_epsilon
 u13220_1586-2066,forkhead_protein_freac-2_mrna,_partial_cds
 u54999_1795-2287,lgn_protein_mrna,_complete_cds
 all_x00734_8016-8239,beta-tubulin_gene_(5-beta)_with_ten_alu_family_members
 x65293cds_1670-2180,mrna_for_protein_kinase_c-epsilon
 all_x71348_2835-3436,vhnf1-c_mrna
 all_x76057_1206-1765,pmi1_mrna_for_phosphomannose_isomerase
 all_x98311_1901-2274,mrna_for_carcinoembryonic_antigen,_cgm2_
 z49205mrna_2454-2976,mrna_for_purinergic_receptor

Metagene 74

l21715_127-631,troponin_i_fast-twitch_isoform_mrna,_complete_cds
 l76687mrna_1823-2291,grb14_mrna,_complete_cds_
 y07596cds_1035-1149:in_reversesequence,_1173-1509,mrna_for_gpi8_protein_
 z19574mrna_1039-1479,gene_for_cytokeratin_17

Metagene 75

hg1227-ht1227_s_at_hg1227-ht1227_collagen,_type_ii,_alpha_1
 all_j00116_4597-4806,alpha-1(ii)_collagen_gene_col2a1,_partial_cds_
 m60299exon_73-163,alpha-1
 1_collagen_type_ii_gene,_exons_1,and/gb=m60299/_ntype=dna/_annot=exon
 u14550_1319-1877,sialyltransferase_sthm_(sthm)_mrna,_complete_cds
 u22322_2205-2587,nuclear_tyrosine_protein_kinase_rak_mrna,_complete_cds
 all_x57830_2409-3016,serotonin_5-ht2_receptor_mrna_

Metagene 76

d50310_731-1127,mrna_for_cyclin_i,_complete_cds
 d87735_127-643,mrna_for_ribosomal_protein_l14,_complete_cds
 hg1515-ht1515_f_at_hg1515-ht1515_transcription_factor_bt3b
 hg3117-ht3293_at_hg3117-ht3293_mps1
 hg384-ht384_at_hg384-ht384_ribosomal_protein_l26_
 hg429-ht429_at_hg429-ht429_b-cell_growth_factor_
 hg613-ht613_at_hg613-ht613_ribosomal_protein_s12_
 hg688-ht688_f_at_hg688-ht688_major_histocompatibility_complex,_ii,_dr_beta_2_
 j03459mrna_1459-1855,leukotriene_a-4_hydrolase_mrna,_complete_cds
 l08666_953-1421,porin_(por)_mrna,_complete_cds_and_truncated_cds
 l36870mrna_3077-3533,map_kinase_kinase(mkk4)_mrna,_complete_cds
 m13934cds#2_41-407:in_reversesequence,_5551-
 5557,_rps14_gene_(unknown_protein)_extracted_fromribosom
 m14199_2-381,laminin_receptor_(2h5_epitope)_mrna,_5'_end_
 m17885mrna_532-946,acidic_ribosomal_phosphoprotein_p0_mrna,_complete_cds_
 m26730cds_3-273:in_reversesequence,_99-204,mitochondrial_ubiquinone-
 binding_protein_gene,_5'_flank_w
 m75126_3159-3537,hexokinase(hkl)_mrna,_complete_cds_

m84711_345-831,v-fos_transformation_effector_protein_(fte-1),_mrna_complete_cds
 u12404_111-651,csa-19_mrna,_complete_cds_
 u14970_122-656,ribosomal_protein_s5_mrna,_complete_cds_
 u14972_103-499,ribosomal_protein_s10_mrna,_complete_cds
 u21049cds_61-319:in_reversesequence,_592-760,dd96_mrna,_complete_cds
 u58682_31-313,ribosomal_protein_s28_mrna,_complete_cds_
 u65092_324-774,melanocyte-specific_gene(msg1)_mrna,_complete_cds
 u70323_3897-4401,ataxin-2_(sca2)_mrna,_complete_cds
 u70439_956-1407,silver-stainable_protein_ssp29_mrna,_complete_cds
 v01516cds_713-1044:in_reversesequence,_1070-
 1293,messenger_fragment_encoding_cytoskeletal_keratin_(t
 all_x04347_618-917,liver_mrna_fragment_dna_binding_protein_upi_homologue_(c-
 terminus)
 x12671mrna_1450-
 1726,_hnrnp_a1_protein_gene_extracted_fromgene_for_heterogeneous_nuclear_ribonu
 cleop
 x15940cds_66-348:in_reversesequence,_379-385,mrna_for_ribosomal_protein_l31_
 x16560cds_1-163:in_reversesequence,_13-
 295,cox_viic_gene_for_subunit_viic_of_cytochrome_c_oxidase_(e
 x53777cds_81-435,l23_mrna_for_putative_ribosomal_protein_
 x55733cds_1611-1773:in_reversesequence,_1840-2056,initiation_factor_4b_cdna
 x55954cds_19-385:in_reversesequence,_427-
 433,mrna_for_hl23_ribosomal_protein_homologue
 x62691cds_13-343,mrna_for_ribosomal_protein_(homologuous_to_yeast_s24)_
 x73460cds_725-1133:in_reversesequence,_1211,mrna_for_ribosomal_protein_l3_
 x76013cds_1933-2257:in_reversesequence,_2328-2394,qgrshs_mrna_for_glutaminy1-
 trna_synthetase_
 x80822cds_13-331:in_reversesequence,_56-578,mrna_for_orf
 x80909cds_297-591:in_reversesequence,_694-754,alpha_nac_mrna
 all_y00339_913-1465,mrna_for_carbonic_anhydrase_ii_(ec_4.2.1.1)
 y08915_749-1235,mrna_for_alphaprotein_

Metagene 77

u12767_4598-
 4922,mitogen_induced_nuclear_orphan_receptor_(minor)_mrna,_complete_cds
 u79298_928-1312,clone_23803_mrna,_partial_cds
 x58987mrna_1801-2299,mrna_for_d-1_dopamine_receptor
 all_x97671_31-566,mrna_for_erythropoietin_receptor_

Metagene 78

af005887_1969-
 2413,atf_family_member_atf6_(atf6)_mrna,_complete_cds/gb=af005887_/ntype=rna
 d00860_1546-
 2020,mrna_for_phosphoribosyl_pyrophosphate_synthetase_(ec_2.7.6.1)_subunit_i_
 d13370exon#5_193-637,apx_gene_encoding_apex_nuclease,_complete_cds_
 d50550_3217-3475,llgl_mrna,_complete_cds_
 d85131_1126-1679,mrna_for_myc-associated_zinc-
 finger_protein_ofislet,_complete_cds
 d87989_597-1095,mrna_for_udp-
 galactose_transporter_related_isozyme_1,_complete_cds_
 hg982-ht982_s_at_hg982-ht982_pre-t/nk-cell-associated_protein_1f6

j03263_667-1218,lysosome-associated membrane glycoprotein (lamp_a)_mrna,_complete_cds
 l04282_1873-2329,caccc_box-binding protein_mrna,_complete_cds
 l15189_1520-2081,mitochondrial_hsp75_mrna,_complete_cds.
 l25876_359-785,protein tyrosine phosphatase (cip2)_mrna,_complete_cds
 l43579_6-403,(clone_110298)_mrna/gb=l43579_/ntype=rna,(clone_110298)_mrna/gb=l43579_/ntype=rna
 m24766_1513-2055,(clone_phaiv2-12)_alpha-2_collagen_type_iv (col4a2)_mrna,_3'_end
 m31169cds_2-71,propionyl-coa_carboxylase_beta-subunit_(beta-pcc)_gene,_partial_cds_(mutant_delta-atc
 m34423_1856-2312,beta-galactosidase (glb1)_mrna,_complete_cds
 m36429_827-1412,transducin_beta-2_subunit_mrna,_complete_cds_
 m60891mrna_6-411,uroporphyrinogen decarboxylase (uro-d)_gene,_partial_cds/gb=m60891_/ntype=dna_/anno
 m94250exon#4-5_43-301:not_in_gb_record,retinoic_acid_inducible_factor_(mk)_gene_exons_1-5,_complete_
 u10323_963-1467,nuclear_factor_nf45_mrna,_complete_cds_
 u14417_567-1017,ral_guanine_nucleotide_dissociation_stimulator_mrna,_partial_cds_
 u28963_567-1143,gps2 (gps2)_mrna,_complete_cds_
 u29171_1340-1742,casein_kinase_i_delta_mrna,_complete_cds
 u35835_2404-2859,dna-pk_mrna,_partial_cds
 u47105_616-1174,h105e3_mrna,_complete_cds
 u50553_2647-3079,helicase_like_protein_mrna,_complete_cds
 u61734cds_461-628:in_reversesequence,_710-767,protein_trafficking_protein_(s31111125)_mrna,_complete
 u72935mrna#1_7752-7898,_atrx_gene_(putative_dna_dependent_atpase_and_helicase)_extracted_fromputativ
 u73477_440-885,acidic_nuclear_phosphoprotein_pp32_mrna,_complete_cds_
 u78722_1523-1965,zinc_finger_protein_165_(zpf165)_mrna,_complete_cds
 u81802_2557-3043,ptdins_4-kinase (pi4kb)_mrna,_complete_cds
 x54199mrna_2616-3006:in_reversesequence,_3118,mrna_for_gars-air-s-gart_
 x55448exon#13_150-670,_g6pd_gene_(glucose-6-phosphate_dehydrogenase)_extracted_fromg6pd_gene_for_glu
 x55544cds_350-626:in_reversesequence,_984-1110,cdna_for_treb_protein
 x55885mrna_587-1049,mrna_for_a_presumptive_kdel_receptor_
 x58521cds_1250-1544:in_reversesequence,_1701-1785,mrna_for_p62_nucleoporin
 x66397cds_6605-6977:in_reversesequence,_7352-7442,tpr_mrna
 all_x66503_1125-1690,adenylosuccinate_synthetase_mrna
 all_x78925_1966-2447,hzf2_mrna_for_zinc_finger_protein_
 x90872cds_288-600:in_reversesequence,_799,mrna_for_gp25l2_protein_
 z49107cds_619-947:in_reversesequence,_1046-1259,mrna_for_galectin_
 z54367cds_13580-14031:in_reversesequence,_14140,gene_for_plectin
 z97054cds#2_428-968,dna_sequence_from_pac_339a18_on_chromosome_xp11.2contains_kiaa0178_gene,_similar

Metagene 79

u00802_1922-2463,drebrin_e2_mrna_(dbn1),_complete_cds
 u77594_245-599,tazarotene-induced_gene(tig2)_mrna,_complete_cds_

u86136_8094-8472,telomerase-associated protein_tp-1_mrna,_complete_cds_
x82494mrna_3527-3965,mrna_for_fibulin-2

Metagene 80

hg2479-ht2575_at_hg2479-ht2575_helix-loop-helix_protein_sef2-1d
m55682cds_1132-1467:in_reversesequence,_439-
571, cartilage_matrix_protein_(cmp)_gene_
s77583_4-
66,_hervk10/hummtv_reverse_transcriptase_homolog_{clone_rt244}_[human,_multiple
sclerosis,

Metagene 81

d78335_242-770,mrna_for_5'_-terminal_region_of_umk,_complete_cds_
hg2724-ht2820_at_hg2724-ht2820_oncogene_tls/chop,_fusion_activated_
l09234_2517-3075,vacuolar_atpase_(isoform_ho68)_mrna,_complete_cds_
all_x02751_1835-2430,n-ras_mrna_and_flanking_regions_

Metagene 82

ab000460_4262-4724,_clone_res4-22b,_complete_cds
af007551_16-
574,bet1p_homolog_(hbet1)_mrna,_complete_cds/gb=af007551_/ntype=rna_
d12763_882-1314,mrna_for_st2_protein_
d21337_5825-6353,mrna_for_collagen_
d31797exon_752-1274,cd40_ligand_(cd40l)_gene,_5'_flanking_region_and_
d84276_909-1185:in_reversesequence,_1299-1305,mrna_for_cd38,_complete_cds_
d87024cds#5_85-283:in_reversesequence,_2475-
39492,(lambda)_dna_for_immunoglobulin_light_chain_
d87119_3614-4160,cancellous_bone_osteoblast_mrna_for_gs3955,_complete_cds
l14542_664-982,lectin-like_type_ii_integral_membrane_protein_(nkg2-
e)_mrna,_complete_cds_
l32140_1681-2227,afamin_mrna,_complete_cds_
l41870_4412-
4814,retinoblastoma_susceptibility_protein_(rb1)_mrna_and_mutations_
m27394cds_459-860:in_reversesequence,_1054-1101,b-lymphocyte_cell-
surface_antigen_b1_(cd20)_
m77698_1764-2310,gli-kruppel_related_protein_(yy1)_mrna,_complete_cds_
u03105_1538-1916,b4-2_protein_mrna,_complete_cds_
u41344mrna_1478-1988,prolargin_(prelp)_gene,_5'_flanking_sequence_and
u73499mrna_29-200,hepatic_nuclear_factor_1-alpha_(tcf-1-
alpha)_gene,_promoter_region_and_partial_cds
x51804cds_400-532:in_reversesequence,_820-
1162,pmi_gene_for_a_putative_receptor_protein_
y10204mrna_49-505,mrna_for_cd77_protein/gb=y10204_/ntype=rna_

Metagene 83

d90224_2791-3319,mrna_for_glycoprotein_34_(gp34)_
hg415-ht415_at_hg415-ht415_lectin,_galactoside-binding,_soluble,_2_
k03204mrna_582-1130,prb1_locus_salivary_proline-
rich_protein_mrna,_clone_cp3,_complete_cds_
m14758mrna#1_4264-4561,p-glycoprotein_(mdr1)_mrna,_complete_cds_
m36653_1448-1663,2-oct_factor_mrna,_complete_cds_
m64231mrna_1264-1624,spermidine_synthase_gene,_complete_cds_
m64358exon_16-189,rhom-3_gene,_exon/gb=m64358_/ntype=dna_/annot=exon_
all_u67368_952-1411,multiple_exostosis(ext2)_gene_
all_x16105_1077-1226,mrna_for_rd_protein,_rna-binding
x58255mrna_2472-2862,flg-2_gene_for_fibroblast_growth_factor_receptor
all_x67235_1087-1595,mrna_for_proline_rich_homeobox_(prh)_protein
y10209mrna_79-331,mrna_for_cd30l_protein/gb=y10209_/ntype=rna
all_z70723_1812-2239,mrna_for_serum_arylalkylphosphatase

Metagene 84

d28589mrna_281-743,mrna_(kiaa00167),_partial_sequence/gb=d28589_/ntype=rna_
d79991_5181-5613,mrna_for_kiaa0169_gene,_partial_cds_
l11573_1101-1665,surfactant_protein_b_mrna,_complete_cds/gb=l11573_/ntype=rna_
u79528_1038-1577,sr31747_binding_proteinmrna,_complete_cds

Metagene 85

d38553_2125-2665,mrna_for_kiaa0074_gene,_partial_cds_
d78367_1372-1810,mrna_for_k12_keratin,_complete_cds_
j03133_2096-2612,transcription_factor_spl_mrna,_3'_end_
l06895_503-
977,antagonizer_of_myc_transcriptional_activity_(mad)_mrna,_complete_cds_
l41816mrna_891-1389,cam_kinase_i_mrna,_complete_cds_
s78085_719-1187,_pdcd2=programmed_cell_death-
2/rp8_homolog_[human,_fetal_lung,_mrna,_1282_ntl]
all_u66083_2217-
2758,contig_of_two_cosmids_from_llnl_x_chromosome_library_(u83f1,_u109h10),_inc
ludin
u89916_375-879,putative_osp_like_protein_mrna,_partial_cds
all_x62048_1820-2343,wee1_hu_gene

Metagene 86

d12485_2904-3444,mrna_for_nucleotide_pyrophosphatase,_complete_cds_
d42123_655-1135,mrna_for_esp1/crp2,_complete_cds_
d63479_5529-6079,mrna_for_kiaa0145_gene,_complete_cds_
m16938_1154-1659,homeo_box_c8_protein,_mrna,_complete_cds_
m59815mrna_5022-5424,complement_component_c4a_gene_
m63167_2039-2429,rac_protein_kinase_alpha_mrna,_complete_cds_
u24266_2533-3103,pyrroline-5-
carboxylate_dehydrogenase_(p5cdh)_mrna,_long_form,_complete_cds_
u33147_43-463,mammaglobin_mrna,_complete_cds_
u68142_1372-1900,ralgds-like(rgl2)_mrna,_partial_cds
u83411_1505-2039,carboxypeptidase_z_precursor,_mrna,_complete_cds.

u94592_1287-1809,uncoupling_protein_homolog_(ucph)_mrna,_complete_cds
all_x78706_1878-2443,mrna_for_carnitine_acetyltransferase

Metagene 87

j05070_1805-2303,type_iv_collagenase_mrna,_complete_cds
u22028utr#1_47-
168:in_reversesequence,_8031,cytochrome_p450_(cyp2a13)_gene,_complete_cds,cytoc
hrome_
u77968_1294-1879,neuronal_pas1_(npas1)_mrna,_complete_cds
x87767exon_4-148,cd89_gene,_exon_s1/gb=x87767_/ntype=dna_/annot=exon_

Metagene 88

d13640_4563-5091,mrna_for_kiaa0015_gene,_complete_cds
hg2414-ht2510_s_at_hg2414-ht2510_prostaglandin_receptor_ep1_subtype
hg3236-ht3413_f_at_hg3236-ht3413_neurofibromatosis_tumor_suppressor
hg3342-ht3519_s_at_hg3342-ht3519_id1_
j03801_911-1418,lysozyme_mrna,_complete_cds_with_an_alu_repeat_in_the_3'_flank_
all_100389_1196-1792,cytochrome_p-450gene_
m11058mrna_2351-2879,3-hydroxy-3-
methylglutaryl_coenzyme_a_reductase_mrna,_complete_cds
m19045_907-1414,lysozyme_mrna,_complete_cds
all_m31551_576-1134,urokinase_inhibitor_(pai-2)_gene_
m31667_f_at_m31667_m31667_4040_in_all_m31667_1679-
2265,cytochrome_p450_(cyp1a2)_gene_
u32576mrna_19-535,apolipoprotein_apoc-iv_(apoc4)_gene,_complete_cds_
u33267_1613-2081,glycine_receptor_beta_subunit_(glrb)_mrna,_complete_cds_
u50361_16-319,calcium,_calmodulin-
dependent_protein_kinase_ii_delta_mrna,_partial_cds/gb=u50361_/nty
u60269cds#2_171-429,endogenous_retrovirus_herv-
k(hml6)_proviral_clone_hml6.17_putative_polymerase_an
u72507mrna_855-1341,40871_mrna_partial_sequence
x14008mrna_926-1433,lysozyme_gene_(ec_3.2.1.17)_
all_x51417_1050-1651,mrna_for_steroid_hormone_receptor_herr2_
y10207mrna_61-475,mrna_for_cd171_protein/gb=y10207_/ntype=rna

Metagene 89

hg2139-ht2208_f_at_hg2139-ht2208_beta-1-glycoprotein_1,_pregnancy-specific_
m22403exon#2_1749-2224,blood_platelet_membrane_glycoprotein_ib-
alpha_(gpib)_gene,_complete_cds,_clon
u31201_cds1_at_u31201_u31201,not_in_gb_record,laminin_gamma2_chain_gene_(lamc2)
,laminin_gamma2_chain
u73167cds#4_1050-1254:in_reversesequence,_13521-
13767:not_in_gb_record,_h_luca14.2a_gene_extracted_f
x58288mrna_4517-4955,hr-ptpu_gene_for_protein_tyrosine_phosphatase_
all_x66276_3221-3734,mrna_for_skeletal_muscle_c-protein

Metagene 90

m16653mrna_652-742,pancreatic_elastase_iib_mrna,_complete_cds
s83513_1328-
1840,_pituitary_adenylate_cyclase_activating_polypeptide_[human,_mrna,_1940_nt]
_u08049exon_19-475,peripheral_myelin_protein-22_(pmp22)_gene,_non-
coding_exon_1a/gb=u08049_/ntype=dna
u24056_1237-1787,inward_rectifier_k+_channel_protein_(hirk2)_mrna,_complete_cds
u43885_1914-2442,grb2-associated_binder-1_mrna,_complete_cds_
z49105mrna_1064-1259,hd21_mrna_

Metagene 91

d50402_1972-2533,mrna_for_nramp1,_complete_cds_
d64159_2585-2828,mrna
m98399_1688-2165,antigen_cd36_(clone_21)_mrna,_complete_cds
u29343_2203-2731,hyaluronan_receptor_(rhamm)_mrna,_complete_cds
u52960_186-630,rna_polymerase_ii_complex_component_srb7_mrna,_complete_cds_
all_x82835_5995-6350,mrna_for_voltage-activated_sodium_channel_

Metagene 92

d14826_834-1163,mrna_for_hcrem_(cyclic_amp-
responsive_element_modulator)_typeprotein,_complete_cds
hg2591-ht2687_s_at_hg2591-ht2687_transcription_factor_itf-1
u13696cds_2138-2563:in_reversesequence,_2600-
2669,homolog_of_yeast_mutl_(hpms2)_gene,_complete_cds
u60269cds#3_237-447:in_reversesequence,_1593-1737,endogenous_retrovirus_herv-
k(hml6)_proviral_clone_
x84740mrna_2847-3309,mrna_for_dna_ligase_iii_
y10275cds_363-633:in_reversesequence,_880-1060,mrna_for_l-3-
phosphoserine_phosphatase_

Metagene 93

d85423_133-439,mrna_for_cdc5,_partial_cds/gb=d85423_/ntype=rna_
u23070_938-1460,putative_transmembrane_protein_(nma)_mrna,_complete_cds
all_x52001_1770-2281,endothelinmrna_
x83863cds_1151-1241,mrna_for_prostaglandin_e_receptor_(ep3f)_
z34822_f_at_z34822_z34822,_4040_in_z34822_6145-6595,(hlcc85)_mrna_for_voltage-
dependent_l-type_ca_ch

Metagene 94

u66581cds_963-1275:in_reversesequence,_1547-1745,putative_g_protein-
coupled_receptor_(gpr22)_gene,_c
u73799_34-265,dynactin_mrna,_partial_cds/gb=u73799_/ntype=rna

u88892_31-241,tenascin-c_mrna,_splice_variant_tncfn-
ad2,_partial_cds/gb=u88892_/ntype=rna
all_x73501_11784-13955,gene_for_cytokeratin_20_
x97249cds_1720-2230,mrna_for_leucine-rich_primary_response_protein_1_
all_x97261_25-
333,mrna_for_metallothionein_isoform_1r,mrna_for_metallothionein_isoform_1r_
all_z32684_4621-5042,xk_mrna_for_membrane_transport_protein

Metagene 95

d13630_2433-2919,mrna_for_kiaa0005_gene,_complete_cds
d14530_55-403,homolog_of_yeast_ribosomal_protein_s28,_complete_cds_
d14658_859-1285,mrna_for_kiaa0102_gene,_complete_cds_
d21090_2298-2868,mrna_for_xp-
c_repair_complementing_protein_(p58/hhr23b),_complete_cds_
d25218_1125-1575,mrna_for_kiaa0112_gene,_partial_cds_
d43948_6033-6549,mrna_for_kiaa0097_gene,_complete_cds_
d45248_389-773,mrna_for_proteasome_activator_hpa28_subunit_beta,_complete_cds_
d50663_235-625,mrna_for_tctel1_gene,_complete_cds_
d61380_258-762,mrna_for_dj-1_protein,_complete_cds_
d63480_2623-3187,mrna_for_kiaa0146_gene,_partial_cds_
d76444mrna_2828-3362,hkf-1_mrna,_complete_cds_
d80005_4364-4862,mrna_for_kiaa0183_gene,_partial_cds_
d87076_5065-5581,mrna_for_kiaa0239_gene,_partial_cds_
d87440_3807-4245,mrna_for_kiaa0252_gene,_partial_cds_
d87466_3602-4124,mrna_for_kiaa0276_gene,_partial_cds_
d87470_6278-6794,mrna_for_kiaa0280_gene,_partial_cds_
d88378_2857-3157,mrna_for_proteasome_inhibitor_hpi31_subunit,_complete_cds_
d90086exon#10_9-
489:not_in_gb_record,pyruvate_dehydrogenase_(ec_1.2.4.1)_beta_subunit_gene,_exo
ns_10
j04543_1215-1725,synexin_mrna,_complete_cds
j04615mrna_833-
1265,lupus_autoantigen_(small_nuclear_ribonucleoprotein,_snrnp,_sm-
d)_mrna,_complete
all_j04982_4001-
5444,heart/skeletal_muscle_atp/adp_translocator_(ant1)_gene,_complete_cds
l06132_1325-1721,voltage-
dependent_anion_channel_isoform(vdac)_mrna,_complete_cds_
l10284_3582-
4038,integral_membrane_protein,_calnexin,(ip90)_mrna,_complete_cds_
l13977_1675-2017,prolylcarboxypeptidase_mrna,_complete_cds_
l19527_31-415,ribosomal_protein_l27_(rpl27)_mrna,_complete_cds_
l32977mrna_680-
1124,(clone_f17252)_ubiquinol_cytochrome_c_reductase_rieske_iron-
sulphur_protein_(uqc
all_m12783_3467-3780,c-sis/platelet-
derived_growth_factor(sis/pdgf2)_mrna,_complete_cds_
all_m19645_4941-5470,78_kdalton_glucose-
regulated_protein_(grp78)_gene,_complete_cds_
m21259_at_m21259_m21259,not_in_gb_record,alu_repeats_in_the_region_5'_to_the_sm
all_nuclear_ribonucle
m22760_142-586,nuclear-
encoded_mitochondrial_cytochrome_c_oxidase_va_subunit_mrna,_complete_cds_
m23613_701-1217,nucleophosmin_mrna,_complete_cds_

all_m32405_2395-2832:in_m32405cds_316-
 347,homologue_of_rat_insulinoma_gene_(rig),_exons_4-jan_
 m80335_574-886,protein_kinase_a_catalytic_subunit_mrna,_3'_end
 m86667_1037-1517,nap_(nucleosome_assembly_protein)_mrna,_complete_cds
 m93036mrna_987-1353:in_reversesequence,_527-545,(clone_21726)_carcinoma-
 associated_antigen_ga733-2_(
 u07231_2329-2647,g-rich_sequence_factor-1_(grsf-1)_mrna,_complete_cds
 u07857_173-677,_humankda_alu_rna_binding_protein_mrna,_complete_cds_
 u09813mrna_225-
 765,mitochondrial_atp_synthase_subunit_9,_p3_gene_copy,_mrna,_nuclear_gene_enco
 ding_m
 u12595_1663-
 2083,tumor_necrosis_factor_typerereceptor_associated_protein_(trap1)_mrna,_partia
 l_cds
 u18062_1678-2152,tfiid_subunit_tafii55_(tafii55)_mrna,_complete_cds
 u44772_1738-2176,palmitoyl_protein_thioesterase_mrna,_complete_cds_
 u50733_1132-1642,dynamin_mrna,_complete_cds
 u58089_1599-1941,hs-cul-3_mrna,_partial_cds
 u62800_181-535,cystatin_m_(cst6)_mrna,_complete_cds
 u66879_394-928,bcl-2_binding_component(bbc6)_mrna,_complete_cds.
 x02317cds_251-371:in_reversesequence,_531-
 831,mrna_for_cu/zn_superoxide_dismutase_(sod)
 all_x52979_759-
 895:not_in_gb_record,_smb_protein_gene_extracted_fromgene_for_small_nuclear_rib
 onucle
 x56468mrna_1303-1789,mrna_for_14.3.3_protein,_a_protein_kinase_regulator_
 x59417cds_319-709:in_reversesequence,_813-861,pros-27_mrna
 all_x75252_1083-1408,phosphatidylethanolamine_binding_protein_mrna_
 all_x91809_980-1533,mrna_for_gaip_protein
 z50749cds_689-1055:in_reversesequence,_1088-1274,sds22-like_mrna

Metagene 96

hg2668-ht2764_at_hg2668-ht2764_bradykinin_receptor_
 u58032_1007-
 1322,myotubularin_related_protein(mtmr1)_gene,_partial_cds/gb=u58032/_ntype=dna
 _/annot=c
 u89012_2087-2639,dentin_matrix_acidic_phosphoprotein(dmp1)_mrna,_complete_cds

Metagene 97

l11244mrna_545-1049,(clone_a12)_c4b-binding_protein_beta-
 chain_mrna,_complete_cds
 all_m29458_440-1017,carbonic_anhydrase_iii_gene
 m57731mrna_617-1032,gro-beta_mrna,_complete_cds
 m90657_581-1163,tumor_antigen_(l6)_mrna,_complete_cds

Metagene 98

ab002559_1302-1746,mrna_for_hunc18b2,_complete_cds_

af006087_237-777, arp2/3_protein_complex_subunit_p20-
 arc(arc20)_mrna,_complete_cds/gb=af006087/_ntyp
 d10511cds_860-1256:in_reversesequence,_165-
 243, gene_for_mitochondrial_acetoacetyl-coa_thiolase
 d26308_241-691, mrna_for_nadph-flavin_reductase,_complete_cds_
 d26598_187-571, mrna_for_proteasome_subunit_hsc10-ii,_complete_cds_
 d31764_1478-1982, mrna_for_kiaa0064_gene,_complete_cds_
 d38047_327-825, mrna_for_26s_proteasome_subunit_p31,_complete_cds_
 d38751_1539-1868: not_in_gb_record, mrna_for_kid_(kinesin-
 like_dna_binding_protein),_complete_cds_
 d43947_6379-6901, mrna_for_kiaa0100_gene,_complete_cds_
 d50645_502-1006, mrna_for_sdf2,_complete_cds_
 d85433_109-439, murr1_mrna,_sequence/gb=d85433/_ntype=rna_
 hg3638-ht3849_s_at_hg3638-
 ht3849_amyloid_beta_(a4)_precursor_protein,_altssplice_2,_a4(751)_
 j04444cds_596-944:in_reversesequence,_3590-3740, cytochrome_c-
 1_gene,_complete_cds_
 l20320cds_605-
 953:in_reversesequence,_1218, protein_serine/threonine_kinase_stk1_mrna,_complet
 e_cds_
 l37042mrna_960-1314, casein_kinase_i_alpha_isoform_(csnk1a1)_mrna,_complete_cds_
 l40410mrna_296-803, thyroid_receptor_interactor_(trip3)_mrna,_3'_end_of_cds_
 l41559mrna_61-475, pterin-4a-
 carbinolamine_dehydratase_(pcbd)_mrna,_complete_cds_
 m15661mrna_3-338, ribosomal_protein_mrna,_complete_cds_
 m19483cds_1127-1559:in_reversesequence,_2162-
 2204, atp_synthase_beta_subunit_gene
 m29971_282-750, 6-o-methylguanine-
 dna_methyltransferase_(mgmt)_mrna,_complete_cds_
 m55153_2794-3232, transglutaminase_(tgase)_mrna,_complete_cds_
 u34343_110-560, 13kd_differentiation-
 associated_protein_mrna,_partial_cds/gb=u34343/_ntype=rna_
 u43923_888-1410, transcription_factor_supt4h_mrna,_complete_cds_
 u65093_466-838, msg1-related_gene(mrg1)_mrna,_complete_cds_
 u79262_878-1007, deoxyhypusine_synthase_mrna,_complete_cds_
 u79718_532-1012, endonuclease_iii_homolog(octs3)_mrna,_complete_cds_
 all_x90857_2739-3184, mrna_for_-14_gene,_containing_globin_regulatory_element_
 x94910_333-861: not_in_gb_record, mrna_for_erp31_protein
 y08766cds_1803-1893:in_reversesequence,_2190-
 2239, mrna_for_splicing_factor,_sf1-bo_isoform
 y12478_210-750, mrna_for_chd5_protein_

Metagene 99

ac002450cds_13-535, bac_clone_gs244b22_from_7q21-
 q22,_complete_sequence/gb=ac002450/_ntype=dna/_annot
 af006041_300-762, fas-
 binding_protein_(daxx)_mrna,_partial_cds/gb=af006041/_ntype=rna_
 d80006_4068-4596, mrna_for_kiaa0184_gene,_partial_cds_
 d83779_4499-4967, mrna_for_kiaa0195_gene,_complete_cds_
 hg4310-ht4580_at_hg4310-ht4580_cellular_retinol_binding_protein_ii_
 j04501_3032-3482, muscle_glycogen_synthase_mrna,_complete_cds_
 j04513mrna_6156-
 6714, basic_fibroblast_growth_factor_(bfgf)_22.5_kd,_21_kd_andkd_protein_mrna,_c
 omple

m16276mrna_1281-1569,mhc_ii_hla-dr2-dw12_mrna_dqw1-beta,_complete_cds
 m74099_4835-5327,displacement_protein_(ccaat)_mrna_
 m97388_786-1332,tata_binding_protein-
 associated_phosphoprotein_(dr1)_mrna,_complete_cds
 s77575_11-
 59,_erv9_reverse_transcriptase_homolog_{clone_rt11}_{human,_multiple_sclerosis,
 _brain_plaq
 u75679_1214-1622,histone_stem-loop_binding_protein_(slbp)_mrna,_complete_cds_
 u91616_1484-1988,i_kappa_b_epsilon_(ikbe)_mrna,_complete_cds_
 all_x54925_1537-1904,mrna_for_type_i_interstitial_collagenase
 all_x73882_2585-3120,e-map-115_mrna

Metagene 100

d28423_53-100,mrna_for_pre-
 mrna_splicing_factor_srp20,_5'_utr_(sequence_from_the_5'_cap_to_the_start
 all_d89377_1587-2173,mrna_for_msx-2,_complete_cds,mrna_for_msx-2,_complete_cds
 l13943_1963-2019,glycerol_kinase_(gk)_mrna_exons_1-4,_complete_cds_
 m37197mrna_2687-3065,ccaat-box-binding_factor_(cbf)_mrna,_complete_cds_
 m68520_1708-2170,cdc2-related_protein_kinase_mrna,_complete_cds
 s67970_962-
 1538,_znf75=krab_zinc_finger_[human,_lung_fibroblast,_mrna,_1563_nt]_
 s70585mrna_138-612,_thyroid-
 stimulating_hormone_alpha_subunit_[human,_genomic,_1327_ntsegments]_
 s82471_77-298,_ssx3=kruppel-
 associated_box_containing_ssx_gene_[human,_testis,_mrna_partial,_675_nt]
 u04209_1396-1834,associated_microfibrillar_protein_mrna,_complete_cds
 u12978_1713-2247,sperm_membrane_protein_bs-84_(hsd-1)_mrna,_partial_cds
 u15555_1003-1489,serine_palmitoyltransferase_(lcb2)_mrna,_partial_cds
 u18271_cds1_at_u18271_u18271,not_in_gb_record,thymopoietin_(tmpo)_gene,thymopoi
 etin_(tmpo)_gene
 u39226_6864-7440,myosin_viiia_(ush1b)_mrna,_complete_cds
 u43843_813-1374,h-neuro-d4_protein_mrna,_complete_cds
 u82321_1608-2112,clone_14.9b_mrna_sequence_
 all_x59618_1970-2475,rr2_mrna_for_small_subunit_ribonucleotide_reductase_
 x98482mrna_2-
 46,tnnt2_gene_exon/gb=x98482_/ntype=dna_/annot=mrna,tnnt2_gene_exon/gb=x98482_/
 ntype=dn

Metagene 101

d13814_960-1532,mrna_for_angiotensin_ii_type_1b_receptor,_complete_cds_
 m63175_1221-1689,autocrine_motility_factor_receptor_mrna_
 u22029_1690-2227,cytochrome_p450_(cyp2a7)_mrna,_complete_cds_
 x13930cds_1147-1454:in_reversesequence,_1650-1695,cyp2a4_mrna_for_p-
 450_iia4_protein
 x63187mrna_91-511,he4_mrna_for_extracellular_proteinase_inhibitor_homologue

Metagene 102

d25215_4320-4839,mrna_for_kiaa0032_gene,_complete_cds

d86974_5077-5308,mrna_for_kiaa0220_gene,_partial_cds_
hg3123-ht3299_at_hg3123-ht3299_homeotic_protein_gbx2_
l20861_3555-4089,proto-oncogene_(wnt-5a)_mrna,_complete_cds_
l29339mrna_1862-2324,na+/glucose_co-transporter_(sglt1)_gene
m91083mrna_989-1469,dna-binding_protein_(hrc1)_mrna,_complete_cds
m96684_609-867,pur_(pur-alpha)_mrna,_complete_cds
s90469_1802-
2300,_cytochrome_p450_reductase_[human,_placenta,_mrna_partial,_2403_nt]
u05237_2192-2570,fetal_alz-50-reactive_clone(fac1)_mrna,_complete_cds_
u13896_2487-3015,homolog_of_drosophila_discs_large_protein,_isoform(hdlg-
2)_mrna,_complete_cds
u47054_853-1357,putative_mono-adv-
ribosyltransferase_(htmart)_mrna,_complete_cds_
u50327mrna_1463-2020,protein_kinase_c_substrate_80k-h_gene_(prkcsh)
u66615_4601-5165,swi/snf_complex_155_kda_subunit_(baf155)_mrna,_complete_cds_
u79288_1035-1509,clone_23682_mrna_sequence_
all_x69878_3909-4372,flt4_mrna_for_transmembrane_tyrosine_kinase_
all_x83618_1574-1995,mrna_for_3-hydroxy-3-methylglutaryl_coenzyme_a_synthase_
x96506cds_96-441:in_reversesequence,_600-631,mrna_for_nc2_alpha_subunit_

Metagene 103

u59877_295-750,low-mr_gtp-binding_protein_(rab31)_mrna,_complete_cds_
x51441cds_28-
65:in_reversesequence,_228,mrna_for_serum_amyloid_a_(saa)_protein_partial,_clon
e_pas3-a
all_x52075_5011-5273,gene_for_sialophorin_(cd43)
all_z11559_2897-3480,mrna_for_iron_regulatory_factor_
all_z29331_1560-1981,(23k/3)_mrna_for_ubiquitin-conjugating_enzyme_ubch2_

Metagene 104

d78611_1893-2331,mest_mrna,_complete_cds_
l01406_1010-1562,growth_hormone-releasing_hormone_receptor_mrna,_complete_cds
m20919cds_478-568:in_reversesequence,_899-
927,dna_with_a_hepatitis_b_virus_surface_antigen_(hbsag)_g

Metagene 105

u38276_2969-3509,semaphorin_iii_family_homolog_mrna,_complete_cds
all_x17093_3834-4023,hla-f_gene_forleukocyte_antigen_f
all_x59798_3705-4192,prad1_mrna_for_cyclin_

Metagene 106

hg2007-ht2056_s_at_hg2007-ht2056_proto-oncogene_sno,_altspllice_n_

Metagene 107

d00591exon#14_597-1041,rccl_gene,_complete_cds_
d28114_780-1278,mrna_for_mobp_(myelin-
associated_oligodendrocytic_basic_protein),_complete_cds,_clon
d50532_839-1283,mrna_for_macrophage_lectin_2,_complete_cds_
d56495_1102-1600,mrna_for_reg-related_sequence_derived_peptide-2_
l21993_1527-2013,adenylyl_cyclase_mrna,_3'_end_of_cds
m32313mrna_1537-2047,steroid_5-alpha-reductase_mrna,_complete_cds
all_z46788_1637-2082,mrna_for_cylicin_ii_

Metagene 108

ab003102_956-1442,mrna_for_proteasome_subunit_p44.5,_complete_cds
d14659_648-1134,mrna_for_kiaa0103_gene,_complete_cds_
d21260_5600-6002,mrna_for_kiaa0034_gene,_complete_cds
d31885_1773-2169,mrna_for_kiaa0069_gene,_partial_cds_
d38551_3082-3592,mrna_for_kiaa0078_gene,_complete_cds
d38555_3911-4421,mrna_for_kiaa0079_gene,_complete_cds
d64142mrna_625-1177,mrna_for_histone_h1x,_complete_cds_
d78129_568-
1024,adult_(34_year_old)_male_liver_mrna_for_squalene_epoxidase,_partial_cds/gb
=d78129_/n
d85429exon#3_813-1347,dna_for_heat_shock_protein_40,_complete_cds
d86972_4190-4610,mrna_for_kiaa0218_gene,_complete_cds
d87120_1936-2314,cancellous_bone_osteoblast_mrna_for_gs3786,_complete_cds
hg2788-ht2896_at_hg2788-ht2896_calcyclin_
hg2874-ht3018_at_hg2874-ht3018_ribosomal_protein_l39_homolog_
l09604_339-819,differentiation-dependent_a4_protein_mrna,_complete_cds
l19779_7-496,histone_h2a.2_mrna,_complete_cds_
l38928mrna_274-832,5,10-methenyltetrahydrofolate_synthetase_mrna,_complete_cds
l42542mrna_3353-3803,rlip76_protein_mrna,_complete_cds_
m31642mrna_802-
1288,hypoxanthine_phosphoribosyltransferase_(hprt)_mrna,_complete_cds_
m58460_1311-1490,75-kd_autoantigen_(pm-scl)_mrna,_complete_cds_
all_m59830_2432-2661,mhc_iii_hsp70-2_gene_(hla),_complete_cds
m60922_1971-2427,surface_antigen_mrna,_complete_cds
all_m90516_2559-3058,glutamine:fructose-6-
phosphate_amidotransferase_(gfat)_mrna,_complete_cds_
u76992_2137-2533,tat-sf1_mrna,_complete_cds
x55079mrna_3257-3366:not_in_gb_record,gaa_gene_extracted_fromlysosomal_alpha-
glucosidase_gene_exon_
x57985mrna#1_1652-
2168,gl105_gene_(histone_h2b)_extracted_fromgenes_for_histones_h2b.1_and_h2a_
y07867cds_643-787:in_reversesequence,_1087-1237,mrna_for_pirin,_isolate_1_

Metagene 109

hg1327-ht1327_s_at_hg1327-ht1327_statherin_
hg2723-ht2819_at_hg2723-ht2819_proto-oncogene_n-cym
hg3971-ht4241_at_hg3971-ht4241_transcription_factor
hg4332-ht4602_at_hg4332-ht4602_zinc_finger_protein_znfpt1
l07949_1619-2075,gnrh_receptor_mrna,_complete_cds_

m11722_1473-2037,terminal_transferase_mrna,_complete_cds_
 m13143_1762-
 2224,_nucleotide_sequence_of_the_cdna_insert_of_lambda_pk129_coding_forplasma_p
 rekallikr
 m83363_4104-4614,plasma_membrane_calcium-
 pumping_atpase_(pmca4)_mrna,_complete_cds_
 s69369_779-
 1115,_pax3a=transcription_factor_[human,_adult_cerebellum,_mrna,_1248_nt]
 s69965_171-597,_beta-synuclein_[human,_brain,_mrna,_730_nt]
 u83117_1201-1477,sentrin_mrna,_complete_cds
 all_x64594_1290-1855,mrna_for_50_kda_erythrocyte_plasma_membrane_glycoprotein

Metagene 110

d13705_1151-1722,mrna_for_fatty_acids_omega-hydroxylase_(cytochrome_p-
 450hkv),_complete_cds
 d16105_2703-2979,mrna_for_leukocyte_tyrosine_kinase,_complete_cds
 d83017_2365-2810,mrna_for_nel-related_protein,_complete_cds
 hg2255-ht2344_f_at_hg2255-
 ht2344_phosphoribosyl_pyrophosphate_synthetase,_subunit_iii
 hg2797-ht2906_s_at_hg2797-ht2906_clathrin,_light_polypeptide_altsplice_2
 k03192_566-964,cytochrome_p-450_mrna,_partial
 m13058exon#3_1-372,acidic_proline-rich_protein_(prh2)_gene,_complete_cds_
 m13149_1540-2008,histidine-rich_glycoprotein_mrna,_complete_cds
 all_m29335_62-94,mhc_ii_do-alpha_mrna,_partial_cds,mhc_ii_do-
 alpha_mrna,_partial_cds
 all_m32879_690-1129,steroid_11-beta-hydroxylase_(cyp11b1)_gene,steroid_11-beta-
 hydroxylase_(cyp11b1)
 m33772mrna_69-631,fast_skeletal_muscle_troponin_c_gene_
 m55513mrna_2274-2767,potassium_channel_(hpcn1)_mrna,_complete_cds
 m62303_726-872,retinoic_acid_receptor-
 beta_associated_open_reading_frame,_complete_sequence
 m64269cds_389-718:in_reversesequence,_7859-
 7876,mast_cell_chymase_gene,_complete_cds
 m74587mrna_953-1425,insulin-
 like_growth_factor_binding_protein_(higfbp1)_gene,_complete_cds_
 m83652_932-1457,complement_component_properdin_mrna,_complete_cds_
 s77576_3-
 60,_erv9_reverse_transcriptase_homolog_{clone_rt18}_[human,_multiple_sclerosis,
 _brain_plaqu
 u05012_2204-2720,receptor_tyrosine_kinase_trkc_(ntrk3)_mrna,_complete_cds
 u11862_1844-2402,clone_hp-dao1_diamine_oxidase,_copper/topa_quinone-
 containing_mrna,_complete_cds
 u12140_3433-3673,tyrosine_kinase_receptor_p145trk-b_(trk-b)_mrna,_complete_cds_
 u23850_8177-8697,inositol_1,4,5_trisphosphate_receptor_typemrna,_partial_cds
 u24488_2519-3042,tenascin-x_(xa)_mrna,_complete_cds
 u25771_1383-1821,adp-ribosylation_factor_mrna,_complete_cds
 u52373_1810-2355,serine/threonine_kinase_mnb_(mnb)_mrna,_complete_cds
 u57623exon#1-4_51-
 240:in_reversesequence,_6798,fatty_acid_binding_protein_fabp_gene,_complete_cds
 _
 u80034_1785-
 2283,mitochondrial_intermediate_peptidase_precursor_(mipep)_mrna,_mitochondrial
 _gene_enc
 u81599_751-1273,homeodomain_protein_hoxb13_mrna,_complete_cds

u86214_1736-2000,fas-associated_death_domain_protein_interleukin-1b-
 converting_enzymemrna,_complete_
 u88898_561-757,endogenous_retroviral_h_protease/integrase-
 derived_orf1_mrna,_complete_cds,_and_putat
 all_x07618_880-1388,mrna_for_cytochrome_p450_db1_variant_a_
 all_x07730_1535-1680,mrna_for_prostate_specific_antigen
 all_x14253_1410-2003,mrna_for_cripto_protein_
 all_x66867_1864-2066:in_x66867cds#2_310,_max_gene_extracted_frommax_gene_
 x94628mrna_952-1510,mecp-2_gene_
 x99688_3790-4270,mrna_from_tyl_gene
 all_y08613_599-1164,alternative_3'_utr_of_nup88_mrna/gb=y08613_/ntype=rna
 z35227cds_385-547:in_reversesequence,_1162-1318,ttf_mrna_for_small_g_protein

Metagene 111

d14694_2143-2455,mrna_for_kiaa0024_gene,_complete_cds
 d21261_957-1305,mrna_for_kiaa0120_gene,_complete_cds_
 d25328_2086-2536,mrna_for_platelet-type_phosphofructokinase,_complete_cds
 d26599_167-707,mrna_for_proteasome_subunit_hsc7-i,_complete_cds
 d26600_354-822,mrna_for_proteasome_subunit_hsn3,_complete_cds
 d31890_1375-1909,mrna_for_kiaa0070_gene,_partial_cds_
 d38521_5541-5997,mrna_for_kiaa0077_gene,_partial_cds_
 d38550_3195-3735,mrna_for_kiaa0075_gene,_partial_cds_
 d38583_109-475,mrna_for_calgizzarin,_complete_cds
 d43642mrna_759-1215,yl-1_mrna_for_yl-1_protein_(nuclear_protein_with_dna-
 binding_ability),_complete_
 d49489_1267-1759,mrna_for_protein_disulfide_isomerase-
 related_protein_p5,_complete_cds_
 d50916_5465-5999,mrna_for_kiaa0126_gene,_complete_cds
 d80009_3652-4048,mrna_for_kiaa0187_gene,_complete_cds
 d80012_2697-3237,mrna_for_kiaa0190_gene,_partial_cds_
 d86978_5648-6086,mrna_for_kiaa0225_gene,_partial_cds_
 d87953_2449-2935,mrna_for_rtp,_complete_cds
 hg2259-ht2348_s_at_hg2259-ht2348_tubulin,_alpha_1,_isoform_44
 hg3494-ht3688_at_hg3494-ht3688_nuclear_factor_nf-il6_
 hg4541-ht4946_s_at_hg4541-ht4946_transformation-related_protein
 j03827_970-1438,_y_box_binding_protein-1_(yb-1)_mrna
 l08246_3333-3819,myeloid_cell_differentiation_protein_(mcl1)_mrna
 l17131mrna#1_1646-2198,high_mobility_group_protein_(hmg-i(y))_gene_exons_1-
 8,_complete_cds
 l19871_1361-1793,activating_transcription_factor(atf3)_mrna,_complete_cds_
 l20298_2250-2790,transcription_factor_(cbfb)_mrna,_3'_end_
 l39059mrna_3327-3831,transcription_factor_sl1_mrna,_complete_cds
 l77886_5390-5696,protein_tyrosine_phosphatase_mrna,_complete_cds_
 m14328mrna_1144-1704,alpha_enolase_mrna,_complete_cds
 m23254_2672-3164,ca2-
 activated_neutral_protease_large_subunit_(canp)_mrna,_complete_cds
 m31303mrna_933-1407,oncoprotein(op18)_gene,_complete_cds
 m37721_3297-3705,peptidylglycine_alpha-
 amidating_monooxygenase_mrna,_complete_cds
 m69066_3272-3824,moesin_mrna,_complete_cds_
 m83088_1722-2271,phosphoglucomutase(pgm1)_mrna,_complete_cds
 u24105_4121-4355,coatmer_protein_(hepcop)_mrna,_complete_cds
 u26173_1295-1775,bzip_protein_nf-il3a_(il3bp1)_mrna,_complete_cds
 u28368_841-1249,id-related_helix-loop-helix_protein_id4_mrna,_complete_cds_

u46692mrna_84-480,cystatin_b_gene,_complete_cds_
u51711_at_u51711_u51711,not_in_gb_record,desmocollin-2_mrna,_3'_utr_
u58334_3933-
4485,bcl2,_p53_binding_protein_bbp/53bp2_(bbp/53bp2)_mrna,_complete_cds
u90651_1122-
1576,embryonic_ectoderm_development_protein_homolog_(eed)_mrna,_partial_cds
all_v00572_1364-1731,mrna_encoding_phosphoglycerate_kinase_
all_x07834_515-1026,mrna_for_manganese_superoxide_dismutase_(ec_1.15.1.1)
x53416cds_7595-7889:in_reversesequence,_8097-8319,mrna_for_actin-
binding_protein_(filamin)_(abp-280)
all_x54941_194-687,ckshs1_mrna_for_cks1_protein_homologue
all_x54942_31-572,ckshs2_mrna_for_cks1_protein_homologue_
all_x76534_2145-2614,nmb_mrna
x86018cds_1630-1822:in_reversesequence,_1834-2062,mrna_for_mufl_protein

Metagene 112

j04621mrna_2879-3347,heparan_sulfate_proteoglycan_(hspg)_core_protein,_3'_end
all_m27749_245-348,immunoglobulin-
related_14.1_protein_mrna,_complete_cds,immunoglobulin-related_14.
all_x51730_4462-5003,mrna_and_promoter_dna_for_progesterone_receptor_

Metagene 113

110102mrna#1_392-794,sex-determining_region_y_(sry)_gene,_complete_cds_
134081mrna_1055-1601,bile_acid_coa:_amino_acid_n-
acyltransferase_mrna,_complete_cds
m34353_6763-7342,transmembrane_tyrosine-
specific_protein_kinase_(ros1)_mrna,_complete_cds
m61156_1122-1308,activator_protein_2b_(ap-2b)_mrna,_complete_cds_
m95767_1065-1563,di-n-acetylchitobiase_mrna,_complete_cds_
all_x02956_1039-1253,interferon_alpha_gene_ifn-alpha_5_
all_x07994_5703-6244,mrna_for_lactase-phlorizin_hydrolase_lph_(ec_3.2.1.23-62)_
x68994exon_4-55,creb_gene,_exon_y
all_x78686_706-1121,ena-78_mrna
all_x95239_863-1362,mrna_for_cysteine-rich_secretory_protein-2/type_i
y10508mrna_370-660,mrna_for_cd190_protein/gb=y10508_/ntype=rna_

Metagene 114

hg3928-ht4198_s_at_hg3928-ht4198_surfacant_protein_sp-a1_delta_
105597cds_729-1071:in_reversesequence,_1307-
1499,serotonin_receptor_gene,_complete_cds
u76189_49-355,extl3_mrna,_partial_cds/gb=u76189_/ntype=rna_

Metagene 115

all_m16441_2260-
 2855, lymphotoxin_gene_extracted_fromtumor_necrosis_factor_and_lymphotoxin_gene
 s,_co

Metagene 116

d63412_1299-1713,mrna_for_aquaporin,_complete_cds
 hg2981-ht3938_s_at_hg2981-ht3938_epican,_altsplise_12
 u61849_4650-5040,neuronal_pentraxin(nptx1)_mrna,_complete_cds_

Metagene 117

all_m21642_180-
 301,(dysfunctional)_antithrombin_iii_(atiii)_utah_gene,(dysfunctional)_antithro
 mbin_i
 m83772_1565-2015,flavin-
 containing_monooxygenase_form_ii_(fmo2)_mrna,_complete_cds_
 y07829exon#1_7-
 283,_exon_fromgene_encoding_ring_finger_protein/gb=y07829_/ntype=dna_/annot=exo
 n,_exo

Metagene 118

d12620_1535-1965,mrna_for_cytochrome_p-450ltbv_
 d38522_3436-3958,mrna_for_kiaa0080_gene,_partial_cds_
 d63861exon#10_90-656,dna_for_cyclophilin_40,_complete_cds
 hg831-ht831_at_hg831-ht831_potassium_channel_
 j02883mrna_55-493,colipase_mrna,_complete_cds
 l40393mrna_1754-2222,(clone_s171)_mrna,_complete_cds
 m94172_6837-7328,n-type_calcium_channel_alpha-1_subunit_mrna,_complete_cds_
 u05589_877-1453,ribosomal_protein_s1_homolog_mrna,_partial_cds_
 u08854_1612-
 2040,udp_glucuronosyltransferase_precursor_(ugt2b15)_mrna,_complete_cds
 u16954_1099-1579,(af1q)_mrna,_complete_cds_
 u17327_6523-7081,neuronal_nitric_oxide_synthase_(nos1)_mrna,_complete_cds
 u35637_8831-9367,nebulin_mrna,_partial_cds/gb=u35637_/ntype=rna
 u47926_1546-1996,unknown_protein_b_mrna,_complete_cds
 u90546_1301-
 1344,butyrophilin_(btf4)_mrna,_complete_cds,butyrophilin_(btf4)_mrna,_complete_
 cds
 x02158mrna_949-1219,gene_for_erythropoietin_
 all_x06562_3951-4396,mrna_for_growth_hormone_receptor
 x14474cds_669-710,mrna_for_microtubule-associated_tau_protein
 all_x86400_560-1155,mrna_for_gamma_subunit_of_sodium_potassium_atpase
 all_x98176_772-1022,mrna_for_mach-beta-1_protein/gb=x98176_/ntype=rna
 z69030cds_838-1186,mrna_for_gammaisofrom_of_61kda_regulatory_subunit_of_pp2a

Metagene 119

d00003_1681-1981,liver_cytochrome_p-450_mrna,_complete_cds,liver_cytochrome_p-450_mrna,_complete_cds
 m74047_1878-2316,steroid_5-alpha-reductase(srd5a2)_mrna,_complete_cds_
 s53911_2110-
 2584,_cd34=glycoprotein_expressed_in_lymphohematopoietic_progenitor_cells_{alte
 rnatively
 u42360mrna_867-1346,n33_gene
 x54867mrna_783-1293,mrna_for_nkg2-a_gene_
 x65663cds_83-137,sox-6_mrna/gb=x65663_/ntype=rna_
 y11174cds_48-
 516:in_reversesequence,_600,mrna_for_rp3_gene/gb=y11174_/ntype=rna_

Metagene 120

121998_15275-15677,intestinal_mucin_(muc2)_mrna,_complete_cds
 126234mrna_298-
 796,apolipoprotein_b_mrna_editing_enzyme,_catalytic_polypeptide(apobec1)_mrna,_
 comple
 m55905_1340-
 1820,mitochondrial_nad(p)+_dependent_malic_enzyme_mrna,_complete_cds_
 m96956_2590-2639,(clone_cr-3)_teratocarcinoma-
 derived_growth_factor(tdgf3)_mrna,_complete_cds_
 u00952_488-998,clone_a9a2brb7_(cac)n/(gtg)n_repeat-containing_mrna_
 u01062mrna_8334-8778,typeinositol_1,4,5-
 trisphosphate_receptor_(itpr3)_mrna,_complete_cds_
 u17418_1591-2071,parathyroid_hormone/parathyroid_hormone-
 related_peptide_receptor_mrna,_complete_cds
 u31099_13-469,dp_prostanoid_receptor_(ptgdr)_mrna,_partial_cds.
 u33838_2-188,nf-kappa-
 b_p65delta3_mrna,_spliced_transcript_lacking_exonsand_7,_partial_cds/gb=u33838
 u40622_999-1449,xrcc4_mrna,_complete_cds_
 u40705_2127-2625,telomeric_repeat_binding_factor_(trf1)_mrna,_complete_cds
 u66561_2158-2614,kruppel-related_zinc_finger_protein_(znf184)_mrna,_partial_cds
 u90313_212-758,glutathione-s-transferase_homolog_mrna,_complete_cds
 u94333_2877-3429,clq/mb1/spa_receptor_clqr(p)_mrna,_complete_cds.
 x89576_1772-2255,mrna_for_putative_mt4-mmp_protein_
 z19002cds_1508-1994:in_reversesequence,_2075-
 2081,of_plzf_gene_encoding_kruppel-like_zinc_finger_pro

Metagene 121

d00749exon_346-525,t_cell_surface_antigen_cd7_gene_
 hg1877-ht1917_s_at_hg1877-ht1917_myelin_basic_protein,_altsplice_form_4
 hg4126-ht4396_at_hg4126-ht4396_zinc_finger_protein_hzf4
 m97287_2345-2885,mar/sar_dna_binding_protein_(satb1)_mrna,_complete_cds
 x98178cds_567-607,mrna_for_mach-beta-4_protein/gb=x98178_/ntype=rna
 y07755exon#2-3_16-204,s100a2_gene,_exon_1,and_3_
 z30426_at_z30426_z30426,not_in_gb_record,gene_for_early_lymphocyte_activation_a
 ntigen_cd69,_exon_1

Metagene 122

af000234_1038-1578,p2x_purinoceptor_mrna,_complete_cds
 d79989_3469-3919,mrna_for_kiaa0167_gene,_complete_cds
 d87463_2511-2997,mrna_for_kiaa0273_gene,_complete_cds
 hg1071-ht1071_at_hg1071-ht1071_bone_morphogenetic_protein_
 hg2028-ht2082_at_hg2028-ht2082_laminin,_a_polypeptide
 hg3790-ht4060_at_hg3790-ht4060_immunoglobulin_heavy_chain,_fd_fragment_
 hg884-ht884_s_at_hg884-ht884_oncogene_e6-ap,_papillomavirus
 j04605mrna_1389-1833,prolidase_(imidodipeptidase)_mrna,_complete_cds_
 l05425_1712-2162,autoantigen_mrna,_complete_cds_
 l13258_2109-2463,renal_na/pi-cotransporter_mrna,_complete_cds_
 l20316_1565-2003,glucagon_receptor_mrna,_complete_cds
 l40387cds_31-
 433,thyroid_receptor_interactor_(trip14)_gene,_3'_end_of_cds/gb=l40387_/ntype=d
 na_/anno
 l40395mrna_861-1395,(clone_s20iii15)_mrna,_3'_end_of_cds
 m21985_1548-2004,steroid_receptor_tr2_mrna,_complete_cds_
 m24461exon#11_528-780,pulmonary_surfactant-associated_protein_sp-
 b_(sftp3)_mrna,_complete_cds
 m32373mrna_2201-2753,arylsulfatase_b_(asb)_mrna,_complete_cds
 m33374mrna_19-427,cell_adhesion_protein_(sqm1)_mrna,_complete_cds
 m34667_3969-4305,phospholipase_c-gamma_mrna,_complete_cds
 m35416mrna_864-1302,gtp-binding_protein_(ralb)_mrna,_complete_cds
 m62958_2486-2942,retinal_degradation_slow_(rds)_mrna_
 m64497_1307-1559,apolipoprotein_ai_regulatory_protein_(arp-
 1)_mrna,_complete_cds_
 m65214_492-997,(hela)_helix-loop-helix_protein_he47_(e2a)_mrna,_3'_end_
 m76125_2612-3170,tyrosine_kinase_receptor_(axl)_mrna,_complete_cds_
 m77144mrna_1332-1630,_3-beta-
 hydroxysteroid_dehydrogenase_gene_extracted_fromtype_ii_3-beta_hydroxys
 m91463mrna_2634-3168,glucose_transporter_(glut4)_gene,_complete_cds_
 s69189_2575-3007,_peroxisomal_acyl-
 coenzyme_a_oxidase_[human,liver,mrna,3086_nt]_
 s76965_1718-2066,_protein_kinase_inhibitor_[human,neuroblastoma_cell_line_sh-
 sy-5y,mrna,2147_nt]_
 s77361_25-
 184,_transcript_ch132_[human,rf1,rf48_stomach_cancer_cell_lines,mrna,216_nt]
 /gb=s77361_
 u04840_3088-3646,onconeural_ventral_antigen-1_(nova-1)_mrna,_complete_cds
 u09414_1994-2462,zinc_finger_protein_znf137_mrna,_complete_cds_
 u16282_2336-2744,ell_mrna,_complete_cds
 u17163_1086-1644,transcription_factor_etv1_mrna,_complete_cds
 u21551_728-1076,eca39_mrna,_complete_cds/gb=u21551_/ntype=rna
 u28749_3491-4033,high-mobility_group_phosphoprotein_isoform_i-
 c_(hmgic)_mrna,_complete_cds_
 u32519_1294-1708,gap_sh3_binding_protein_mrna,_complete_cds
 u60060_1090-1540,fez1_mrna,_complete_cds_
 u64520_308-650,synaptobrevin-3_mrna,_complete_cds
 u87459_331-703,autoimmunogenic_cancer/testis_antigen_ny-eso-
 1_mrna,_complete_cds_
 u93553_1729-2251,alpha1-
 fetoprotein_transcription_factor_(hftf)_mrna,_complete_cds.
 x15376mrna_1216-1684,mrna_for_gaba-a_receptor,_gammasubunit_
 all_x51405_1974-2413,mrna_for_carboxypeptidase_e_(ec_3.4.17.10)
 all_x51435_8408-8982,prdii-bf1_gene_for_a_dna-binding_protein
 x56411mrna_1990-
 2470,adh4_gene_for_ii_alcohol_dehydrogenase_(pi_subunit),_exon_1

x56465cds_1607-
 2069:in_reversesequence,_3400,znf6_mrna_for_zinc_finger_transcription_factor_
 x59065exon_2834-3254,fgf_gene,_exon_3
 all_x63097_2195-2670,mrna_for_rhesus_polypeptide_(rhxiil)
 all_x64624_2881-3429,mrna_for_rdc-1_pou_domain_containing_protein
 y10659cds_1011-1239:in_reversesequence,_1342-1552,il-13ra_mrna
 all_z18956_3398-3951,mrna_for_taurine_transporter

Metagene 123

d90064_1806-2184,cgm6_mrna_for_cd66b_(nca-95)
 m87507_751-1177:in_reversesequence,_1012-1130,_homo_sapien_interleukin-
 1_beta_convertase_(il1bce)_mr
 m91556_4785-5343,voltage-gated_sodium_channel_mrna,_complete_cds.
 u82275_1335-1647,immunoglobulin-like_transcriptmrna,_complete_cds_
 x15675mrna_1522-1840,ptr7_mrna_for_repetitive_sequence/gb=x15675_/ntype=rna

Metagene 124

all_x00038_599-718,h4_histone_gene_

Metagene 125

d14827_1564-1966,mrna_for_tax_helper_protein_1,_complete_cds_
 all_d26561_2433-
 3022,_orf_for_l1_protein_gene_extracted_frompapillomavirus_5b_genome_integrated
 _into
 l34060_2124-2502,cadherin-8_mrna,_complete_cds
 m94167_1894-2326,heregulin-beta2_gene,_complete_cds
 s83390_2318-2865,_t3_receptor-associating_cofactor-
 1_[human,_fetal_liver,_mrna,_2930_nt]
 u03398_1069-1576,receptor_4-1bb_ligand_mrna,_complete_cds
 u52152_2642-
 3020,inwardly_rectifying_potassium_channel_kir3.3_mrna,_complete_cds_
 u64871cds_870-1212:in_reversesequence,_1665-1773,putative_g_protein-
 coupled_receptor_(gpr19)_gene,_c
 u95626mrna#2_1641-
 2133,_ccr2_gene_(ccr2a)_extracted_fromccr2b_(ccr2),_ccr2a_(ccr2),_ccr5_(ccr5)_a
 nd_
 x77094cds_634-994:in_reversesequence,_1136-1214,mrna_for_p40phox

Metagene 126

d38437_37-604,dna_mismatch_repair_mrna_
 hg1604-ht1604_at_hg1604-ht1604_adrenergic,_beta,_receptor_kinase_2_
 hg651-ht5209_s_at_hg651-ht5209_adducin,_alpha_subunit,_altsplice_3_
 j03915_1313-1721,chromogranin_a_mrna,_complete_cds_
 k03183cds_2-326,chorionic_gonadotropin_beta_subunit_gene_

s75256_32-
 446, hnl=neutrophil_lipocalin_[human, ovarian_cancer_cell_line_oc6, mrna_partia
 l, 534_nt]/
 u08989_1383-1857, glutamate_transporter_mrna, complete_cds
 u17280_1004-
 1562, steroidogenic_acute_regulatory_protein_(star)_mrna, complete_cds
 all_u21689_2955-3116, glutathione_s-transferase-plc_gene, complete_cds
 u31973_2396-2914, phosphodiesterase_a'_subunit_(pde6c)_mrna, complete_cds_
 u33822_2053-2563, tax1-binding_protein_txbp181_mrna, complete_cds_
 u40372_1565-
 2021, 3', 5' cyclic_nucleotide_phosphodiesterase_(hspde1c3a)_mrna, partial_cds
 all_u73167_4971-
 35099, h_luca14.2a_gene_extracted_fromcosmid_luca14, h_luca14.2a_gene_extracted
 from
 all_x07496_2066-2268, tangier_apoa-i_gene_
 x58964cds_2500-2914, gene_for_mhc_ii_regulatory_factor_rfx
 x85178_267-627, surf-5_mrna_
 x98258cds_481-619:in_reversesequence, 625-829, mrna_for_m-
 phase_phosphoprotein, mpp9
 x99479_f_at_x99479_x99479, 40_in_x99479cds_951-
 1047: 30_in_reversesequence, 1065-1461, mrna_for_nk_re

Metagene 127

124470_1905-2403, prostanoid_fp_receptor_mrna, complete_cds
 all_m36089_2244-2797, dna-repair_protein_(xrccl)_mrna, complete_cds_
 m74161_2469-2991, inositol_polyphosphate_5-phosphatase_(5ptase)_mrna, 3'_end
 s57235_1085-
 1664, cd68=110kda_transmembrane_glycoprotein_[human, promonocyte_cell_line_u937
 , mrna, 1
 u48231exon#2_1478-2015, bradykinin_b1_receptor_(bdkrb1)_gene, first_
 x51630mrna_2403-2955:in_reversesequence, 2961-
 2979, wilms_tumor_wt1_mrna_for_zinc_finger_protein, kru
 x98261cds_121-352:in_reversesequence, 388-583, mrna_for_m-
 phase_phosphoprotein, mpp5_

Metagene 128

d31765_3735-4191, mrna_for_kiaa0061_gene, partial_cds_
 d84239_15949-16339, mrna_for_igg_fc_binding_protein, complete_cds_
 hg36-ht4101_s_at_hg36-ht4101_polymyositis/scleroderma_(pm-
 scl)_autoantigen, altssplice_2
 l10665mrna_1623-2049, gtp-binding_protein_superfamily, g_protein_alpha-
 olf_subunit_(olfactory)_mrna, _
 l13203_1536-2064, hnf-3/fork-head_homolog-3_hfh-3_mrna, complete_cds
 l34075_7342-7912, fkbp-rapamycin_associated_protein_(frap)_mrna, complete_cds_
 all_m10942_421-1762, metallothionein-ie_gene_(hmt-ie)_
 m21389mrna_1754-2192, keratin_type_ii_(58_kd)_mrna, complete_cds
 m21812_61-592, (clone_pwhlc2-24)_myosin_light_chainmrna, complete_cds
 m57399_434-998, nerve_growth_factor_(hbnf-1)_mrna, complete_cds_
 m96803_6960-7482, general_beta-spectrin_(sptbn1)_mrna, complete_cds_
 u06863_1416-1938, follistatin-related_protein_precursor_mrna, complete_cds
 u08815_2346-2676, splicesomal_protein_(sap_61)_mrna, complete_cds_

Metagene 129

108010exon#6_94-211:not_in_gb_record,reg_gene_homologue,_complete_cds
 l32831exon_463-1036,g_protein-coupled_receptor_(gpr3)_gene,_complete_cds
 m19888_58-580,small_proline_rich_protein_(spri)_mrna,_clone_128
 m19989_cds1_at_m19989_m19989,not_in_gb_record,platelet-
 derived_growth_factor_(pdgfa)_a_chain_gene,pl
 all_m59216_1586-2163:in_m59216cds_1091,gamma-aminobutyric_acid-a_(gaba-
 a)_receptor_beta-1_subunit_
 u58681cds_807-1116:in_reversesequence,_1191-
 1434:not_in_gb_record,neurogenic_basic-helix-loop-helix_
 all_x63337_548-1101,hb2a_gene_for_high_sulfur_keratin
 z29572cds_52-322:in_reversesequence,_95-605,antisense_mrna_for_bcma_peptide
 z48511exon#4_572-1148,xg_mrna_(clone_pep11)

Metagene 130

ab002315_4819-5347,mrna_for_kiaa0317_gene,_complete_cds/gb=ab002315_/ntype=rna_
 ab002382_4858-5320,mrna_for_kiaa0384_gene,_complete_cds/gb=ab002382_/ntype=rna_
 ac002115mrna#2_3349-
 7559:not_in_gb_record,_cox6b_gene_(coxg)_extracted_fromdna_from_overlapping_chr
 o
 af002020_4090-4600,niemann-
 pick_c_disease_protein_(npc1)_mrna,_complete_cds/gb=af002020_/ntype=rna
 d14657_355-775,mrna_for_kiaa0101_gene,_complete_cds
 d25248_4510-5050,randomly_sequenced_mrna_
 d25304_4431-4701,mrna_for_kiaa0006_gene,_partial_cds_
 d25547_779-864,mrna_for_pimt_isozyme_i,_complete_cds_
 d28476_5899-6385,mrna_for_kiaa0045_gene,_complete_cds
 d55716_1952-2378,mrna_for_plcdc47,_complete_cds
 d63876_3171-3717,mrna_for_kiaa0154_gene,_partial_cds_
 d79998_3100-3562,mrna_for_kiaa0176_gene,_partial_cds_
 d83004_644-1148,epidermoid_carcinoma_mrna_for_ubiquitin-
 conjugating_enzyme_e2_similar_to_drosophila_
 d83785_5214-5634,mrna_for_kiaa0200_gene,_complete_cds
 d85181_1502-2018,mrna_for_fungal_sterol-c5-desaturase_homolog,_complete_cds
 d86550_5888-6338,mrna_for_serine/threonine_protein_kinase,_complete_cds
 d87451_2622-3162,mrna_for_kiaa0262_gene,_complete_cds
 d87969_1206-1686,mrna_for_cmp-sialic_acid_transporter,_complete_cds
 hg2492-ht2588_at_hg2492-ht2588_glutamate_receptor_subunit
 hg4557-ht4962_at_hg4557-ht4962_small_nuclear_ribonucleoprotein_u1,_lsnrp_
 l07758_1288-1762,ief_ssp_9502_mrna,_complete_cds_
 l13738mrna_4076-4490,activated_p21cdc42hs_kinase_(ack)_mrna,_complete_cds
 all_119314_3362-3789,hry_gene,_complete_cds
 l20859_2655-3159,leukemia_virus_receptor(glvrl1)_mrna,_complete_cds
 l21936_1796-
 2222,succinate_dehydrogenase_flavoprotein_subunit_(sdh)_mrna,_complete_cds_
 l27706_1445-1985,chaperonin_protein_(tcp20)_gene_complete_cds
 l34600_1958-2426,nuclear-
 encoded_mitochondrial_initiation_factor_mrna,_complete_cds
 all_m22877_1917-2434,somatic_cytochrome_c_(hcs)_gene,_complete_cds_
 m29960mrna_1721-2141,steroid_receptor_(tr2-11)_mrna,_complete_cds

m31932mrna_1771-
 2341,igg_low_affinity_fc_fragment_receptor_(fcrla)_mrna,_complete_cds_
 m32011mrna_1623-2157,neutrophil_oxidase_factor_(p67-phox)_mrna,_complete_cds_
 m33336_2441-3005,camp-dependent_protein_kinase_type_i-
 alpha_subunit_(prkar1a)_mrna,_complete_cds_
 m75715_1635-2185,tb3-1_mrna,_complete_cds
 u07559_1832-2366,isl-1_(islet-1)_mrna,_complete_cds
 u11872_36-72,interleukin-
 8_receptor_type_b_(il8rb)_mrna,_splice_variant_il8rb1,_partial_cds/gb=u1187
 u15642_975-1472,transcription_factor_e2f-5_mrna,_complete_cds
 u47927_2598-3132,isopectidase_t_(isot)_mrna,_complete_cds
 u48296_1629-
 2175,protein_tyrosine_phosphatase_ptpcaax1_(hptpcaax1)_mrna,_complete_cds
 u52154_2352-2610,g_protein-
 coupled_inwardly_rectifying_potassium_channel_kir3.4_mrna,_complete_cds_
 u63541mrna_431-977,mrna_expressed_in_hc/hcc_livers_and_molt-
 4_proliferating_cells,_partial_sequence
 u77456_2006-2414,nucleosome_assembly_proteinmrna,_complete_cds
 u84720_1431-1611,mrna_export_protein_rael_(rael)_mrna,_complete_cds
 u89336exon#34-35_35-
 87: not_in_gb_record,_unknown_gene_extracted_fromhla_iii_region_containing_notch
 4
 u94832_2732-2958,kh_type_splicing_regulatory_protein_ksrp_mrna,_complete_cds.
 u94836_3450-3894,erprot_213-21_mrna,_complete_cds
 all_x06272_2379-
 2854,mrna_for_docking_protein_(signal_recognition_particle_receptor)_
 all_x17567_432-1018,rna_for_snrnp_protein_b
 all_x63741_3695-4230,pilot_mrna
 x66113cds_2199-2633:in_reversesequence,_2682-
 2729,mrna_for_pm/scl_100kd_nucleolar_protein
 all_x67155_2735-3228,mrna_for_mitotic_kinesin-like_protein-1_
 all_x79888_965-1500,auh_mrna_
 x87613cds_1996-2236:in_reversesequence,_2780-
 2912,mrna_for_skeletal_muscle_abundant_protein_
 all_x95632_1680-1784,mrna_for_arg_protein_tyrosine_kinase-binding_protein
 y07707_1136-1634,mrna_for_itba4_gene/gb=y07707_/ntype=rna
 z84721cds#1_81-390:in_reversesequence,_15248-
 15488,dna_sequence_from_cosmid_gg1_from_a_contig_from_t
 reverse_z86000_20444-20634,dna_sequence_from_pac_151b14_on_chromosome_22q12-
 qter_contains_somatostat

Metagene 131

112723_1781-2360,heat_shock_protein_70_(hsp70)_mrna,_complete_cds
 114922_4053-4395,dna-binding_protein_(po-ga)_mrna,_complete_cds_
 138932mrna_1076-1466,gt197_partial_orf_mrna,_3'_end_of_cds
 m27891exon_13-58:in_reversesequence,_145-
 370: not_in_gb_record,cystatin_c_(cst3)_gene_
 m81057_749-1223,procarboxypeptidase_b_mrna,_complete_cds_
 s69272_853-
 1403,_cytoplasmic_antiproteinase=38_kda_intracellular_serine_proteinase_inhibit
 or_[human,
 u14603_937-1483,protein-tyrosine_phosphatase_(hu-pp-1)_mrna,_partial_sequence
 u46689_3317-3863,microsomal_aldehyde_dehydrogenase_(ald10)_mrna,_complete_cds
 u84388_905-1055,death_domain_containing_protein_cradd_mrna,_complete_cds_

all_x65724_1307-1746,dna_for_orf1_and_orf2_from_chromosome_x_
 x84002cds_210-456:in_reversesequence,_706-
 862,tafii20_mrna_for_transcription_factor_tfiid_
 z19585cds_2522-2858:in_reversesequence,_2909-2939,mrna_for_thrombospondin-4_
 z49878cds_367-565:in_reversesequence,_734-968,mrna_for_guanidinoacetate_n-
 methyltransferase_
 z84718mrna#1_424-982,dna_sequence_from_bac_322b1_on_chromosome_22q11.2-
 qter_contains_gstt1,_gstt2_gl

Metagene 132

d37781_4150-4705,mrna_for_protein-tyrosine_phosphatase_hptpeta,_complete_cds_
 j00209mrna_366-878,leukocyte_interferon_(ifn-alpha)_alpha-c_mrna,complete_cds_
 m90696_1168-1738,cathepsin_s_(ctss)_mrna,_complete_cds_
 u03735exon#3_970-1517,mage-3_antigen_(mage-3)_gene,_complete_cds_

Metagene 133

all_d00726_1842-2413,mrna_for_ferrochelatase_(ec_4.99.1.1)_
 d16217_1904-2414,mrna_for_calpastatin,_complete_cds_
 d63390_600-1164,mrna_for_acetylhydrolase_ib_beta-subunit,_complete_cds_
 d87464_2481-2961,mrna_for_kiaa0274_gene,_complete_cds_
 hg2850-ht4814_s_at_hg2850-ht4814_biliary_glycoprotein,_altsplice_5,_a
 hg3578-ht3781_at_hg3578-ht3781_autoimmune_antigen,_thyroid_disease-
 related_antigen_
 hg417-ht417_s_at_hg417-ht417_cathepsin_b_
 hg4234-ht4504_at_hg4234-ht4504_methylenetetrahydrofolate_reductase_
 hg4660-ht5073_at_hg4660-ht5073_microtubule-associated_protein_1b_
 hg945-ht945_s_at_hg945-ht945_nucleic_acid-binding_protein_
 j05213_430-958,sialoprotein_mrna,_complete_cds_
 l07033_967-1507,hydroxymethylglutaryl-coa_lyase_mrna,_complete_cds_
 l38486mrna_1162-1720,microfibril-
 associated_glycoprotein(mfap4)_mrna,_3'_end_of_cds_
 m71243mrna_25-
 38:not_in_gb_record,glycophorin_sta_(type_a)_exonsand_4,_partial/gb=m71243_/nty
 pe=dna_
 m76424gene_6565-7070,carbonic_anhydrase_vii_(ca_vii)_gene_
 u01824_1402-1912,glutamate/aspartate_transporter_ii_mrna,_complete_cds_
 u07000cds#4_558-810:in_reversesequence,_97660-
 97876,_bcr_gene_(unknown)_extracted_frombreakpoint_clu_
 u13044_1429-1945,nuclear_respiratory_factor-2_subunit_alpha_mrna,_complete_cds_
 u19948_1058-1616,protein_disulfide_isomerase_(pdip)_mrna,_complete_cds_
 u27831cds_1110-1578:in_reversesequence,_1602-1680,striatum-
 enriched_phosphatase_(step)_mrna,_partial_
 u44059_429-909,thyrotroph_embryonic_factor_(tef)_mrna,_complete_cds_
 u49441_258-
 648,mitochondrial_trifunctional_protein_beta_subunit_mrna,_partial_cds/gb=u4944
 1_/ntype=r
 u51205_333-873,cop9_homolog_(hcop9)_mrna,_complete_cds_
 u59057_226-754,beta-a4_crystallin_(cryba4)_mrna,_complete_cds_
 u59736_2496-2772,transcription_factor_(nfatc.b)_mrna,_complete_cds_
 u63455mrna_4412-4868,sulfonylurea_receptor_(sur1)_gene_
 u67988_1623-2163,guanylate_kinase_associated_protein_(gkap)_mrna,_complete_cds_

u86358_296-818, chemokine_(teck)_mrna, _complete_cds/gb=u86358_/ntype=rna
u90918_1794-2094, clone_23654_mrna_sequence_
u96769mrna_1266-1746, chondroadherin_gene, _5'_flanking_region_and_
u96781mrna#1_2433-2961, _atp2a1_gene_(ca2+_atpase_of_fast-
twitch_skeletal_muscle_sarcolemmal_reticulum)
x65633cds_585-870:in_reversesequence, _1568-1766, acth-
r_gene_for_adrenocorticotrophic_hormone_receptor
x66114mrna_564-1074, gene_for_2-oxoglutarate_carrier_protein_
all_x77197_2631-3166, mrna_for_chloride_channel_
x83973cds_2262-2538:in_reversesequence, _2738-2822, mrna_for_ttf-i
x91117mrna_1655-2033, hg_net_gene_exon_1_
x92521cds_1127-1484:in_reversesequence, _1618-1768, mrna_for_mmp-19_protein_
x93996mrna_2570-3113, mrna_for_afx_protein_
x95406exon#1-2_12-17:not_in_gb_record, cyclin_e_gene.
y07847exon#3_36-582, mrna_for_rrp22_protein_
z71389mrna_85-295, mrna_for_skin-antimicrobial-peptide(sap1).

Metagene 134

hg4128-ht4398_at_hg4128-ht4398_anion_exchanger_3, _cardiac_isoform
j03934_1835-2371, _human, nad(p)h:menadione_oxidoreductase_mrna, _complete_cds
l00634_734-1246, farnesyl-protein_transferase_alpha-subunit_mrna, _complete_cds
l09717mrna_1316-1778, lysosomal_membrane_glycoprotein-
2_(lamp2)_gene, _5'_end_and_flanking_region
l10413_1331-1589, farnesyltransferase_alpha-subunit_mrna, _complete_cds
l20852_2574-3150, leukemia_virus_receptor(glv2)_mrna, _complete_cds
l37199_977-1313, (clone_cd24-
1)_huntington_disease_candidate_region_mrna_fragment
l42025mrna_1988-2504, cellular_co-factor_(rab)_gene, _complete_cds_
m23114mrna_3623-4085, calcium-atpase_(hkl)_mrna, _complete_cds
m55150mrna_978-1422, fumarylacetoacetate_hydrolase_mrna, _complete_cds_
m91592_1971-2325, zinc-finger_protein_(znf76)_gene, _partial_cds_
s82447_42-397, _gcn5-
like_1=gcn5_homolog/putative_regulator_of_transcriptional_activation_{clone_gcn
5
u10324_2934-3444, nuclear_factor_nf90_mrna, _complete_cds
u24169_723-1197, jtv-1_(jtv-1)_mrna, _complete_cds_
u24183_2457-3031, phosphofructokinase_(pfkm)_mrna, _complete_cds_
u29091_960-1368, selenium-
binding_protein_(hsbp)_mrna, _complete_cds/gb=u29091_/ntype=rna
u29463mrna_2121-2681, cytochrome_b561_gene
u40462_3034-3574, ikaros/lyf-1_homolog_(hik-1)_mrna, _complete_cds_
u52153_2069-
2513, inwardly_rectifying_potassium_channel_kir3.2_mrna, _complete_cds_
u65676_3144-3648, hermansky-pudlak_syndrome_protein_(hps)_mrna, _complete_cds
u66669_785-1240:not_in_gb_record, 3-hydroxyisobutyryl-
coenzyme_a_hydrolase_mrna, _complete_cds
u68063_1453-1915, transformer-2_beta_(htra-2_beta)_mrna, _complete_cds_
u74612_2915-3425, hepatocyte_nuclear_factor-3/fork_head_homolog_11a_(hfh-
11a)_mrna_complete_cds.
u75370_3396-
3732, mitochondrial_rna_polymerase_mrna, _nuclear_gene_encoding_mitochondrial_pro
tein, _com
u76272mrna_161-689, diadenosine_triphosphate_(ap3a)_hydrolase_(fhit)_gene, _5'_of
u91316_891-1461, acyl-coa_thioester_hydrolase_mrna, _complete_cds

all_x06825_679-1154,mrna_for_skeletal_beta-tropomyosin_
 x15187cds_2089-2380:in_reversesequence,_2521-
 2737,tra1_mrna_forhomologue_of_murine_tumor_rejection_a
 x61970cds_299-677:in_reversesequence,_758-860,mrna_for_macropain_subunit_zeta_
 all_x70944_2459-3030,mrna_for_ptb-associated_splicing_factor_
 all_x77922_1492-2000,gd3_synthase_mrna_
 x85134mrna_2737-3007,rbq-3_mrna_
 all_x87176_2148-2593,mrna_for_17-beta-hydroxysteroid_dehydrogenase_
 all_x91788_857-1284,mrna_for_icln_protein
 x95586exon#3_56-248:in_reversesequence,_5872-6088:not_in_gb_record,mb1_gene
 x97795cds_1954-2218:in_reversesequence,_2342-
 2564,mrna_homologous_to_scerevisiae_rad54
 y08682mrna_2358-2552,mrna_for_carnitine_palmitoyltransferase_i_type_i_
 y11251_4297-4822,mrna_for_novel_member_of_serine-
 arginine_domain_protein,_srrp129
 z17227_1268-1850,mrna_for_transmembrane_receptor_protein_
 z68129mrna#1_3-469:in_fullsequence,_16183-16321:not_in_gb_record,_h-
 idh_gamma_gene_(nad(h)-specific_

Metagene 135

l40396mrna_1542-2028,(clone_s22i71)_mrna_fragment_
 m21186_122-650,neutrophil_cytochrome_b_light_chain_p22_phagocyte_b-
 cytochrome_mrna,_complete_cds_
 m98833_2383-2899,ergb_transcription_factor_(fli-1_homolog)_mrna,_complete_cds_
 u27655_2169-2577,rgp3_mrna,_complete_cds_

Metagene 136

ac000064cds#2_102-372:in_fullsequence,_6375-
 6621,_wugsc:h_rg083m05.2_gene_extracted_frombac_clone_rg
 ac000064cds#1_1287-1581:in_reversesequence,_16950-
 17160,_wugsc:h_rg083m05.2_gene_extracted_frombac_c
 af000177_293-851,sm-
 like_protein_casm_(casm)_mrna,_complete_cds/gb=af000177_/ntype=rna
 af000231_1768-2308,rab11a_gtpase_mrna,_complete_cds.
 af015950_3501-3909,telomerase_reverse_transcriptase_(htrt)_mrna,_complete_cds.
 d10656_988-1528,mrna_for_crk-ii,_complete_cds
 d63391_341-773,mrna_for_platelet_activating_factor_acetylhydrolase_ib_gamma-
 subunit,_complete_cds
 d86959_5435-5867,mrna_for_kiaa0204_gene,_complete_cds
 hg3104-ht3280_at_hg3104-ht3280_serine_protease_met1
 l34820_566-938,nad+-dependent_succinate-
 semialdehyde_dehydrogenase_(ssadh)_mrna,_3'_end
 m37400mrna_1352-1886,cytosolic_aspartate_aminotransferase_mrna,_complete_cds_
 m63483_757-1255,major_nuclear_matrix_protein_mrna
 m68891_2398-2686,gata-binding_protein_(gata2)_mrna,_complete_cds_
 s72370_3422-3962,_pyruvate_carboxylase_[human,_kidney,_mrna,_4017_nt]_
 u01160_1056-1635,transmembranesuperfamily_protein_(sas)_mrna,_complete_cds
 u39412_675-1209:not_in_gb_record,platelet_alpha_snap_mrna,_complete_cds_
 u44755_965-1487,pse-binding_factor_ptf_delta_subunit_mrna,_complete_cds
 u44839_2566-3088,putative_ubiquitin_c-
 terminal_hydrolase_(uhx1)_mrna,_complete_cds_

u66469_819-1209, cell_growth_regulator_cgr19_mrna, _complete_cds_
u87972_91-373, nad+-
isocitrate_dehydrogenase_mrna, _partial_cds/gb=u87972_/ntype=rna_
all_x12433_1247-1734, phs1-
2_mrna_with_orf_homologous_to_membrane_receptor_proteins_
all_x17025_1254-1807, homolog_of_yeast_ipp_isomerase

Metagene 137

af005037_574-
1030, secretory_carrier_membrane_protein_(scamp1)_mrna, _complete_cds/gb=af005037
_/ntype=
d87449_5359-5785, mrna_for_kiaa0260_gene, _partial_cds_
100972_2064-2202, cystathionine-beta-synthase_(cbs)_mrna
149218exon_4-
91, retinoblastoma_susceptibility_protein_(rb1)_e413kbp_deletion_mutant_(resulti
ng_in_pr
m88163_3059-
3581, global_transcription_activator_homologous_sequence_mrna, _complete_cds_
u79296_1366-1876, dihydrolipoamide_acetyl_transferase_mrna, _partial_cds.

Metagene 138

af003743_28-235, delayed_rectifier_potassium_channel_(kvlqt1-
iso5)_mrna, _5'_utr_and_partial_cds/gb=af
d10495_1562-2054, mrna_for_protein_kinase_c_delta-type
all_d13897_1402-
1545, _peptide_yy_precursor_gene_extracted_fromdna_for_peptide_yy, _complete_cds
d16583exon#12_473-1001, gene_for_l-histidine_decarboxylase, _complete_cds
d17532_3624-4104, mrna_for_rck, _complete_cds
d28416_5-
55, mrna_for_esterase_d, _5'_utr_(sequence_from_the_5'_cap_to_the_start_codon)/gb
=d28416_/nty
d42044_5131-5635, mrna_for_kiaa0090_gene, _partial_cds_
d42046_3648-4077, mrna_for_kiaa0083_gene, _partial_cds_
d55696_1285-1807, mrna_for_cysteine_protease, _complete_cds
d63484_2642-3188, mrna_for_kiaa0150_gene, _partial_cds_
d83542_2250-2808, mrna_for_cadherin-15, _complete_cds
d83780_3502-4060, mrna_for_kiaa0196_gene, _complete_cds
d83784_5115-5445, mrna_for_kiaa0198_gene, _partial_cds_
d87937_88-
502, mrna_for_alpha(1,2) fucosyltransferase, _5'_utr_partial_sequence/gb=d87937_/n
type=rna
hg1602-ht1602_at_hg1602-ht1602_utrophin
hg2247-ht2332_at_hg2247-ht2332_major_intrinsic_protein_
hg2348-ht2444_s_at_hg2348-ht2444_peptide_yy
hg2994-ht4850_s_at_hg2994-ht4850_elastin, _altssplice_2
hg3148-ht3324_s_at_hg3148-
ht3324_major_histocompatibility_complex, _iii, _rp1, _altssplice_1_
hg3437-ht3628_s_at_hg3437-ht3628_myelin_proteolipid_protein, _altssplice_2_
hg3565-ht3768_r_at_hg3565-ht3768_zinc_finger_protein_
hg3566-ht3769_at_hg3566-ht3769_zinc_finger_protein_
hg4018-ht4288_at_hg4018-ht4288_opioid-binding_cell_adhesion_molecule_

hg4264-ht4534_s_at_hg4264-ht4534_guanine_nucleotide-binding_protein_rab5c-like_protein_
 hg4638-ht5050_at_hg4638-ht5050_spliceosomal_protein_sap_49_
 hg4724-ht5166_at_hg4724-ht5166_atp-binding_cassette_protein
 hg4749-ht5197_at_hg4749-ht5197_calmitine_calcium-binding_protein_mitochondrial
 hg880-ht880_at_hg880-ht880_mucin_6_gastric
 j02871_1475-1931_lung_cytochrome_p450_(iv_subfamily)_bi_protein_complete_cds
 j02947mrna_839-1349_extracellular-superoxide_dismutase_(sod3)_mrna_complete_cds_
 j03241_1918-2438_transforming_growth_factor-beta(tgf-beta3)_mrna_complete_cds_
 l22454_2803-2944_nuclear_respiratory_factor-1_(nrf-1)_mrna_complete_cds_
 l33799_1065-1455_procollagen_c-proteinase_enhancer_protein_(pcolce)_mrna_complete_cds_
 l40402mrna_593-1157_(clone_zap2)_mrna_fragment
 m11749cds_141-405:in_reversesequence_1501-1747_thy-1_glycoprotein_gene_complete_cds_
 m13929mrna_421-974_c-myc-p64_mrna_initiating_from_promoter_p0_(hlmyc2.5)_partial_cds_
 m16336mrna_923-1463_t-cell_surface_antigen_cd2_(t11)_mrna_complete_cds_clone_pb1_
 m28882_2907-3186_muc18_glycoprotein_mrna_complete_cds_
 m29932cds_637-1180_beta-3-adrenergic_receptor_gene_
 m31211mrna_150-714_myosin_light_chainslow_a_(mlc1sa)_mrna_complete_cds_
 m37238mrna_3630-4187_phospholipase_c_mrna_complete_cds_
 m37763cds_350-740:in_reversesequence_965-989_neurotrophin-3_(nt-3)_gene_complete_cds_
 m59916_1784-2300_acid_sphingomyelinase_(asm)_mrna_complete_cds_
 m64673_1541-2084_heat_shock_factor(tcf5)_mrna_complete_cds_
 m79463_2979-3514_pml-2_mrna_complete_cds_
 m85085_1449-1953_cleavage_stimulation_factor_complete_cds_
 m93284_879-1407_pancreatic_lipase_related_protein(plrp2)_mrna_complete_cds_
 m95627mrna_1227-1587_angio-associated_migratory_cell_protein_(aamp)_mrna_complete_cds_
 s39329_948-1368_glandular_kallikrein-1_{alternatively_spliced}_[human_prostate_mrna_1541_nt]
 s83309_1291-1856_germ_cell_nuclear_factor_[human_embryonal_carcinoma_nt2/d1_mrna_1916_nt]
 u01038_1649-2123_plk_mrna_complete_cds_
 u07664exon#2_535-973_hb9_homeobox_gene_
 u08198mrna_313-805_complement_c8_gamma_subunit_precursor_(c8g)_gene_complete_cds_
 u09937mrna_1176-1581_urokinase-type_plasminogen_activator_receptor_gene_extracted_fromurokinase-type
 u11877_7-139_interleukin-8_receptor_type_b_(il8rb)_mrna_splice_variant_il8rb9_partial_cds/gb=u1187
 u14187_824-962_receptor_tyrosine_kinase_ligand_lerk-3_(eplg3)_mrna_complete_cds_
 all_u15637_1727-2315_cd40_binding_protein_(cd40bp)_mrna_complete_cds_
 u18018_1732-2290_e1a_enhancer_binding_protein_(e1a-f)_mrna_partial_cds_
 u18235_61-493_atp-binding_cassette_protein_(abc2)_mrna_hfbcd04_clone_partial_cds_
 u18300_1231-1657_damage-specific_dna_binding_protein_p48_subunit_(ddb2)_mrna_complete_cds_
 u19261_1792-2320_epstein-barr_virus-induced_protein_mrna_complete_cds_
 u32645_3566-4112_myeloid_elf-1_like_factor_(mef)_mrna_complete_cds_
 u38372_13-331_huntingtin_associated_protein_(hhap1)_mrna_partial_cds_

u40998_760-1312,retinal_protein_(hrp4)_mrna,_complete_cds
 u43965_3313-3389,ankyrin_g119_(ank3)_mrna,_complete_cds
 u46570_974-1364,tetratricopeptide_repeat_protein_(tpr1)_mrna,_complete_cds_
 u49070_411-951,peptidyl-
 prolyl_isomerase_and_essential_mitotic_regulator_(pin1)_mrna,_complete_cds_
 u50079_1013-1569,histone_deacetylase_hd1_mrna,_complete_cds
 u50136mrna_106-640,leukotriene_c4_synthase_(ltc4s)_gene,_complete_cds_
 u52100_167-605,xmp_mrna,_complete_cds
 u56417_1673-2063,lysophosphatidic_acid_acyltransferase-alpha_mrna,_complete_cds
 all_u57450_305-546,epc-1_gene
 u67674exon_2279-2813,ileal_sodium_dependent_bile_acid_transporter
 u70426_1863-2301,a28-rgs14p_mrna,_complete_cds_
 u73377_3059-3363,p66shc_(shc)_mrna,_complete_cds.
 u76456_587-1145,tissue_inhibitor_of_metalloproteinase_mrna,_complete_cds.
 u83192_3401-3905,post-synaptic_density_protein_95_(psd95)_mrna,_complete_cds_
 u83410_2256-2772,cul-2_(cul-2)_mrna,_complete_cds
 u83598_519-
 790,death_domain_receptorsoluble_form_(ddr3)_mrna,_partial_cds,death_domain_rec
 eptorsolub
 u85611_385-919,dna-pk_interaction_protein_(kip)_mrna,_complete_cds_
 u86409cds_61-
 523,hyaluronan_synthase_(has3)_gene,_partial_cds/gb=u86409_/ntype=dna_/annot=cds
 u88629cds_1508-
 1898,rna_polymerase_ii_elongation_factor_ell2,_complete_cds/gb=u88629_/ntype=dn
 a_/ann
 u89278_1958-2402,polyhomeotichomolog_(hph2)_mrna,_complete_cds
 u89355_3288-3618,clone_crt16_creb-binding_protein_mrna,_partial_cds.
 all_x04828_1116-1702,mrna_for_g(i)_protein_alpha-
 subunit_(adenylate_cyclase_inhibiting_gtp-binding_p
 all_x07315_341-864,gene_for_pp15_(placental_protein_15)
 x52192cds_2144-2426:in_reversesequence,_2525-2717,rna_for_c-fes_
 x52611cds_962-1273:in_reversesequence,_1441-
 1555,mrna_for_transcription_factor_ap-2_
 all_x52638_1152-1723,mrna_for_6-phosphofructo-2-kinase/fructose-2,6-
 biphosphatase_(ec_2.7.1.105,_ec
 x59373mrna_531-1071,hox4d_mrna_for_a_homeobox_protein
 all_x60104_1532-2110,mrna_for_zinc_finger_protein
 x62025mrna_877-1180,rod_cg-pde_g_gene_for_3',_5'-
 cyclic_nucleotide_phosphodiesterase
 x62153cds_1930-2398:in_reversesequence,_2459-2494,mrna_for_p1_protein_(p1.h)
 x63380_1061-1613,mrna_for_rsrfr2_
 all_x65463_1187-1734,mrna_for_mhc_i_promoter_binding_protein_
 x68688mrna_111-134,znf33b_gene
 x70991_1597-2089,mader_mrna
 all_x74295_178-695,mrna_for_alpha_7b_integrin
 x77588cds_154-679,te2_mrna_for_ard-1_n-acetyltransferase_homologue.
 x86428cds_626-
 920:not_in_gb_record,gene_for_phosphotyrosyl_phosphatase_activator_(exon_1)_
 x92715_3170-3701,mrna_for_znf74_protein
 x95463cds_793-1222,mrna_for_ox19_protein_
 y00970cds_756-1236:in_reversesequence,_1264-
 1312,mrna_for_acrosin_(ec_3.4.21.10)
 y08302cds_807-1122:in_reversesequence,_1385-
 1445,mrna_for_map_kinase_phosphatase_4
 y08836mrna_37-181,mrna_for_hrx-like_protein/gb=y08836_/ntype=rna_
 y09022cds_805-1291:in_reversesequence,_1328-1406,mrna_for_not56-like_protein
 y11416mrna_1639-2209,mrna_for_p73

all_z14978_1422-1673,mrna_for_actin-related_protein
 z33905mrna_1190-1598,gene_for_43kd_acetylcholine_receptor-
 associated_protein_(rapsyn)

Metagene 139

hg4518-ht4921_r_at_hg4518-ht4921_transcription_factor_bt3_homolog_
 s81083mrna_3078-3438,_<beta>-
 add_gene_extracted_from_beta_#name?_beta_subunit_63_kda_isoform/membran
 all_x86019_2045-2574,mrna_for_prpl-2_protein_

Metagene 140

ab002365_5053-5617,mrna_for_kiaa0367_gene,_partial_cds/gb=ab002365_/ntype=rna
 hg3729-ht3999_f_at_hg3729-ht3999_homeotic_protein_hpx-5
 107077_3277-3661,enyol-coa:_hydratase_3-hydroxyacyl-
 coa_dehydrogenase_(ehhadh)_mrna,_complete_cds_wi
 111353_1698-2202:in_reversesequence,_2208-2214,moesin-ezrin-radixin-
 like_protein_mrna,_complete_cds_
 all_112052_3408-3871,camp_phosphodiesterase_mrna,_3'_end_
 127050_1166-1508,apolipoprotein_f_(apof)_mrna,_complete_cds
 136847cds_1044-1578,(clone_p17/90)_rearranged_iduronate-2-
 sulphatase_homologue_gene/gb=136847_/ntype
 176569mrna_6762-
 7284,(clones_cyg3,_b5p6c4)_fragile_x_e_mental_retardation_syndrome_protein_(fmr
 2)_mr
 m21535_2603-3101,_m17390erg_protein_(ets-related_gene)_mrna,_complete_cds
 u28687_1710-
 1983,zinc_finger_containing_protein_znf157_(znf157)_mrna,_complete_cds_
 u34380_rnal_s_at_u34380_u34380,not_in_gb_record,_tec_gene_extracted_fromprotein
 _tyrosine_kinase_tec_
 z35309cds_3385-3727,mrna_for_adenylyl_cyclase
 all_z79693_2421-3018,mrna_for_protein-tyrosine_phosphatase_nc-ptpcom1

Metagene 141

u19180_535-925,b_melanoma_antigen_(bage)_mrna,_complete_cds
 u30828_1078-1630,splicing_factor_srp55-2_(srp55)_mrna,_complete_cds
 u51269_3408-3900,armadillo_repeat_protein_mrna,_complete_cds_

Metagene 142

d43772_1616-2168,squamous_cell_carcinoma_of_esophagus_mrna_for_grb-
 7_sh2_domain_protein,_complete_cd
 d50920_2969-3419,mrna_for_kiaa0130_gene,_complete_cds
 109229_2642-3099,long-chain_acyl-
 coenzyme_a_synthetase_(fac11)_mrna,_complete_cds
 111370_3486-4038,protocadherin_42_mrna,_complete_cds_for_abbreviated_pc42
 all_m12036_1553-1732,tyrosine_kinase-type_receptor_(her2)_gene,_partial_cds

m24899_1750-2284,triiodothyronine_(ear7)_mrna,_complete_cds
 m80783_3001-3451,b12_protein_mrna,_complete_cds
 u47634_1341-1623,beta-tubulin_iii_isotype_(beta-3)_mrna,_complete_cds
 u90914_1369-1795,clone_23587_mrna_sequence_
 all_x03363_3873-4408,c-erb-b-2_mrna
 x63527cds_99-549:in_reversesequence,_637-655,mrna_for_ribosomal_protein_l19_
 all_x65233_1966-2429,mrna_for_zinc-finger_protein_(znfpt17)
 all_x80198_1398-1939,mln64_mrna
 all_x80199_3718-4223,mln51_mrna
 all_x80692_3409-3878,erk3_mrna_
 y09836_999-1335,mrna_for_3' utr_of_unknown_protein_
 z38026cds_63-483:in_reversesequence,_536-542,mrna_for_fall-
 39_peptide_antibiotic

Metagene 143

d14663_785-1259,mrna_for_kiaa0107_gene,_complete_cds_
 d38496_3615-4170,mrna_for_lztr-1,_complete_cds_
 d42084_2112-2610,mrna_for_kiaa0094_gene,_partial_cds_
 d49400_115-655,fetus_brain_mrna_for_vacuolar_atpase,_complete_cds
 d84294mrna_8552-9020,mrna_for_tprdi,_complete_cds
 d86988_4716-5220,mrna_for_kiaa0221_gene,_complete_cds
 d87445_6334-6892,mrna_for_kiaa0256_gene,_complete_cds
 hg1322-ht5143_s_at_hg1322-
 ht5143_small_nuclear_ribonucleoprotein,_polypeptide_altsplice_2_
 hg3484-ht3678_s_at_hg3484-ht3678_protein_kinase
 j04794mrna_567-1071,aldehyde_reductase_mrna,_complete_cds
 l09209_3114-3666,amyloid_protein_homologue_mrna,_complete_cds_
 l35249mrna_2225-2690,vacuolar_h+-
 atpase_mr_56,000_subunit_(ho57)_mrna,_complete_cds_
 l49380mrna_2916-3414,clone_b4_transcription_factor_zfml_mrna,_complete_cds
 ml4483mrna_41-
 443,_ptma_gene_extracted_fromprothymosin_alpha_mrna,_complete_cds_
 m26708_549-1008,prothymosin_alpha_mrna_(prot-alpha),_complete_cds
 m91432mrna_1664-2144,medium-chain_acyl-coa_dehydrogenase_(mcad)_gene_
 u00115_3001-3451,zinc-finger_protein_(bcl-6)_mrna,_complete_cds
 u09825_3156-3522,acid_finger_protein_mrna,_complete_cds
 u22970mrna#1_205-749,_16-jun_gene_(interferon-
 inducible_peptide_precursor)_extracted_frominterferon-
 u26424_2237-2735,ste20-like_kinase_(mst2)_mrna,_complete_cds_
 u45328_591-1079,ubiquitin-conjugating_enzyme_(ube2i)_mrna,_complete_cds
 u60061_905-1325,fez2_mrna,_partial_cds_
 u61397_875-1173,ubiquitin-homology_domain_protein_pic1_mrna,_complete_cds
 u80017mrna#3_892-
 l444,_btf2p44_gene_(basic_transcription_factorp44)_extracted_frombasic_transcri
 ptio
 u91930_4196-4682,ap-3_complex_delta_subunit_mrna,_complete_cds_
 u91931_3081-3489,ap-3_complex_beta3a_subunit_mrna,_complete_cds
 u91932_778-1210,ap-3_complex_sigma3a_subunit_mrna,_complete_cds
 u92014_817-1366,clone_121711_defective_mariner_transposon_hsmar2_mrna_sequence_
 all_x03484_2418-2947,mrna_for_raf_oncogene_
 x60787mrna_2434-3000,mrna_for_transcription_factor_ilf_
 all_x62534_726-1137,hmg-2_mrna_
 all_x63692_4825-5348,mrna_for_dna_(cytosin-5)-methyltransferase
 x65784cds_58-399,car_gene

all_x66899_1902-2323,ews_mrna
 x69838cds_2756-2924:in_reversesequence,_3043-3331,mrna_for_g9a
 all_x69910_2339-2892,p63_mrna_for_transmembrane_protein
 all_x70394_2591-3156,ozf_mrna
 all_x72889_5441-5844,hbrm_mrna
 all_x73478_2042-2637,htpa_mrna
 all_x79536_1005-1156,mrna_for_hnrnpcore_protein_a1.
 all_x86691_5882-6399,mrna_for_218kd_mi-2_protein_
 all_x89750_1061-1512,mrna_for_tgif_protein_
 all_x95404_482-1047,mrna_for_non-muscle_type_cofilin_
 x95735_1628-2168,mrna_for_zyxin_2
 all_x98743_2619-3112,mrna_for_rna_helicase_(myc-regulated_dead_box_protein)
 all_y00815_7107-7684,mrna_for_lca-
 homologlar_protein_(leukocyte_antigen_related)_
 all_y08614_3715-4118,mrna_for_crml_protein_
 all_z24724_1263-1840,polya_site_dna
 z26491exon#5_388-430,gene_for_catechol_o-methyltransferase_
 all_z29505_1140-1468,mrna_for_nucleic_acid_binding_protein_sub2.3

Metagene 144

ab006782_1392-1672,mrna_for_galectin-
 9_isoform,_complete_cds/gb=ab006782/_ntype=rna_
 d32129_920-1425,mrna_for_hla-i_(hla-a26)_heavy_chain,_complete_cds_(clone_cmiy-
 1)
 all_d49824_945-978,hla-b_null_allele_mrna,hla-b_null_allele_mrna
 hg2915-ht3059_f_at_hg2915-ht3059_major_histocompatibility_complex,_i,_e
 hg2917-ht3061_f_at_hg2917-ht3061_major_histocompatibility_complex,_i,_e
 hg3597-ht3800_f_at_hg3597-ht3800_major_histocompatibility_complex,_i_
 hg658-ht658_f_at_hg658-ht658_major_histocompatibility_complex,_i,_c
 j00105_24-520,beta-2_microglobulin_gene_mrna,_3'_end_
 j04080mrna_2136-2604,complement_component_c1r_mrna,_complete_cds_
 m13690mrna_1190-1739,plasma_protease_(c1)_inhibitor_mrna,_complete_cds_
 m14058_1982-2438,complement_c1r_mrna,_complete_cds_
 m58286_1533-2054,tumor_necrosis_factor_receptor_mrna,_complete_cds
 m63838_2097-2643,interferon-gamma_induced_protein_(ifi_16)_gene,_complete_cds
 m64099_1873-2371,gamma-glutmyl_transpeptidase-related_protein_(ggt-
 rel)_mrna,_complete_cds_
 m92357_3609-4131,b94_protein_mrna,_complete_cds_
 m94880_f_at_m94880_m94880,_4040_in_m94880_515-1055,mhc_i_(hla-a*8001)_mrna
 m97935_3412-3886,transcription_factor_isgf-3_mrna_sequence_
 u49020mrna#1_4711-5228,_mef2a_gene_(myocyte-
 specific_enhancer_factor_2a,_c9_form)_extracted_frommyoc
 u70451_2097-
 2607,myleoid_differentiation_primary_response_protein_myd88_mrna,_complete_cds.
 all_x07696_1300-1685,mrna_for_cytokeratin_15_
 x12451mrna_974-1496,mrna_for_pro-cathepsin_l_(major_excreted_protein_mep)_
 x53587mrna_5160-5688,mrna_for_integrin_beta_4
 all_x82200_2236-2801,staf50_mrna_
 x83416exon_1688-2160,prp_gene,_exon_2
 all_z19554_1243-1734,vimentin_gene_

Metagene 145

ab000450_1298-1730,mrna_for_vrk2,_complete_cds_
 ab000464_3281-3743,_clone_res4-24a,_exon_1,_2,_3,_4_
 ab001106_3542-4088,mrna_for_glia_maturation_factor,_complete_cds_
 d00723_642-
 1110,mrna_for_hydrogen_carrier_protein,_a_component_of_an_enzyme_complex,_glyci
 ne_synthas
 d11151exon_1936-2434,dna_for_endothelin-a_receptor,_5'_flanking_region_and_
 d12625_2036-
 2219,mrna_for_nf1_protein_isoform_(neurofibromin_isoform),_complete_cds
 d12676_1884-2220,mrna_for_lyosomal_sialoglycoprotein,_complete_cds
 d13635_4583-5117,mrna_for_kiaa0010_gene,_complete_cds
 d13789_1594-2062,mrna_for_n-acetylglucosaminyltransferase_iii,_complete_cds
 d14662_1082-1592,mrna_for_kiaa0106_gene,_complete_cds
 d21163_3183-3693,mrna_for_kiaa0031_gene,_complete_cds
 d86549_609-969,mrna_for_p97_homologous_protein,_partial_cds
 d88532_3016-3328,mrna_for_p55pik,_complete_cds_
 104733_1785-2265,kinesin_light_chain_mrna,_complete_cds_
 108488_1206-1644,inositol_polyphosphate_1-phosphatase_mrna,_complete_cds_
 113434_2304-2850,chromosome_3p21.1_gene_sequence,_complete_cds_
 122009_1642-2056,hnrnp_h_mrna,_complete_cds
 127476_3901-4429,x104_mrna,_complete_cds_
 138933mrna_883-
 1393,_the_longest_open_reading_frame_predicts_a_protein_of_202_amino_acids,_wit
 h_fair
 141939mrna_3197-3731,(clone_fbk_iii_11c)_protein-
 tyrosine_kinase_(drt)_mrna,_complete_cds_
 m37190mrna_1220-1796,ras_inhibitor_mrna,_3'_end
 all_m54968_5180-5775,k-ras_oncogene_protein_mrna,_complete_cds_
 m64936_2808-3264,retinoic_acid-inducible_endogenous_retroviral_dna
 m91029exon#3_2581-2977,amp_deaminase_(ampd2)_mrna_
 s59049_786-1314,_bl34=b_cell_activation_gene_[human,_mrna,_1398_nt]_
 s73149mrna_293-827,_insulin-
 like_growth_factor_ii_{intron_7}_[human,_genomic,_1702_nt]/gb=s73149_/nt
 u08023_3037-3529,cellular_proto-oncogene_(c-mer)_mrna,_complete_cds
 u08316_1719-2235,insulin-stimulated_protein_kinase(ispk-1)_mrna,_complete_cds_
 u15782_2237-2681,cleavage_stimulation_factor_77kda_subunit_mrna,_complete_cds
 u23028_1702-2236,eukaryotic_initiation_factor_2b-epsilon_mrna,_partial_cds_
 u39487_3877-4339,xanthine_dehydrogenase/oxidase_mrna,_complete_cds_
 u85658_2310-2736,transcription_factor_erf-1_mrna,_complete_cds_
 x62083_3969-4029,mrna_for_drosophila_female_sterile_homeotic_(fsh)_homologue_
 all_x69962_4188-4308,fmr-1_mrna
 all_x82125_2007-2368,hok-2_mrna_for_zinc_finger_protein

Metagene 146

x12556mrna_3159-3483,mrna_for_dbl_proto-oncogene_
 all_x52011_699-1144,myf6_gene_encoding_a_muscle_determination_factor_

Metagene 147

all_ac0000061_18132-57268:in_ac0000061cds#1_720-
 760,_wugsc:h_133k23.1c_gene_extracted_frombac_clone_13

ac000062_110059-110206:in_all_ac000062_109961-109993,pac_clone_2g3a_from_13q12-13q13
 d50640exon_700-1132,dna_for_phosphodiesterase_3b_

Metagene 148

d13644_4013-4523,mrna_for_kiaa0019_gene,_complete_cds
 l35545mrna_689-
 1223,endothelial_cell_protein_c/apc_receptor_(epcr)_mrna,_complete_cds_
 m33882_2348-2762,p78_protein_mrna,_complete_cds
 m60750cds_3-
 348,histone_h2b.1_(h2b)_gene,_complete_cds/gb=m60750_/ntype=dna_/annot=cds_
 u78798_1699-2203,tnf_receptor_associated_factor(traf6)_mrna,_complete_cds.
 all_y08319_1743-2272,mrna_for_kinesin-2
 y12556_427-877,mrna_for_amp-activated_protein_kinase_beta-
 1/gb=y12556_/ntype=rna_

Metagene 149

d00097exon#2_152-
 710,serum_amyloid_p_component_(sap)_gene_with_upstream_promoter_
 d14533_812-1322,mrna_for_xpac_protein
 d16815_1642-2086,mrna_for_ear-1r,_complete_cds_
 d87683_6419-6941,mrna_for_kiaa0243_gene,_partial_cds_
 hg2510-ht2606_at_hg2510-ht2606_ras-specific_guanine_nucleotide-releasing_factor
 j00314mrna#1_4079-4173,beta-tubulin_gene,_clone_m40
 j05200mrna_14740-15238,ryanodine_receptor_mrna,_complete_cds
 l11329_1162-1630,protein_tyrosine_phosphatase_(pac-1)_mrna,_complete_cds
 l12760exon#9_396-
 721,phosphoenolpyruvate_carboxykinase_(pck1)_gene,_complete_cds_with_repeats
 all_l35263_3222-3721,csaids_binding_protein_(csbp1)_mrna,_complete_cds_
 m22976mrna_21-303:in_reversesequence,_668-728,cytochrome_b5_mrna,_3'_end
 m62397_3586-4126,colorectal_mutant_cancer_protein_mrna,_complete_cds_
 all_m83554_3167-3576,lymphocyte_activation_antigen_cd30_mrna,_complete_cds_
 m84424exon_1073-1217,cathepsin_e_(ctse)_gene_
 all_m93311_1950-2085,metallothionein-iii_gene,_complete_cds
 s83549_19-571,na+/h+_exchanger_isoform_nhe-
 2_[human,_various_tissues,_mrna_partial,_595_nt]/gb=s835
 u02082_1643-
 2201,guanine_nucleotide_regulatory_protein_(tim1)_mrna,_complete_cds_
 u14528_2357-2807,sulfate_transporter_(dtd)_mrna,_complete_cds
 u18009_1900-2338,chromosome_17q21_mrna_clone_lf113_
 u19517_1692-2010,(apoargc)_long_mrna,_complete_cds_
 u22680_6048-6558,x2_box_repressor_mrna,_complete_cds_
 u36601_2620-3166,heparan_n-deacetylase/n-sulfotransferase-2_mrna,_complete_cds_
 u49436_1303-1783,translation_initiation_factor(eif5)_mrna,_complete_cds_
 u53003_1093-1609,gt335_mrna,_complete_cds
 u73338_6615-7113,methionine_synthase_mrna,_complete_cds
 u73682_2255-2651,meningioma-expressed_antigen(mea11)_mrna,_partial_cds_
 u78876_1789-2317,mek_kinase_mrna,_complete_cds_
 u80811_1092-1536,lysophosphatidic_acid_receptor_homolog_mrna,_complete_cds_
 x02176cds_1397-1656:in_reversesequence,_1681-
 1859,mrna_fragment_for_complement_component_c9

x05997cds#1_726-1158:in_reversesequence,_1280-1316,mrna_for_gastric_lipase
 x51956mrna_1881-2397,eno2_gene_for_neuron_specific_(gamma)_enolase
 all_x60483_975-1171,h4/d_gene_for_h4_histone_
 x67325cds_31-337:in_reversesequence,_43-541,p27_mrna
 x67683cds_34-319:in_reversesequence,_13,mrna_for_keratin/gb=x67683_/ntype=rna
 x68149exon#2_2249-2687,blr1_gene_for_burkitt_lymphoma_receptor_1_
 x85133mrna_2399-2897,rbq-1_mrna
 x85372cds_18-210:in_reversesequence,_19-115,mrna_for_sm_protein_f_
 all_x87342_2921-3456,mrna_for_giant_larvae_homolog_
 x90908cds_11-353,mrna_for_i-15p_(i-babp)_protein_
 all_y00978_2012-2535,mrna_for_dihydrolipoamide_acetyltransferase_(pdc-
 e2)_(ec_2.3.1.12)
 y12393_346-819,mrna_for_srp1-like_protein,_partial_
 z24459exon#1_13-
 199,_exon2a_frommtcp1_gene,_exons_2a_to(and_joined_mrna)/gb=z24459_/ntype=dna_
 annot

Metagene 150

d17390_2313-2829,mrna_for_mdc_protein
 d49410exon_48-534,gene_for_interleukinreceptor_alpha_subunit
 hg3063-ht3224_at_hg3063-ht3224_major_histocompatibility_complex,_i_
 hg3355-ht3532_at_hg3355-ht3532_peroxisome_proliferator_activated_receptor
 hg4417-ht4687_f_at_hg4417-ht4687_homeotic_protein_hpx-2
 l11931_1454-
 1644,cytosolic_serine_hydroxymethyltransferase_(shmt)_mrna,_complete_cds_
 m21056cds_193-403:in_reversesequence,_165-345,pancreatic_phospholipase_a-
 2_(pla-2)_gene_
 m76231_292-790,sepiapterin_reductase_mrna,_complete_cds
 m81379_1126-1546,alpha-3_type_iv_collagen_(col4a3)_mrna,_3'_end
 m86383_1007-
 1527,nicotinic_acetylcholine_receptor_alphasubunit_mrna,_complete_cds_
 m86407_2299-2833,alpha_actinin(actn3)_mrna,_complete_cds_
 m95678_3990-4494,phospholipase_c-beta-2_mrna,_complete_cds
 u06643_71-463,keratinocyte_lectin(hkl-14)_mrna,_complete_cds.
 u16127_3025-3589,glutamate/kainate_receptor_subunit_(eaa5)_mrna,_complete_cds
 u43142_1456-
 1972,vascular_endothelial_growth_factor_related_protein_vrp_mrna,_complete_cds_
 u59913_1640-2168,chromosomemad_homolog_smad5_mrna,_complete_cds_
 u62437_1943-
 2393,nicotinic_acetylcholine_receptor_beta2_subunit_precursor,_mrna,_complete_c
 ds
 u71300_1307-
 1703,snrna_activating_protein_complex_50kd_subunit_(snap50)_mrna,_complete_cds_
 all_x15217_2292-2875,sno_oncogene_mrna_for_snoa_protein,_ski-related_
 all_x54741_2389-2918,cypxib2_gene_for_aldosterone_synthase_
 x60592mrna_415-973,cdw40_mrna_for_nerve_growth_factor_receptor-related_b-
 lymphocyte_activation_molec
 x60655mrna_990-1474,evx1_mrna
 x62891mrna_57-390,mutant_coseg_gene_for_vasopressin-neurophysin_precursor
 x91257_1281-1797,mrna_for_seryl-trna_synthetase
 x92475_905-1295,mrna_for_itba1_protein_
 x95191cds_707-848,mrna_for_delta-sarcoglycan/gb=x95191_/ntype=rna
 all_y11215_971-1446,mrna_for_skap55_protein/gb=y11215_/ntype=rna
 z22865cds_164-578:in_reversesequence,_620,dermatopontin_mrna,_complete_cds

reverse_z49155_27087-
27346,dna_from_cosmid_183d3,_huntington's_disease_region,_chromosome_4p16.3_

Metagene 151

ac002464cds_799-
1345,bac_clone_rg331p03,_complete_sequence/gb=ac002464_/ntype=dna_/annot=cds_
d87457_1568-2060,mrna_for_kiaa0281_gene,_complete_cds
hg4109-ht4379_at_hg4109-ht4379_olfactory_receptor_or17-30
u31215_3797-
4037,metabotropic glutamate_receptoralpha_(mglur1alpha)_mrna,_complete_cds
x03473cds_270-552:in_reversesequence,_1054-1150,gene_for_histone_h1(0)
x06948cds_482-680:in_reversesequence,_918-
1146,mrna_for_high_affinity_ige_receptor_alpha-subunit_(fc
all_z12173_1808-2361,gns_mrna_encoding_glucosamine-6-sulphatase

Metagene 152

hg3115-ht3291_at_hg3115-ht3291_golli-mbp_
102950_673-1177,mu-crystallin_mrna,_complete_cds_
all_m10950_57-304,alpha-fetoprotein_(afp)_gene
m64572_3431-3923,protein_tyrosine_phosphatase_mrna,_complete_cds_
s68134_500-665,_crem=cyclic_amp-
responsive_element_modulator_beta_isoform_[human,_mrna,_1030_nt]
u41898_73-505,sodium_cotransporter_rkst1_mrna,_partial_cds/gb=u41898_/ntype=rna
u50708_946-1384,branched_chain_alpha-
ketoacid_dehydrogenase_e1_beta_subunit_mrna,_complete_cds_

Metagene 153

hg4245-ht4515_at_hg4245-ht4515_forkhead_family_afx1
m84349mrna_1366-1852,transmembrane_protein_(cd59)_gene_

Metagene 154

d00408_1373-1921,fetal_liver_cytochrome_p-450_(p-
450_hfla),_complete_cds,fetal_liver_cytochrome_p-45
d13638_5003-5557,mrna_for_kiaa0013_gene,_complete_cds
hg2320-ht2416_at_hg2320-ht2416_integrin,_betasubunit
m24351_cds2_at_m24351_m24351,not_in_gb_record,_pthlh_gene_(parathyroid_hormone-
like_protein_a)_extra
m73489_3312-3660,heat-stable_enterotoxin_receptor_mrna,_complete_cds_
u73330exon_13-77,pac_85d2,_complete_sequence/gb=u73330_/ntype=dna_/annot=exon
x95425cds_2672-3061:in_reversesequence,_3810-3857,mrna_for_ehk-
1_receptor_tyrosine_kinase_

Metagene 155

m26683_416-510,interferon_gamma_treatment_inducible_mrna_
 m60314_1582-2044,transforming_growth_factor-beta_(tgf-beta)_mrna,_complete_cds_
 u02310_2946-3372,fork_head_domain_protein_(fkhr)_mrna,_complete_cds
 u57796_3322-3784,zinc_finger_protein_(ld5-1)_mrna,_complete_cds
 all_u60116_905-966:not_in_gb_record,skeletal_muscle_lim-
 protein_slim2_mrna,_partial_cds_

Metagene 156

hg2887-ht3031_r_at_hg2887-ht3031_sry-related_hmg-boxprotein
 hg4099-ht4369_s_at_hg4099-ht4369_adrenergic_receptor,_alpha_1b_
 l04947_3659-
 4199,(clones_bt3.081.8,_bt3.129.5_and_bt4.169)_receptor_tyrosine_kinase_(kdr)_m
 rna,_3'_e
 m74088_8374-8717,apc_gene_mrna,_complete_cds_
 m96738cds_719-1221,somatostatin_receptor_subtype(ssstr3)_gene,_complete_cds
 m99435_2069-2325,transducin-like_enhancer_protein_(tle1)_mrna,_complete_cds
 s72487_1134-1582,_orf1_5'_to_pd-ecgf/tp...orf2_5'_to_pd-
 ecgf/tp_[human,_epidermoid_carcinoma_cell_li
 u28043_1989-
 2499,plasma_membrane_na+/h+_exchanger_isoform(nhe3)_mrna,_complete_cds
 u28049_1684-2221,tbx2_(txb2)_mrna,_complete_cds
 u51003_2591-3169,dlx-2_(dlx2)_mrna,_complete_cds_
 u62739_986-1430,branched-
 chain_amino_acid_aminotransferase_(eca40)_mrna,_complete_cds
 u72509mrna_2-
 255,alternatively_spliced_b8_(b7)_mrna,_partial_sequence/gb=u72509_/ntype=rna_
 u79300_930-1404,clone_23629_mrna_sequence
 all_x69654_4-422,mrna_for_ribosomal_protein_s26
 x79439cds_16-277,notchdna_sequence/gb=x79439_/ntype=dna_/annot=cds
 x82850cds_722-1090:in_reversesequence,_1108-
 1238,mrna_for_thyroid_transcript_factor_1_
 y00414cds_1266-1537:in_reversesequence,_1573-
 1785,mrna_for_tyrosine_hydroxylase_type_3
 all_y08265_1306-1834,mrna_for_dan26_protein,_partial_
 z49254cds_75-435:in_reversesequence,_549-651,123-related_mrna_

Metagene 157

af008445_895-
 1387,phospholipid_scamblase_mrna,_complete_cds/gb=af008445_/ntype=rna_
 d29640_5767-6325,mrna_for_kiaa0051_gene,_complete_cds
 j04088_4377-4587,dna_topoisomerase_ii_(top2)_mrna,_complete_cds
 l11239exon_358-802,homeobox_protein_(hox)_gene,_3'_end
 l32179mrna_1028-1556,arylacetamide_deacetylase_mrna,_complete_cds
 m21551mrna_158-590,neuromedin_b_mrna,_complete_cds
 m24069mrna_1401-1543,dna-binding_protein_a_(dbpa)_gene,_3'_end_
 m26311_27-504,cystic_fibrosis_antigen_mrna,_complete_cds.
 all_m36200_67-428:in_m36200cds_194-339,synaptobrevin(syb1)_gene
 m36634_1340-1450,vasoactive_intestinal_peptide_(vip)_mrna,_complete_cds
 all_x04741_413-924,mrna_for_protein_gene_product_(pgp)_9.5_
 y09267_1148-1664,mrna_for_flavin-containing_monooxygenase/gb=y09267_/ntype=rna

Metagene 158

m92843_1144-1583,zinc_finger_transcriptional_regulator_mrna,_complete_cds
 u62015_1475-1841,cyr61_mrna,_complete_cds_
 v01512mrna#2_1533-2061,cellular_oncogene_c-fos_(complete_sequence)
 all_x51345_1604-1744,jun-b_mrna_for_jun-b_protein
 all_x52541_2549-3102,mrna_for_early_growth_response_protein(hegr1)
 all_x68277_1459-1952,cl_100_mrna_for_protein_tyrosine_phosphatase
 all_x75918_2858-3417,mrna_for_not

Metagene 159

d78514cds_73-409:in_reversesequence,_511-565,mrna_for_ubiquitin-
 conjugating_enzyme,_complete_cds
 m30448mrna_1936-2447,casein_kinase_ii_beta_subunit_mrna,_complete_cds
 all_x74794_2662-2906,p1-cdc21_mrna_

Metagene 160

d14811_644-1124,mrna_for_kiaa0110_gene,_complete_cds_
 d14889_760-1240,mrna_for_small_gtp-binding_protein,_s10,_complete_cds
 d21878_816-1386,mrna_for_bst-1,_complete_cds_
 hg3288-ht3465_at_hg3288-ht3465_xanthine_dehydrogenase
 j04102_1830-2184,erythroblastosis_virus_oncogene_homolog(ets-
 2)_mrna,_complete_cds
 125798_1061-1589,3-hydroxy-3-
 methylglutaryl_coenzyme_a_synthase_mrna,_complete_cds
 l41349mrna_3238-3646,phospholipase_c_beta(plcb4)_mrna,_complete_cds
 m17219_758-1286,brain_guanine_nucleotide-binding_protein_alpha-
 i_subunit_mrna,_5'_end
 u55054_3199-3697,k-cl_cotransporter_(hkcc1)_mrna,_complete_cds_
 u57094_502-1018,small_gtp-binding_protein_mrna,_complete_cds_
 u93091_4410-4806,toll_protein_homolog_mrna,_complete_cds_and_line-
 1_reverse_transcriptase_homolog,_p

Metagene 161

ab006781_528-1007,mrna_for_galectin-4,_complete_cds/gb=ab006781/_ntype=rna
 af007111_1609-2017,mdm2-like_p53-binding_protein_(mdmx)_mrna,_complete_cds
 d49357_958-1438,mrna_for_s-adenosylmethionine_synthetase,_complete_cds_
 d86984_5659-6139,mrna_for_kiaa0231_gene,_partial_cds_
 hg2261-ht2351_s_at_hg2261-ht2351_antigen,_prostate_specific,_altsplice_form_2
 hg3527-ht3721_f_at_hg3527-ht3721_luteinizing_hormone,_beta_subunit_
 hg3994-ht4264_at_hg3994-ht4264_cpg-enriched_dna,_clone_s16_
 hg4058-ht4328_at_hg4058-ht4328_oncogene_aml1-evi-1,_fusion_activated_
 hg4533-ht4938_at_hg4533-ht4938_kallistatin,_protease_inhibitor_4_
 j04739mrna_1212-
 1650,bactericidal_permeability_increasing_protein_(bpi)_mrna,_complete_cds_

115309_2444-2960,zinc_finger_protein_(znf141)_mrna,_complete_cds_
 117075_1130-1607,tnfrsf25_receptor_type_1_mrna,_complete_cds_
 124774_272-757,delta3,_delta2-coa-isomerase_mrna,_3'_end
 142583cds_1334-1665:in_reversesequence,_305-
 528,keratinisoform_k6a_(krt6a)_gene_
 all_m24900_1501-
 2054,triiodothyronine_receptor_(thra1,_ear1),_and_ear2_genes,_lastexons_each_
 m27093_2049-2509,nuclear-encoded_mitochondrial_branched_chain_alpha-
 keto_acid_dehydrogenase_transacylase_mrna,_complete_cds_
 m36067mrna_2602-3040,dna_ligase_i_mrna,_complete_cds_
 m73077_2770-3178,glucocorticoid_receptor_repression_factor(grf-
 1)_mrna,_complete_cds_
 m94055_5925-6285,voltage-gated_sodium_channel_mrna,_complete_cds_
 all_u17894_870-1231,alpha(1,2)fucosyltransferase_(fut2)_gene,_complete_cds_
 u38545_3056-3578,arf-activated_phosphatidylcholine-
 specific_phospholipase_d1a_(hpld1)_mrna,_complete_cds_
 u45448_2014-2535,p2x1_receptor_mrna,_complete_cds_
 u68727_2868-3414,homeobox-containing_protein_mrna,_complete_cds_
 u90550_2991-3513,butyrophilin_(btfd2)_mrna,_complete_cds_
 x76029cds_141-453:in_reversesequence,_636-756,mrna_for_neuromedin_u_
 all_x99226_4853-5412,mrna_for_faa_protein

Metagene 162

hg3242-ht4231_s_at_hg3242-ht4231_calcium_channel,_voltage-
 gated,_alpha_1e_subunit,_altsplice_3_
 hg4258-ht4528_at_hg4258-ht4528_kinase_inhibitor_p27kip1,_cyclin-dependent
 hg4411-ht4681_at_hg4411-ht4681_mucin,_gastric
 hg4677-ht5102_s_at_hg4677-ht5102_oncogene_ret/ptc2,_fusion_activated_
 k01900mrna_655-1213,lymphocyte_interferon_alpha_type_201_mrna,_complete_cds_
 l32961_1584-1679,4-aminobutyrate_aminotransferase_(gabat)_mrna,_complete_cds_
 l78267mrna_2573-3113,par-5_mrna,_probable_5'_end
 m10612cds_17-275:in_reversesequence,_2926-
 3822:not_in_gb_record,apolipoprotein_c-ii_gene,_complete_c
 m13686_388-897,pulmonary_surfactant-
 associated_protein_mrna,_complete_cds,_clone_mpsap-6a
 m16591mrna_1446-1933,hemopoietic_cell_protein-
 tyrosine_kinase_(hck)_gene,_complete_cds,_clone_lambda
 m81829cds_915-1137:in_reversesequence,_1260-
 1476,somatostatin_receptor_isoformgene,_complete_cds_
 s38953cds_611-820:in_reversesequence,_4446-4527,_xa_[human,_genomic,_6873_nt]
 s79281_25-
 463,_pancreatic_ribonuclease_[human,_mrna_recombinant_partial,_491_nt]/gb=s7928
 1_/ntype=rn
 u25826cds_795-1017:in_reversesequence,_4190-
 4436,transcription_factor_(sc1)_gene,_complete_cds_
 u29725_2517-2937,bmk1_alpha_kinase_mrna,_complete_cds_
 u31986_877-1381,cartilage-specific_homeodomain_protein_cart-
 1_mrna,_complete_cds_
 u36798_4071-4551,platelet_cgi-pde_mrna,_complete_cds_
 u48936_15-139,amiloride-
 sensitive_epithelial_sodium_channel_gamma_subunit_mrna,_5'_end,_partial_cds/
 u49248_4807-
 5251,canalicular_multispecific_organic_anion_transporter_(cmoat),_gene,_complet
 e_cds_

u49837_684-1218,lim_protein_mlp_mrna,_complete_cds_
 u53174_1639-2059,cell_cycle_checkpoint_control_protein_mrna,_complete_cds_
 u56814_495-957,dnase_i_homologous_protein_(dhp2)_mrna,_complete_cds_
 u60062_1060-1550,fez1-t_mrna,_alternatively_spliced_form,_complete_cds_
 u63090_1303-1813,gal_beta-1,3_galnac_alpha-
 2,3_sialyltransferase_(st3gal_ii)_mrna,_complete_cds_
 u79295_817-1345,clone_23961_mrna_sequence
 all_x65857_1542-2053,hgmp07e_gene_for_olfactory_receptor_
 x70070cds_954-1194:in_reversesequence,_1608-1800,mrna_for_neurotensin_receptor_
 x77307cds_1244-1382:in_reversesequence,_1491-1701,mrna_for_5-
 ht2b_serotonin_receptor
 all_x87160_2768-3339,mrna_for_gamma_subunit_of_epithelial_amiloride-
 sensitive_sodium_channel_
 all_x95095_487-1058,mrna_for_pdgfralpha_protein/gb=x95095_/ntype=rna_
 z26653cds_8896-9286:in_reversesequence,_9383-
 9509,mrna_for_laminin_m_chain_(merosin)
 all_z37976_6411-6916,mrna_for_latent_transforming_growth_factor-
 beta_binding_protein_(ltbp-2)
 all_z38133_5578-5993,mrna_for_myosin_
 all_z49825_1747-2253,mrna_for_hepatocyte_nuclear_factoralpha
 z70276cds_2-294,mrna_for_fibroblast_growth_factor(partial).
 z83805_199-463,mrna_for_axonemal_dynein_heavy_chain_(partial,_id_hdhc8)

Metagene 163

d63882_1015-1568,hslim15_mrna_for_hslim15,_complete_cds_
 hg2188-ht2258_at_hg2188-ht2258_paired_box_hup1_
 m37825_624-1044,fibroblast_growth_factor-5_(fgf-5)_mrna,_complete_cds_
 m60092mrna_1743-2295,myoadenylate_deaminase_(ampd1)_mrna,_complete_cds_
 s67798_1420-1930,_ph-20_[human,_testis,_mrna,_1973_nt]
 u49065_1400-1922,interleukin-1_receptor-
 related_protein_mrna,_complete_cds/gb=u49065_/ntype=rna
 u82671mrna#2_1536-1776:in_reversesequence,_106561-106657,_hsp1-
 a_gene_extracted_fromcosmids_qc14e2,_
 all_u83303_1160-2035,_gcp-2_gene_(granulocyte_chemotactic_protein-
 2)_extracted_fromline-1_reverse_tr
 all_x91148_3331-3824,mrna_for_microsomal_triglyceride_transfer_protein_

Metagene 164

af009674_2870-3308,axin_(axin)_mrna,_partial_cds_
 d13748_812-1352,mrna_for_eukaryotic_initiation_factor_4ai
 d16562_514-1042,mrna_for_atp_synthase_gamma-subunit_(l-type),_complete_cds_
 d28473_3882-4418,t-lymphocyte_mrna_for_isoleucyl-trna_synthetase,_complete_cds_
 d29643_1079-1469,mrna_for_kiaa0115_gene,_complete_cds_
 d32050_2761-3307,mrna_for_alanyl-trna_synthetase,_complete_cds_
 d42073_1551-2049,mrna_for_reticulocalbin,_complete_cds_
 d50063_1139-1553,mrna_for_proteasome_subunit_p40/_mov34_protein,_complete_cds_
 d63478_2816-3308,mrna_for_kiaa0144_gene,_complete_cds_
 d80000_5250-5754,mrna_for_kiaa0178_gene,_partial_cds_
 d86970_5998-6400,mrna_for_kiaa0216_gene,_complete_cds_
 d87071_5779-6223,mrna_for_kiaa0233_gene,_complete_cds_
 d87437_4613-5039,mrna_for_kiaa0250_gene,_complete_cds_

d89052_428-938,mrna_for_proton-atpase-like_protein,_complete_cds_
 hg1153-ht1153_at_hg1153-ht1153_nucleoside_diphosphate_kinase_nm23-h2s
 hg2279-ht2375_at_hg2279-ht2375_triosephosphate_isomerase_
 j03191mrna_192-684,profilin_mrna,_complete_cds_
 j04031_2529-3057,methylenetetrahydrofolate_dehydrogenase-
 _methenyltetrahydrofolate_cyclohydrolase-fo
 j04988cds_1925-2147:in_reversesequence,_7591-
 7831,90_kd_heat_shock_protein_gene,_complete_cds_
 l10678_1128-1650,profilin_ii_mrna,_complete_cds_
 l11669_1355-1715,tetracycline_transporter-like_protein_mrna,_complete_cds_
 l14076_1469-2051,pre-mrna_splicing_factor_srp75_mrna,_complete_cds_
 l16842_1402-1792,ubiquinol_cytochrome-
 c_reductase_core_i_protein_mrna,_complete_cds_
 l20010_7717-8185,hcf1_gene_related_mrna_sequence_
 l33243mrna_13655-
 14051,polycystic_kidney_diseaseprotein_(pkd1)_mrna,_complete_cds_
 l38696_961-1375,autoantigen_p542_mrna,_3'_end_of_cds_
 m11433_115-403,cellular_retinol-binding_protein_mrna,_complete_cds_
 m31606mrna_1102-1528,phosphorylase_kinase_(psk-c3)_mrna,_complete_cds_
 all_m34677_1486-1913,nested_gene_protein_gene,_complete_cds_
 m57567_491-953,adp-ribosylation_factor_(harf5)_mrna,_complete_cds_
 m61832_1472-2002,s-adenosylhomocysteine_hydrolase_(ahcy)_mrna,_complete_cds_
 m81601_2039-2483,transcription_elongation_factor_(sii)_mrna,_complete_cds_
 m86400_2239-2743,phospholipase_a2_mrna,_complete_cds_
 m88458_585-1095,elp-1_mrna_sequence
 m94362_3717-4179,lamin_b2_(lamb2)_mrna,_partial_cds_
 m97856_2016-2430,histone-binding_protein_mrna,_complete_cds_
 s75463_1145-
 1565,_p43=mitochondrial_elongation_factor_homolog_[human,_liver,_mrna,_1644_nt]
 _
 all_u02493_2130-2485,54_kda_protein_mrna,_complete_cds_
 u02619_6437-6965,tfiic_box_b-binding_subunit_mrna,_complete_cds_
 u18321_1065-
 1569,ionizing_radiation_resistance_conferring_protein_mrna,_complete_cds_
 u20285_1283-1811,gps1_(gps1)_mrna,_complete_cds_
 u25988_680-720,pregnancy-specific_glycoprotein(psg13'_)_mrna,_complete_cds_
 u28386_1405-
 1933,nuclear_localization_sequence_receptor_hsrplalpha_mrna,_complete_cds_
 u31556_1445-1679,transcription_factor_e2f-5_mrna,_complete_cds_
 u33053_2381-2879,lipid-activated_protein_kinase_prk1_mrna,_complete_cds_
 u36764_721-997,tgf-beta_receptor_interacting_proteinmrna,_complete_cds_
 u39400_1407-1887,nof1_mrna,_complete_cds_
 u47077_13025-13463,dna-dependent_protein_kinase_catalytic_subunit_(dna-
 pkcs)_mrna,_complete_cds_
 u51586_1262-1676,siah_binding_protein(siahbp1)_mrna,_partial_cds_
 u62136_660-
 1050,putative_enterocyte_differentiation_promoting_factor_mrna,_partial_cds_
 u66711mrna_556-1102,ly-6-related_protein_-9804_gene,_complete_cds_
 u73379_193-661,cyclin-selective_ubiquitin_carrier_protein_mrna,_complete_cds_
 u81375_1669-
 2119,placental_equilibrative_nucleoside_transporter(hent1)_mrna,_complete_cds_
 v00599mrna_903-1380,mrna_fragment_encoding_beta-tubulin(from_clone_d-beta-1)_
 all_x02152_1090-1625,mrna_for_lactate_dehydrogenase-a_(ldh-a,_ec_1.1.1.27)_
 all_x04366_2448-
 2986,mrna_for_calcium_activating_neutral_protease_large_subunit_(mucanp,_calpain
 ,_ec_

all_x05130_1362-1876,mrna_for_prolyl_4-hydroxylase_beta_subunit_(ec_1.14.11.2)_(procollagen-1-proline
 all_x14850_1122-1555,h2a.x_mrna_encoding_histone_h2a.x_
 all_x52142_2163-2734,mrna_for_ctp_synthetase_(ec_6.3.4.2)
 x58079mrna_43-565,mrna_for_s100_alpha_protein
 x67951cds_312-576:in_reversesequence,_642-888,mrna_for_proliferation-associated_gene_(pag)_
 all_x75208_3276-3781,hek2_mrna_for_protein_tyrosine_kinase_receptor
 all_x97335_3247-3704,mrna_for_kinase_a_anchor_protein
 y10807_650-1227,mrna_for_arginine_methyltransferase,_splice_variant,_1262_bp_
 z27113cds_73-325:in_reversesequence,_439-463,gene_for_rna_polymerase_ii_subunit_14.4_kd_
 z48501cds_957-1429,mrna_for_polyadenylate_binding_protein_ii/gb=z48501/_ntype=rna
 z48950exon#4_794-1100,hh3.3b_gene_for_histone_h3.3_

Metagene 165

af000959_759-1269,transmembrane_protein_mrna,_complete_cds
 d28364_4-118,mrna_for_annexin_ii,_5'_utr_(sequence_from_the_5'_cap_to_the_start_codon)/g
 b=d28364/_nt
 hg2239-ht2324_at_hg2239-ht2324_potassium_channel_protein_
 hg3075-ht3236_s_at_hg3075-ht3236_focal_adhesion_kinase_
 m28214_255-723,gtp-binding_protein_(rab3b)_mrna,_complete_cds_
 m91368_2656-3189,na+/ca+_exchanger_(cnc)_mrna,_complete_cds_
 u79734_4119-4683,huntingtin_interacting_protein_(hip1)_mrna,_complete_cds_
 x71345mrna_222-798,mrna_for_trypsinogen_iv_b-form
 all_x83535_1791-2208,mrna_for_membrane-type_matrix_metalloproteinase_

Metagene 166

af001359_2-27,dna_mismatch_repair_protein_(hmlh1)_mrna,_alternatively_spliced,_partial_cds
 /gb=af0013
 hg627-ht5097_s_at_hg627-ht5097_rhesus_(rh)_blood_group_system_ce-antigen,_altsplice_2,_rhvi
 hg627-ht5098_s_at_hg627-ht5098_rhesus_(rh)_blood_group_system_ce-antigen1,_altsplice_3,_rhviii
 l05144_2488-2598,(clone_lamda-hpec-3)_phosphoenolpyruvate_carboxykinase_(pck1)_mrna,_complete_cds_
 all_l05187_2284-2339,small_proline-rich_protein(sprrla)_gene,_complete_cds_
 l18877exon#2_980-1530,mage-12_protein_gene,_complete_cds_
 l20469_499-996,truncated_dopamine_d3_receptor_mrna,_complete_cds.
 m23323mrna_779-1309,membrane_protein_(cd3-epsilon)_gene
 s72503_1692-1870,_hrk1=inward_rectifier_potassium_channel_[human,_hippocampus,_mrna,_1913_n
 t]_
 ul2707_1280-1744,wiskott-aldrich_syndrome_protein_(wasp)_mrna,_complete_cds
 ul5641_760-1283,transcription_factor_e2f-4_mrna,_complete_cds
 u20979_2612-3068,chromatin_assembly_factor-i_p150_subunit_mrna,_complete_cds_

u73167cds#2_79-
 834,_h_luca14.2a_gene_extracted_fromcosmid_luca14,_h_luca14.2a_gene_extracted_f
 romcos
 x87344mrna#26_769-945,dma,_dmb,_hla-
 z1,_ipp2,_lmp2,_tap1,_lmp7,_tap2,_dob,_dqb2_and_ring8,_9,andgene
 x97064cds_1988-2210:in_reversesequence,_2435-
 2678,mrna_for_sec23a_isoform,_2748bp
 z30644cds_1860-1918:in_reversesequence,_2130-
 2138,mrna_for_chloride_channel_(putative)_2163bp_

Metagene 167

hg4704-ht5146_at_hg4704-ht5146_glial_growth_factor
 m19301mrna_944-1448,branched-chain_alpha-
 keto_acid_dehydrogenase_(e2)_mrna,_complete_cds_
 m95610_1971-2493,alphatype_ix_collagen_(col9a2)_mrna,_partial_cds_
 u65437mrna_7-307,homeodomain-containing_protein_(hanf)_gene,_partial_cds

Metagene 168

d00761_252-750,mrna_for_proteasome_subunit_hc5_
 d00762_237-777,mrna_for_proteasome_subunit_hc8_
 d13435_526-832,mrna_for_pig-f_(phosphatidyl-inositol-glycan_f),_complete_cds_
 d13969_1638-2148,mrna_for_mel-18_protein,_complete_cds_
 d29677_5709-6231,mrna_for_kiaa0054_gene,_complete_cds_
 d31762_6385-6775,mrna_for_kiaa0057_gene,_complete_cds_
 d31766_2024-2552,mrna_for_kiaa0060_gene,_complete_cds_
 d38449_2311-2791,mrna_for_g_protein-coupled_receptor,_complete_cds_
 d38535_2583-2973,mrna_for_pk-120_
 d43950_1355-1739,mrna_for_kiaa0098_gene,_partial_cds_
 d50487_3756-4098,mrna_for_rna_helicase_(hrh1),_complete_cds_
 d50863_1908-2370,mrna_for_tesk1,_complete_cds_
 d50922_1972-2452,mrna_for_kiaa0132_gene,_complete_cds_
 d50923_5018-5528,mrna_for_kiaa0133_gene,_complete_cds_
 d78586_6497-6923,cad_mrna_for_multifunctional_protein_cad,_complete_cds_
 d79993_2741-3167,mrna_for_kiaa0171_gene,_complete_cds_
 d79997_1881-2415,mrna_for_kiaa0175_gene,_complete_cds_
 d80010_4778-5198,mrna_for_kiaa0188_gene,_partial_cds_
 d83776_4596-5166,mrna_for_kiaa0191_gene,_partial_cds_
 d83782_3411-3915,mrna_for_kiaa0199_gene,_partial_cds_
 d84557_2412-2874,mrna_for_hsmcm6,_complete_cds_
 d86968_4437-4899,mrna_for_kiaa0213_gene,_partial_cds_
 d86971_4851-5325,mrna_for_kiaa0217_gene,_partial_cds_
 d86976_3592-4060,mrna_for_kiaa0223_gene,_partial_cds_
 hg1019-ht1019_at_hg1019-ht1019_serine_kinase_psk-h1
 hg1879-ht1919_at_hg1879-ht1919_ras-like_protein_tc10_
 hg2190-ht2260_at_hg2190-ht2260_crystallin,_beta_b3_
 hg2379-ht3997_s_at_hg2379-
 ht3997_serine_hydroxymethyltransferase,_cytosolic,_altsplice_3_
 hg2649-ht2745_s_at_hg2649-ht2745_serine/threonine_protein_kinase_cdk3
 hg3033-ht3194_r_at_hg3033-ht3194_spliceosomal_protein_sap_62_
 hg3327-ht3504_s_at_hg3327-ht3504_dna-binding_protein_hrfx2_
 hg3945-ht4215_at_hg3945-ht4215_phospholipid_transfer_protein_

hg4094-ht4364_s_at_hg4094-ht4364_transcription_factor_lsf-id_
 hg4433-ht4703_at_hg4433-ht4703_cyclin_d1_promoter
 hg511-ht511_at_hg511-ht511_ras_inhibitor_inf_
 all_j03764_14604-15049,_human,_plasminogen_activator_inhibitor-
 1_gene,_exonsto_9_
 l04953_2585-3065,x11_protein_(x11)_mrna,_3'_end
 l09260_781-1171,(chromosome_3p25)_membrane_protein_mrna
 l11284_1672-2122,_homosapiens_erk_activator_kinase_(mek1)_mrna
 l12711_1468-2000,transketolase_(tk)_mrna,_complete_cds
 l16991_679-1132,thymidylate_kinase_(cdc8)_mrna,_complete_cds_
 l25286_4549-5081,alpha-1_type_xv_collagen_mrna,_complete_cds
 l32976_2969-3533,protein_kinase_(mlk-3)_mrna,_complete_cds_
 l36529mrna_1491-2043,(clone_n5-4)_protein_p84_mrna,_complete_cds_
 l36983mrna_3012-3546,dynamin_(dnm)_mrna,_complete_cds_
 l37347_1301-1835,integral_membrane_protein_(nramp2)_mrna,_partial
 all_m13241_5990-6537,n-myc_gene,_exonsand_3_
 all_m15205_12942-
 l3411,thymidine_kinase_gene,_complete_cds,_with_clustered_alu_repeats_in_the_in
 tron
 m16707mrna_6-
 357,histone_h4_gene,_complete_cds,_clone_fo108,histone_h4_gene,_complete_cds,_c
 lone_fo1
 m20747_1519-2034,insulin-
 responsive_glucose_transporter_(glut4)_mrna,_complete_cds_
 m21121_958-1129,t_cell-specific_protein_(rantes)_mrna,_complete_cds
 m21154mrna_1234-1756,s-adenosylmethionine_decarboxylase_mrna,_complete_cds_
 m23668exon_743-1271,adrenodoxin_gene
 m24470mrna_911-1355,glucose-6-phosphate_dehydrogenase,_complete_cds
 m25280_1753-2299,lymph_node_homing_receptor_mrna,_complete_cds_
 m28249_4850-5306,very_late_antigen-2_(vla-2)/collagen_receptor_alpha-
 2_subunit_mrna,_complete_cds
 m29536_1025-1361,translational_initiation_factorbeta_subunit_(elf-2-
 beta)_mrna,_complete_cds
 m34539_1051-1477,fk506-binding_protein_(fkbp)_mrna,_complete_cds_
 m38591_120-600,cellular_ligand_of_annexin_ii_(p11)_mrna,_complete_cds_
 m54915_2208-2236,h-pim-1_protein_(h-pim-1)_mrna,_complete_cds
 m60091_1118-1248,galactose-1-phosphate_uridyl_transferase_mrna,_complete_cds_
 m60450_1932-2404,voltage-gated_potassium_channel_(hk1)_mrna,_complete_cds
 m60527mrna_1877-2369,deoxycytidine_kinase_mrna,_complete_cds_
 m63180_2055-2505,threonyl-trna_synthetase_mrna,_complete_cds_
 m69013_1053-1515,guanine_nucleotide-binding_regulatory_protein_(g-y-
 alpha)_mrna,_complete_cds
 m69039_625-1171,pre-mrna_splicing_factor_sf2p32,_complete_sequence_
 m86852_1041-1557,peroxisome_assembly_factor-1_mrna,_complete_cds_
 m87339_875-1361,replication_factor_37-kda_subunit_mrna,_complete_cds
 m87434_2316-2862,71_kda_2'_5'_oligoadenylate_synthetase_(p69_2-
 5a_synthetase)_mrna,_complete_cds_
 s77356_3-
 41,_transcript_ch21=oligomycin_sensitivity_conferral_protein_oscp_homolog_[huma
 n,_rf1,rf48_
 s78187_2548-3064,_cdc25hu2=cdc25+_homolog_[human,_mrna,_3118_nt]
 u04810_2050-2536,tastin_mrna,_complete_cds_
 u05681exon#7_111-544,proto-oncogene_bcl3_gene
 u10362_848-1352,gp36b_glycoprotein_mrna,_complete_cds
 u14391_4095-4623,myosin-ic_mrna,_complete_cds
 u15131_3802-4252,p126_(st5)_mrna,_complete_cds_
 u20428_2450-2840,snc19_mrna_sequence_

u24704_790-1264,antisecretory_factor-1_mrna,_complete_cds
 u29607_1974-2148,methionine_aminopeptidase_mrna,_complete_cds
 u34683_1261-1735,glutathione_synthetase_mrna,_complete_cds_
 u41668_520-976,deoxyguanosine_kinase_mrna,_complete_cds
 u52828_1418-1882,cri-du-chat_region_mrna,_clone_niba2
 u53347_2278-2812,neutral_amino_acid_transporter_b_mrna,_complete_cds_
 u56402_2969-
 3471,chromatin_structural_protein_homolog_(supt5h)_mrna,_complete_cds
 u58766_741-1299,fx_protein_mrna,_complete_cds
 u59752_524-938,sec7p-like_protein_mrna,_partial_cds
 u59919_2047-2575,smg_gds-associated_protein_smap_mrna,_complete_cds
 u60325_3700-
 4252,dna_polymerase_gamma_mrna,_nuclear_gene_encoding_mitochondrial_protein,_co
 mplete_cd
 u62293mrna_2576-3152,_limk1_gene_(lim-kinase1)_extracted_fromlim-
 kinase1_and_alternatively_spliced_l
 u69127_2758-3106,fuse_binding_protein(fbp3)_mrna,_partial_cds_
 u71374_617-1157,hspex13p_mrna,_complete_cds/gb=u71374_/ntype=rna_
 all_u73167_4971-
 35099,_h_luca14.2a_gene_extracted_fromcosmid_luca14,_h_luca14.2a_gene_extracted
 _from
 u83463_1406-1862,scaffold_protein_pbp1_mrna,_complete_cds
 u86070_629-1205,phosphomannomutase_mrna,_complete_cds
 u87269_1976-2468,p120e4f_transcription_factor_mrna,_complete_cds.
 u91985_1014-1320,dna_fragmentation_factor-45_mrna,_complete_cds
 u94319_2044-2404,autoantigen_dfs70_mrna,_partial_cds.
 all_x03794_570-1150,embryonic_mrna_3'_end_with_homoeo_box_(clone_hhoc10)_
 all_x05299_2010-2572,mrna_(~95%)_for_major_centromere_autoantigen_cenp-b_
 all_x06389_1582-2087,mrna_for_synaptophysin_(p38)
 all_x07695_1175-1722,mrna_for_cytokeratinc-terminal_region
 all_x15331_813-1194,mrna_for_phosphoribosylpyrophosphate_synthetase_subunit_one
 x15722cds_931-1411:in_reversesequence,_1569-
 1575,mrna_for_glutathione_reductase_(ec_1.6.4.2)
 x15822cds_18-222:in_reversesequence,_13-379,cox_viia-1_mrna_for_liver-
 specific_cytochrome_c_oxidase_
 x17620mrna_257-
 677,mrna_for_nm23_protein,_involved_in_developmental_regulation_(homologto_dros
 ophila
 x54637cds_3359-3539:in_reversesequence,_3857-4133,tyk2_mrna_for_non-
 receptor_protein_tyrosine_kinase
 all_x59727_3618-4201,63_kda_protein_kinase_related_to_rat_erk3_
 x63417cds_170-524:in_reversesequence,_560,irlb_mrna_
 all_x63522_1800-1997,mrna_daudi6_for_retinoic_acid_x_receptor_b
 x63657mrna_1683-2169,fvt1_mrna_
 x63679cds_587-1073,mrna_for_tramp_protein
 all_x69115_718-998,znf37a_mrna_for_zinc_finger_protein_
 x71129cds_213-705,mrna_for_electron_transfer_flavoprotein_beta_subunit_
 x74330cds_788-1154:in_reversesequence,_1281-
 1335,mrna_for_dna_primase_(subunit_p48)_
 x74801cds_1282-1552:in_reversesequence,_1636-1837,cctg_mrna_for_chaperonin
 x74874mrna_5857-
 6262,_rna_polymerase_ii_largest_subunit_gene_extracted_fromgene_for_rna_pol_ii_
 large
 x78992cds_1349-1373,erf-2_mrna_
 all_x80910_3085-3566,ppp1cb_mrna_
 x81788_397-799,ds-1_mrna_

x92720cds_1540-1888:in_reversesequence,_1978-
 2086,mrna_for_phosphoenolpyruvate_carboxykinase
 x93510cds_548-956:in_reversesequence,_1021-
 1069,mrna_for_37_kda_lim_domain_protein
 x97544cds_291-453:in_reversesequence,_508-
 724,mrna_for_tim17_preprotein_translocase_
 x98248mrna_3140-3698,mrna_for_sortilin
 x98534exon#10_287-798,vasp_gene,_exonsto_13_
 x99947_2580-2922:in_reversesequence,_2994-3084,mrna_dynein-related_protein
 y00636cds_586-688:in_reversesequence,_739-
 985,mrna_for_lymphocyte_function_associated_antigen-3_(lfa
 all_y11681_529-
 1040,mrna_for_mitochondrial_ribosomal_protein_s12/gb=y11681_/ntype=rna_
 z23064_1461-1755,mrna_gene_for_hnrnp_g_protein_
 all_z48042_2679-3232,mrna_encoding_gpi-anchored_protein_p137_
 all_z70219_4-188,mrna_for_5'utr_for_unknown_protein_(clone_icrfp507c0696)
 z84497cds_1915-2230:in_fullsequence,_18383-
 18624,dna_sequence_from_cosmid_o14_on_chromosomecontains_

Metagene 169

d50928_2629-3019,mrna_for_kiaa0138_gene,_complete_cds
 hg2417-ht2513_at_hg2417-ht2513_dynein,_heavy_chain,_cytoplasmic
 m15958cds_12-282:in_reversesequence,_6718-6778,gastrin_gene,_complete_cds_
 u68162mrna_3059-
 3585,_mpl_gene_(thrombopoietin_receptor)_extracted_fromthrombopoietin_receptor_
 (mpl)
 all_x60484_683-858,h4/e_gene_for_h4_histone
 x68505_2403-2879,mrna_for_myocyte-specific_enhancer_factor(mef2)

Metagene 170

109230_933-1460,c-c_chemokine_receptor_type(c-c_ckr-1)_mrna,_complete_cds_
 147276_383-934,(cell_line_hl-60)_alpha_topoisomerase_truncated-
 form_mrna,_3'_utr/gb=147276_/ntype=rn
 m13150mrna_776-1337,mas_proto-oncogene_mrna,_complete_cds
 m20137mrna_400-820,interleukin(il-3)_mrna,_complete_cds,_clone_pcd-sr-alpha_
 u33202_104-354,mdm2-d_(mdm2)_mrna,_complete_cds/gb=u33202_/ntype=rna_
 all_x66894_3881-4417,facc_mrna_from_complementation_group_c_(fa(c))
 all_y08263_1373-1902,mrna_for_aad14_protein,_partial_
 all_y09980_16580-17121,hoxd3_gene_

Metagene 171

hg1111-ht1111_at_hg1111-ht1111_ras-like_protein_tc21_
 k02100mrna_983-
 1421,ornithine_transcarbamylase_(otc)_mrna,_complete_coding_sequence
 u08015mrna_2388-2700,nf-atc_mrna,_complete_cds_
 u09413_1957-2389,zinc_finger_protein_znf135_mrna,_complete_cds_
 u70862_1029-1248,nuclear_factor_i_b3_mrna,_complete_cds

all_x01059_941-
 1512,placenta_mrna_for_luteinizing_hormone_releasing_hormone_precursor_(lhrh)_
 all_x66436_1427-1980,hsr1_mrna_(partial)_
 x80507cds_1020-1314:in_reversesequence,_1624-1828,yap65_mrna_
 all_x99141_1411-1715,mrna_for_hair_keratin,_hkb3_

Metagene 172

m22430_300-732,rasf-a_pla2_mrna,_complete_cds
 u80669_863-1403,androgen_regulated_homeobox_protein_(nkx3.1)_mrna,_complete_cds
 z70222cds_3-213:in_reversesequence,_25-37,mrna_for_orf_(clone_icrfp507g2490)

Metagene 173

m24736_3222-3785,endothelial_leukocyte_adhesion_molecule(elam-
 1)_mrna,_complete_cds_
 y07565cds_307-614:in_reversesequence,_833-1024,mrna_for_rin_protein_

Metagene 174

d89289_1431-1947,mrna_for_n-acetyl-beta-d-glucosaminide,_complete_cds
 l05188cds_2-194:in_reversesequence,_281-342,small_proline-
 rich_protein(spr2b)_gene,_complete_cds_
 m74509_7730-8246,endogenous_retrovirus_type_c_oncovirus_sequence.
 s70004_2347-2779,_glycogen_synthase_[human,_liver,_mrna,_2912_nt]_
 u65416mrna_1983-2316,mhc_i_molecule_(micb)_gene,_complete_cds_
 u79285_892-1402,clone_23828_mrna_sequence

Metagene 175

m31661_2134-2674,prolactin_(prl)_receptor_mrna,_complete_cds_
 u12139exon_13-
 151,alpha1(xi)_collagen_(col11a1)_gene,_5'_region_and_exon/gb=u12139_/ntype=dna
 _/annot

Metagene 176

j04027_4061-4343,plasma_membrane_ca2+_pumping_atpase_mrna,_complete_cds
 m11119mrna_722-1011,endogenous_retrovirus_envelope_region_mrna_(pl1)_
 u29656_247-751,dr-nm23_mrna,_complete_cds
 u48251_2308-2651:not_in_gb_record,protein_kinase_c-
 binding_protein_rack7_mrna,_partial_cds
 u68019_1774-2218,rad_protein_homolog_(hmad-3)_mrna,_complete_cds_
 u77604_13-493,microsomal_glutathione_s-transferase_(gst-ii)_mrna,_complete_cds_
 u96922_2336-2822,inositol_polyphosphate_4-phosphatase_type_ii-
 alpha_mrna,_complete_cds/gb=u96922_/nt

x70940cds_1130-1298:in_reversesequence,_1591-
 1722,mrna_for_elongation_factoralpha-2_
 x71973cds_200-530:in_reversesequence,_658-808,gpx-
 4_mrna_for_phospholipid_hydroperoxide_glutathione_
 y07827cds_785-972,mrna_for_putb7,3_molecule_of_cd80-cd60_protein_family

Metagene 177

hg1148-ht1148_at_hg1148-ht1148_lipopolysaccharide-binding_protein
 hg2309-ht2405_at_hg2309-ht2405_insulin-like_growth_factor_ib_
 u70370_1511-
 2012,hindlimb_expressed_homeobox_protein_backfoot_(bft)_mrna,_complete_cds_
 all_x15573_2313-2800,liver-type_1-phosphofructokinase_(pfkl)_mrna,_complete_cds_
 x66365cds_543-957:in_reversesequence,_1080-
 1206,mrna_plstire_for_serine/threonine_protein_kinase
 all_x85786_1751-2262,mrna_for_dna_binding_regulatory_factor
 x86564cds_417-446:not_in_gb_record,fhr-2_gene,_exon_1_
 all_x95240_1487-2056,mrna_for_cysteine-rich_secretory_protein-3

Metagene 178

ab000895_25-385,mrna_for_cadherin_fib1,_partial_cds/gb=ab000895/_ntype=rna
 all_d00408_1838-1946,fetal_liver_cytochrome_p-450_(p-
 450_hfla),_complete_cds,fetal_liver_cytochrome_
 d26018_2865-3381,mrna_for_kiaa0039_gene,_partial_cds_
 d83646_1984-2452,mrna_for_metalloproteinase,_complete_cds
 d83767_917-1319,clone_n9_rep-8_mrna,_complete_cds
 d84307_1321-
 1813,cdna_for_phosphoethanolamine_cytidylyltransferase,_complete_cds_
 hg2714-ht2810_at_hg2714-ht2810_tyrosine_kinase_
 hg3893-ht4163_at_hg3893-ht4163_phosphoglucomutase_1,_altsplice_
 l12701cds_103-283:in_reversesequence,_325-
 463,engrailed_protein_(en2)_gene,_5'_end_
 l37882_1340-1814,frizzled_gene_product_mrna,_complete_cds
 l41919mrna_1877-2450,hic-1_gene_fragment_
 l76937mrna_4642-
 5098,_unnamed_protein_product_gene_extracted_fromwerner_syndrome_gene,_complete_
 _cds
 all_m32053_2900-3489,h19_rna_gene,_complete_cds_(spliced_in_silico)
 all_m58569_4044-4260,fibrinogen_alpha-
 subunit_bipartite_transcript,_complete_cds_of_extended_(alpha-
 m64710cds_64-353:in_reversesequence,_1226-1353,c-
 type_natriuretic_peptide_gene,_complete_cds
 m77829_737-1269,channel-
 like_integral_membrane_protein_(chip28)_mrna,_complete_cds_
 m81830cds_716-1040:in_reversesequence,_1170-
 1326,somatostatin_receptor_isoform(ssr2)_gene,_complete
 u03399_1649-2147,t-complex_protein_10a_(tcp10a)_mrna,_complete_cds_
 u11287_5386-5932,n-methyl-d-
 aspartate_receptor_subunit_nr3_(hnr3)_mrna,_complete_cds_
 u12622_4-
 358,beaded_intermediate_filament_protein_cp115_mrna,_partial_cds/gb=u12622/_nty
 pe=rna_

u22314_2753-3311,rest_protein_mrna,_complete_cds_
 u48436_5739-
 6290,fragile_x_mental_retardation_protein_fmr2p_(fmr2)_mrna,_complete_cds
 u50315_2179-2551,enhancer_of_zeste_homolog(ezh1)_mrna,_complete_cds_
 all_u58658_522-1093,unknown_protein_mrna_within_the_p53_intron_1,_complete_cds_
 u62431_2093-
 2633,nicotinic_acetylcholine_receptor_alpha2_subunit_precursor,_mrna,_complete_cds_
 u87460_3537-4113,putative_endothelin_receptor_type_b-
 like_protein_mrna,_complete_cds_
 u89335exon#30_375-
 909,_notch4_gene_(notch4)_extracted_fromhla_iii_region_containing_notch4_(notch
 4)_
 x62429cds_438-784:in_reversesequence,_877-
 994,mrna_for_transcription_factor_pit-1_
 all_x75315_849-1348,seb4b_mrna_
 x83703mrna_1284-1854,mrna_for_cytokine_inducible_nuclear_protein_
 all_z35102_2543-3018,mrna_for_ndr_protein_kinase_
 z48512exon#4_87-303,xg_mrna_(clone_pep6)/gb=z48512_/ntype=rna
 all_z83742_507-757,hh2a/c_gene.

Metagene 179

d42138_1371-1833,mrna_for_pig-b,_complete_cds
 d45132_5577-6099,kidney_mrna_for_zinc-finger_dna-binding_protein,_complete_cds_
 hg3914-ht4184_s_at_hg3914-ht4184_cell_division_cycle_protein_2-
 related_protein_kinase_(pisslre)
 hg4144-ht4414_at_hg4144-ht4414_zinc_finger_protein_hzf6
 l10333mrna_2590-3166,neuroendocrine-
 specific_protein_a_(nsp)_mrna,_complete_cds_
 m31328mrna_1054-1480,guanine_nucleotide-binding_protein_beta-
 3_subunit_mrna,_complete_cds
 m96944_2724-3252,b-cell_specific_transcription_factor_(bsap)_mrna,_complete_cds
 u25138_676-1168,maxik_potassium_channel_beta_subunit_mrna,_complete_cds
 u57629_2195-
 2735,retinitis_pigmentosa_gtpase_regulator_(rpgr)_mrna,_complete_cds_
 u68494_1290-1764,hbc647_mrna_sequence
 u80457_2243-2645,transcription_factor_sim2_short_form_mrna,_complete_cds_
 x59842mrna_2321-2861,pbx2_mrna
 all_y07759_5956-6377,mrna_for_myosin_heavy_chain_12
 all_y08976_956-1548,mrna_for_fev_protein_
 z50115cds_1782-2011:in_reversesequence,_2181-
 2473,mrna_for_thimet_oligopeptidase_(metalloproteinase)

Metagene 180

m21188mrna_2754-3204,insulin-degrading_enzyme_(ide)_mrna,_complete_cds_
 s66896_1272-
 1638,_squamous_cell_carcinoma_antigen=serine_protease_inhibitor_[human,_mrna,_1
 711_nt]
 u06452_923-1475,melanoma_antigen_recognized_by_t-cells_(mart-1)_mrna_
 u13616_14235-14709,ankyrin_g_(ank-3)_mrna,_complete_cds
 all_x70340_3545-4062,mrna_for_transforming_growth_factor_alpha_

Metagene 181

af000545cds_461-
 983,putative_purinergic_receptor_p2y10_gene,_complete_cds/gb=af000545_/ntype=dn
 a_/an
 d79995_4440-4806,mrna_for_kiaa0173_gene,_complete_cds
 hg2314-ht2410_at_hg2314-ht2410_4-beta-galactosyltransferase
 hg2325-ht2421_at_hg2325-ht2421_retinoic_acid_receptor,_gamma_2_
 j00212mrna_393-761,leukocyte_interferon_(ifn-alpha)_alpha-f_mrna,_complete_cds_
 l40394mrna_1312-1750,(clone_s194)_mrna,_3'_end_of_cds_
 l77566mrna_1103-1655,dgs-i_mrna,_3'_end_
 m15517cds#3_155-419:in_reversesequence,_803-
 923,_ttr_gene_extracted_frommutant_prealbumin_gene_direct
 m55267mrna_573-1035,ev12_protein_gene
 m77235_7902-8418,cardiac_tetrodotoxin-insensitive_voltage-
 dependent_sodium_channel_alpha_subunit_(hh
 m80899_3582-4002,novel_protein_ahnak_mrna,_partial_sequence
 all_m81780_3896-
 4359,_smpd1_gene_(acid_sphingomyelinase)_extracted_fromacid_sphingomyelinase_(s
 mpd1)
 m86934_1529-1973,gs1_(protein_of_unknown_function)_mrna,_complete_cds
 m90820_1286-1742,rapamycin-binding_protein_(fkbp25)_mrna,_complete_cds_
 s77415cds_660-948:in_reversesequence,_1449-1617,_melanocortin-
 4_receptor_[human,_genomic,_1671_nt]_
 u01212cds_153-411:in_reversesequence,_1715-
 1943,olfactory_marker_protein_(omp)_gene,_complete_cds_
 u03187_1505-2015,il12_receptor_component_mrna,_complete_cds
 u09607_3463-3730,jak_family_protein_tyrosine_kinase_(jak3)_mrna,_complete_cds
 u11717_3500-3743,calcium_activated_potassium_channel_(hsl0)_mrna,_complete_cds_
 u12779_1685-1959,map_kinase_activated_protein_kinase_mrna,_complete_cds
 all_u13061_518-1020,dehydroepiandrosterone_sulfotransferase_(std)_gene
 u20325exon#3_57-
 477,cocaine_and_amphetamine_regulated_transcript_cart_(hcart)_gene,_complete_cd
 s_
 u27330_1474-
 1933,alpha_(1,3)_fucosyltransferase_(fut5)_mrna,_minor_transcript_ii,_complete_
 cds_
 u30185_1981-2485,orphan_opioid_receptor_mrna,_complete_cds_
 u32331_1974-2526,rig_mrna,_complete_sequence_
 u46901mrna#1_1088-1640,nacp_gene_
 u48437_1855-2293,amyloid_precursor-like_protein_mrna,_complete_cds_
 u57057cds_1239-1515:in_reversesequence,_1871-
 2069,wd_protein_ir10_mrna,_complete_cds
 u63312exon#1_4-199:not_in_gb_record,cosmid_1112nc01-
 242e1,_etv6_gene,_exons_1b_andand_partial_cds/gb
 u79266_972-1482,clone_23627_mrna,_complete_cds.
 u79302_1414-1906,clone_23855_mrna,_partial_cds.
 u80987_438-
 948,transcription_factor_tbx5_mrna,_complete_cds/gb=u80987_/ntype=rna_
 u82759_406-571,homeodomain_protein_hoxa9_mrna,_complete_cds
 all_x04201_619-1073,skeletal_muscle_1.3_kb_mrna_for_tropomyosin
 x66364cds_454-
 814:in_reversesequence,_922,mrna_pssalre_for_serine/threonine_protein_kinase
 all_x67734_4037-4470,mrna_for_transient_axonal_glycoprotein_(tag-1)

all_x69699_2155-2654,pax8_mrna_
all_x83378_4940-5523,mrna_for_putative_chloride_channel

Metagene 182

d16626_2478-3006,mrna_for_histidase,_complete_cds
d84424_1603-2053,fetal_brain_mrna_for_hyaluronan_synthase,_complete_cds
hg2999-ht4756_s_at hg2999-ht4756_thyroid_peroxidase,_altsplice_2_
l31529cds_1308-1578:in_reversesequence,_1945-2053,beta1-
syntrophin_(snt_b1)_gene,_complete_cds_
m81650mrna_1200-1566,semenogelin_i_(semgi)_gene,_complete_cds_
u46023_4040-4544,xq28_mrna,_complete_cds_
all_z48570_1408-1991,sp17_gene_

Metagene 183

l05628_4400-4969,multidrug_resistance-
associated_protein_(mrp)_mrna,_complete_cds
l07541_950-1436,replication_factor_38-kda_subunit_mrna,_complete_cds
u28413_1440-
1926,cockayne_syndrome_complementation_group_a_csa_protein_(csa)_mrna,_complete_cds

Metagene 184

d13720_3754-4319,mrna_for_lyk,_complete_cds
d30715mrna#3_3-198,_alternative_splicing;_type-2_mrna_from_pap_(pancreatitis-associated_protein)_gene
l39061mrna_1198-1654,transcription_factor_sl1_mrna,_partial_cds_
m34276cds_2066-2228:in_reversesequence,_213-354,plasminogen_gene
u09178_3355-3898,dihydropyrimidine_dehydrogenase_mrna,_complete_cds
u37707_2429-2969,dlg3_mrna,_complete_cds_
u38291mrna_9685-10027,microtubule-associated_protein_1a_(map1a)_genomic_sequence
u66578cds_598-1036:in_reversesequence,_1277,putative_g_protein-coupled_receptor_(gpr23)_gene,_complete_cds_
u69263_474-1002,matrilin-2_precursor_mrna,_partial_cds_
u79667_3199-3522,alpha1a-voltage-dependent_calcium_channel_mrna,_splice_form_bi-1-v2-ggcag,_partial_cds_
u87223_4830-5196,contactin-associated_protein_(caspr)_mrna,_complete_cds_
x01388cds_14-272:in_reversesequence,_349-529,mrna_for_pre-apolipoprotein_ciii_x66358cds#1_633-1041,mrna_kkialre_for_serine/threonine_protein_kinase
x75346cds_788-1157:in_reversesequence,_1205-
1305,mrna_for_map_kinase_activated_protein_kinase_

Metagene 185

af009301_2752-3262,teb4_protein_mrna,_complete_cds/gb=af009301/_ntype=rna_
u73304mrna_4973-5447,cb1_cannabinoid_receptor_(cnr1)_gene,_complete_cds.

x53414mrna_907-1453,mrna_for_peroxisomal_l-alanine:glyoxylate_aminotransferase_
 x59739mrna_5061-5473,zfx_mrna_for_puttranscription_activator,_isoform_2
 x60955cds_2-147:in_reversesequence,_154-168,tyrrp_gene_for_tyrosinase-
 related_protein_(trp-1)_(parti

Metagene 186

m11726exon#1_49-163:in_reversesequence,_1559-
 2534:not_in_gb_record,pancreatic_polypeptide_gene,_comp
 u15590_306-840,heat_shock_protein_27_(hsp27)_mrna,_complete_cds

Metagene 187

l08835mrna#1_3166-
 3367,_dm_kinase_gene_(myotonic_dystrophy_kinase)_extracted_frommyotonic_dystrop
 hy_
 all_m19311_876-
 1059,calmodulin_mrna,_complete_cds,calmodulin_mrna,_complete_cds_
 u53506_1344-1836,type_ii_iodothyronine_deiodinase_mrna,_complete_cds.

Metagene 188

d10537_1359-1876,mrna_for_major_structural_protein_of_myelin,_complete_cds_
 d26443_3282-3822,mrna_for_glutamate_transporter,_complete_cds
 d31897_1050-1548,mrna_for_doc2_(double_c2),_complete_cds_
 d38081_2769-2853,mrna_for_thromboxane_a2_receptor,_complete_cds
 d43767_43-505,mrna_for_chemokine,_complete_cds_
 d50855_2772-3309,mrna_for_ca-sensing_receptor,_complete_cds
 d63940_153-656,mrna_for_mx11_protein,_complete_cds_
 d80007_5240-5768,mrna_for_kiaa0185_gene,_partial_cds_
 d82344_2434-2986,mrna_for_nbphox,_complete_cds_
 d89501exon#3_206-441,pbi_gene,_complete_cds
 hg3405-ht3586_at_hg3405-ht3586_zinc_finger_protein_hzf3
 hg3495-ht3689_at_hg3495-ht3689_collagen,_type_ix,_alpha_1
 hg358-ht358_at_hg358-ht358_homeotic_protein_7,_notch_group_
 hg3921-ht4191_f_at_hg3921-ht4191_homeotic_protein_c6,_i
 hg3962-ht4232_at_hg3962-ht4232_sialyltransferase,_stx
 hg4069-ht4339_s_at_hg4069-ht4339_monocyte_chemotactic_protein_
 hg4318-ht4588_s_at_hg4318-ht4588_lim-domain_transcription_factor_lim-1_
 l07738_717-1125,dhp-
 sensitive_calcium_channel_gamma_subunit_(cacnlg)_mrna,_complete_cds_
 l07765_1443-1923,carboxylesterase_mrna,_complete_cds_
 l10403_834-
 l254,dna_binding_protein_for_surfactant_protein_b_mrna,_complete_cds_
 l31881_929-1385,nuclear_factor_i-x_mrna,_complete_cds
 l38517mrna_766-1228,indian_hedgehog_protein_(ihh)_mrna,_5'_end
 l43338mrna_25-151,(clone_jj1a)_cadherin_mrna_fragment/gb=l43338_/ntype=rna
 l43366mrna_13-157,(clone_jj1b)_cadherin_mrna_fragment/gb=l43366_/ntype=rna
 m15059mrna_1025-1487,fc-
 epsilon_receptor_(ige_receptor)_mrna,_complete_cds_(h107_epitope)

all_m19878_1799-
 1946,calbindin_27_gene,_exonsand_2,_and_alu_repeat/gb=m19878_/ntype=dna_/annot=
 exon,
 m20203cds_242-364,neutrophil_elastase_gene_
 m55047_2637-3207,synaptotagmin_mrna,_complete_cds
 m55067_754-1324,47-
 kd_autosomal_chronic_granulomatous_disease_protein_mrna,_complete_cds_
 m59488mrna_536-1016,s100_protein_beta-subunit_gene_
 all_m60752_611-863,histone_h2a.1_(h2a)_gene,_complete_cds
 m64676mrna_1619-1892,k+_channel_subunit_gene,_complete_cds_
 m80647_1317-1857,thromboxane_synthase_mrna,_complete_cds
 m84371mrna_1318-1824,cd19_gene,_complete_cds
 m85247mrna_141-
 597,dopamine_d1a_receptor_gene,_complete_exon_1,_and_exon_2,_5'_end/gb=m85247_/
 ntype=
 all_m86528_954-1357,neurotrophin-4_(nt-4)_gene,_complete_cds_
 m97639_3533-4037,transmembrane_receptor_(ror2)_mrna,_complete_cds
 m97675_2799-3309,transmembrane_receptor_(ror1)_mrna,_complete_cds
 m97925mrna_121-409,defensin_gene,_complete_cds
 s71824_2437-2881,_n-
 cam=145_kda_neural_cell_adhesion_molecule_[human,_small_cell_lung_cancer_cell_l
 i
 u05659_581-1049,17beta-hydroxysteroid_dehydrogenase_type_mrna,_complete_cds
 u06698_3269-3779,neuronal_kinesin_heavy_chain_mrna,_complete_cds_
 u10485_1906-2326,lymphoid-restricted_membrane_protein_(jaw1)_mrna,_complete_cds
 u11037_19-499,sel-1_like_mrna,_complete_cds
 u11875_48-144,interleukin-
 8_receptor_type_b_(il8rb)_mrna,_splice_variant_il8rb4,_partial_cds/gb=u118
 all_u12471_1014-1255,_thrombospondin-p50_gene_extracted_from_thrombospondin-
 1_gene,_partial_cds
 u16861_1076-1610,inward_rectifying_potassium_channel_mrna,_complete_cds
 u28131_88-283,hmgi-c_chimeric_transcript_mrna,_partial_cds.
 u29700cds_1308-1644:in_reversesequence,_8352-8382,anti-
 mullerian_hormone_type_ii_receptor_precursor_
 u35340_442-868,beta_b1-crystallin_mrna,_complete_cds_
 u38227_3-411,testis-specific_hexokinase(hhk1-
 tb)_mrna,_partial_cds/gb=u38227_/ntype=rna_
 u45982cds_759-1035:in_reversesequence,_1110-1338,g_protein-
 coupled_receptor_gpr-9-6_gene,_complete_c
 u49742cds_744-984:in_reversesequence,_5287-5473,rhodopsin_gene,_complete_cds
 u50146mrna_39-543,type_neuropeptide_y_receptor_(npy_y2)_gene,_partial
 u62433_2748-
 3318,nicotinic_acetylcholine_receptor_alpha4_subunit_precursor,_mrna,_complete_
 cds_
 u76366_4225-4720,treacher_collins_syndrome_(tcof1)_mrna,_complete_cds
 u79303_939-1479,clone_23882_mrna,_complete_cds.
 u83171_2313-2865,macrophage-
 derived_chemokine_precursor_(mdc)_mrna,_complete_cds_
 x05323cds_426-792:not_in_gb_record,mrc_ox-2_gene_signal_sequence
 x14830cds_1033-1423:in_reversesequence,_1547-
 1571,mrna_for_muscle_acetylcholine_receptor_beta-subuni
 x16666cds_422-841:in_reversesequence,_894-984,hox2i_mrna_from_the_hox2_locus
 x64044cds_1066-1402:in_reversesequence,_1538-
 1592,mmrna_for_large_subunit_of_splicing_factor_u2af_
 x71135cds_1083-1308:in_reversesequence,_1752-1977,sox3_gene
 x73113cds_2973-3339:in_reversesequence,_3430-3520,mrna_for_fast_mybp-c
 all_x74496_1967-2520,mrna_for_prolyl_oligopeptidase

x76770mrna_1421-1931,pap_mrna
 x78710mrna_2773-3247,mtf-1_mrna_for_metal-regulatory_transcription_factor
 all_x79200_380-600,mrna_for_syt-
 ssx,_synovial_sarcoma_translocation_junction/gb=x79200_/ntype=rna,mr
 x83572_1392-1920,arsd_mrna_
 all_x93921_942-1471,mrna_for_protein-tyrosine-phosphatase_(tissue_type:_testis)
 y09321cds_1961-2375:in_reversesequence,_2423-2501,tafii105_mrna,_partial
 y09392exon#4_364-884,mrna_for_wsl-lr,_wsl-s1_and_wsl-s2_proteins_
 y10141cds_56-286,dat1_gene,_partial,_vntr/gb=y10141_/ntype=dna_/annot=cds
 z47038cds_267-698,partial_cdna_sequence,_clone_x101,_putative_microtubule-
 associated;_protein_1a_(ma
 z48510exon#5-7_47-
 6:in_reversesequence,_471,xg_mrna_(clone_fb1)/gb=z48510_/ntype=rna
 z68274cds_182-
 632,dna_sequence_from_cosmid_1129h7,_huntington_disease_region,_chromosome_4p16
 .3_cont

Metagene 189

af000562_43-427,uoplakin_ii_mrna,_partial_cds
 d63134mrna_73-439,mrna_for_ets-like_30_kda_protein/gb=d63134_/ntype=rna
 all_j00220_1704-1849,ig_germline_h-chain_g-e-a_region_a:_gamma-
 3_5'_flank,ig_germline_h-chain_g-e-a_
 all_j05253_8895-9496,interstitial_retinol-
 binding_protein_(irbp)_gene,_complete_cds
 l37792mrna_1565-2015,syntaxin_1a_mrna,_complete_cds
 all_m23533_3030-3556,alphaadrenergic_receptor_gene,_complete_cds
 m29610_179-
 451,glycophorin_e_mrna,_complete_cds,glycophorin_e_mrna,_complete_cds
 u13706_3-63,elav-like_neuronal_proteinisoform_hel-n2_(hel-
 n1)_mrna,_partial_cds/gb=u13706_/ntype=rna
 u14383_958-1372,mucin_(muc8)_mrna,_partial_cds_
 u20536_935-1428,cysteine_protease_mch2_isoform_alpha_(mch2)_mrna,_complete_cds_
 u33921_578-1046,_hsu33921cdna_
 u50535_1856-2270,brca2_region,_mrna_sequence_cg006_
 u58970_1284-
 1824,putative_outer_mitochondrial_membrane_34_kda_translocase_htom34_mrna,_comp
 lete_cds
 u66406_2835-3255,putative_eph-related_ptk_receptor_ligand_lerk-
 8_(eplg8)_mrna,_complete_cds
 u90065_615-1178,potassium_channel_kcno1_mrna,_complete_cds_
 v00551mrna_366-878,_messenger_rna_forleukocyte_(alpha)_interferon
 all_x05345_1772-1953,mrna_for_histidyl-trna_synthetase_(hrs)_
 x14448mrna_1017-1299:in_reversesequence,_11301-11319,gla_gene_for_alpha-d-
 galactosidase_a_(ec_3.2.1.
 x86012cds_61-319:in_fullsequence,_6603-
 6795,dna_sequence_from_intron_22_of_the_factor_viii_gene,_xq2
 all_y00477_5141-
 5216,bone_marrow_serine_protease_gene_(medullasin)_(leukocyte_neutrophil_elasta
 se_ge

Metagene 190

126584_3368-3933,(cdc25)_mrna,_complete_cds
 s75168mrna_1515-2079,_matk=megakaryocyte-
 associated_tyrosine_kinase_[human,_genomic,_2617_ntsegments
 u02609_1934-2450,transducin-like_protein_mrna,_complete_cds
 u07882_1382-1730,delta_opioid_receptor_mrna,_complete_cds
 u16307_996-1458,glioma_pathogenesis-related_protein_(glipr)_mrna,_complete_cds_
 u59831mrna_1876-2385,transcription_factor,_forkhead_related_activator(freac-
 4)_gene,_complete_cds
 y10313_1352-1730:not_in_gb_record,mrna_for_nerve_growth_factor-
 inducible_pc4_homologue
 all_z83741_654-1183,hh2a/m_gene

Metagene 191

hg3415-ht3598_at_hg3415-ht3598_poliovirus_receptor_
 j00124exon#8_14-
 227:not_in_gb_record,50_kda_type_i_epidermal_keratin_gene,_complete_cds
 all_100205_358-503,k6b_(epidermal_keratin,_type_ii)_gene_
 l35594mrna_3002-3178,autotaxin_mrna,_complete_cds
 l42611_1374-1954,keratinisoform_k6e_(krt6e)_mrna,_complete_cds_
 m14676_1864-2332,src-like_kinase_(slk)_mrna,_complete_cds
 m95585mrna_3253-3805,hepatic_leukemia_factor_(hlf)_mrna,_complete_cds
 u41518_1761-2253,channel-like_integral_membrane_protein_(aqp-
 1)_mrna,_clone_aqp-1-2344,_partial_cds
 u77180_55-511,macrophage_inflammatory_proteinbeta_(mip-
 3beta)_mrna,_complete_cds
 all_x06182_4474-5069,c-kit_proto-oncogene_mrna_
 x61123mrna_1212-1608,btg1_mrna_

Metagene 192

hg3730-ht4000_s_at_hg3730-ht4000_tyrosine_kinase_syk_
 l19401_3716-4220,myosin_i_homologue_(myh12)_mrna,_3'_end_of_cds
 m96740_2014-2476,nscl-2_gene_sequence
 all_s94421_33-496,_tc_r_eta_#name?_cell_receptor_eta-
 exon_[human,_genomic,_806_nt]_
 all_u27333_2701-
 2753,alpha_(1,3)_fucosyltransferase_(fut6)_mrna,_major_transcript_i,_complete_c
 ds,al
 u33203_73-282,mdm2-e_(mdm2)_mrna,_complete_cds/gb=u33203_/ntype=rna
 u60975_6398-6824,hybrid_receptor_gp250_precursor_mrna,_complete_cds
 x03656mrna_971-1391,_g-
 csf_protein_gene_extracted_fromgene_for_granulocyte_colony-stimulating_factor
 all_x16281_402-898,mrna_for_zinc_finger_protein_(clone_431)
 x66922cds_362-728:in_reversesequence,_848-872,mrna_for_myo-
 insositol_monophosphatase
 x80763cds_202-528:in_reversesequence,_663-850,gene_for_5-ht2c_receptor
 x98307mrna_13-355,mrna_for_uv-b_repressed_sequence,_hur_7
 all_z11685_1974-2425,mrna_for_rna_helicase_
 z29077mrna#1_3-55,_un-named-transcript-
 1_fromcdc25_gene_promoter_region/gb=z29077_/ntype=dna_/annot=

Metagene 193

d78334_496-1018,mrna_for_ankyrin_motif,_complete_cds_
 u59228_407-797,ectodermal_dysplasia_protein_(eda)_mrna,_complete_cds_
 x07384cds_2933-3269:in_reversesequence,_3377-3527,mrna_for_gli_protein
 all_x73608_2895-3478,mrna_for_testican_

Metagene 194

l36642mrna_3940-4474,receptor_protein-
 tyrosine_kinase_(hek11)_mrna,_complete_cds
 l78833cds#3_363-645:in_fullsequence,_17171-
 17279,_brca1_gene_extracted_frombrca1,_rho7_and_vati_gene
 m81886_2390-2861,glutamate_receptor_type(hbgr1)_mrna,_complete_cds
 all_u17579_1465-1982,_growth_hormone-
 releasing_hormone_receptor_form_b_gene_extracted_fromgrowth_hor

Metagene 195

d87461_2959-3517,mrna_for_kiaa0271_gene,_complete_cds
 m26004_3326-3894,cr2/cd21/c3d/epstein-barr_virus_receptor_mrna,_complete_cds_
 m65254_1710-2184,_protein_phosphatase_2a_65_kda_regulatory_subunit-
 beta_mrna,_complete_cds
 s81243_2102-
 2660,_chn=steroid/thyroid_orphan_receptor_homolog_gene_[human,_fetal_brain,_mrn
 a_partial
 u04847_1262-1802,ini1_mrna,_complete_cds_
 u18383mrna_2319-2587,nuclear_respiratory_factor(nrf-1)_gene_
 u19147_34-66,gage-6_protein_mrna,_complete_cds_
 u51920_1447-1927,signal_recognition_particle_(srp54)_mrna,_complete_cds_
 u79290_1380-1770,clone_23908_mrna_sequence_
 u97502mrna_2736-3126,butyrophilin_(bt3.3)_gene_
 all_x51757_1909-2414,heat-shock_protein_hsp70b'_gene_
 x95152mrna_10974-11274,brca2_gene_exon(and_joined_coding_region)_
 y10812_767-1253,mrna_for_fructose-bisphosphatase_

Metagene 196

d37984_1856-2314,mrna_for_dna_helicase_q1,_partial_cds_
 l22214_2335-2857,adenosine_a1_receptor_(adora1)_mrna_exons_1-6,_complete_cds_
 u17743_699-1221,jnk_activating_kinase_(jnk1)_mrna,_complete_cds_
 u21051mrna#1_2326-2647,g_protein-coupled_receptor_(gpr4)_gene,_complete_cds_
 u45975_882-1434,phosphatidylinositol_(4,5)bisphosphate_5-
 phosphatase_homolog_mrna,_partial_cds_
 u50743_13-439,na,k-atpase_gamma_subunit_mrna,_complete_cds_

Metagene 197

ab000114_1818-2208,mrna_for_osteomodulin,_complete_cds_
 ab000905_1045-1253,dna_for_h4_histone,_complete_cds
 af005043_3474-3990,poly(adp-
 ribose)_glycohydrolase_(hparg)_mrna,_complete_cds/gb=af005043_/ntype=rna
 d42108_4054-4414,mrna_for_phospholipase_complete_cds
 d50927_3955-4411,mrna_for_kiaa0137_gene,_complete_cds
 all_d87023_19383-
 19642,_j1_gene_extracted_from(lambda)_dna_for_immunoglobulin_light_chain_
 hg3231-ht3408_at_hg3231-ht3408_protease_receptor-1,_effector_cell
 l40384mrna_22-
 487,thyroid_receptor_interactor_(trip13)_mrna,_partial_cds/gb=l40384_/ntype=rna
 m60052_2004-2280,histidine-
 rich_calcium_binding_protein_(hrc)_mrna,_complete_cds_
 m60315_2334-2838,transforming_growth_factor-beta_(tgf-beta)_mrna,_complete_cds_
 u09368_1908-2298,zinc_finger_protein_znf140
 u36621exon_17-536,y-chromosome_rna_recognition_motif_protein_(yrrm)_gene
 u47414_1449-1959,cyclin_g2_mrna,_complete_cds
 u64198_3571-3955,il-12_receptor_beta2_mrna,_complete_cds_
 y09443_1545-1935,mrna_for_alkyl-dihydroxyacetonephosphate_synthase_precursor_
 all_z17240_956-1014,for_mrna_encoding_hmg2b_

Metagene 198

d37965_913-1393,mrna_for_pdgf_receptor_beta-
 like_tumor_suppressor_(prlts),_complete_cds
 d42047_3472-3970,mrna_for_kiaa0089_gene,_partial_cds_
 d78134_727-1261,mrna_for_glycine-rich_rna_binding_protein_cirp,_complete_cds_
 d87434_4737-5295,mrna_for_kiaa0247_gene,_complete_cds
 hg2238-ht2321_s_at_hg2238-
 ht2321_nuclear_mitotic_apparatus_protein_1,_altsplce_form_2_
 hg2815-ht2931_at_hg2815-ht2931_myosin,_light_chain,_alkali,_smooth_muscle,_non-
 muscle,_altsplce_2_
 hg2815-ht4023_s_at_hg2815-
 ht4023_myosin,_light_chain,_alkali,_smooth_muscle,_smooth_muscle,_altsplc
 hg4679-ht5104_at_hg4679-ht5104_oncogene_ret/ptc,_fusion_activated
 hg651-ht4201_at_hg651-ht4201_adducin,_alpha_subunit,_altsplce_2_
 l27560mrna_986-1262,insulin-like_growth_factor_binding_protein(igfbp5)_mrna_
 l78132_3279-3789,prostate_carcinoma_tumor_antigen_(pcta-1)_mrna,_complete_cds
 m14648_5128-
 5692,cell_adhesion_protein_(vitronectin)_receptor_alpha_subunit_mrna,_complete_
 cds_
 m16447_997-1489,dihydropteridine_reductase_(hdhpr)_mrna,_complete_cds
 m60483mrna_1636-2107,_protein_phosphatase-2a_catalytic_subunit-
 alpha_gene_extracted_fromprotein_phos
 u12778_2243-2621,acyl-coa_dehydrogenase_mrna,_complete_cds_
 u20362_2270-2792,tg737_mrna,_complete_cds
 u37690_31-355,rna_polymerase_ii_subunit_(hsrpb10)_mrna,_complete_cds_
 u40282_1205-1706,integrin-linked_kinase_(ilk)_mrna,_complete_cds_
 x59834mrna_2120-2690,rearranged_mrna_for_glutamine_synthase
 x62654mrna_314-788,_me491_gene_extracted_fromgene_for_me491/cd63_antigen
 x69908mrna_151-
 721,_p2_gene_for_c_subunit_of_mitochondrial_atp_synthase_gene_extracted_fromgen
 e_for_
 all_x75861_1977-2566,tegt_gene_

y00097cds_1757-1982:in_reversesequence, 2114-2324,mrna_for_protein_p68
all_z47087_1065-1438,mrna_for_rna_polymerase_ii_elongation_factor-like_protein_

Metagene 199

ac002086cds_1686-1974:in_reversesequence, 98485,pac_clone_dj525n14_from_xq23
k03218cds_1068-1587:in_reversesequence, 197-230,c-src-1_proto-oncogene
l17418exon_3-
229:not_in_gb_record,_complement_receptorgene_extracted_fromcomplement_receptor
_type(al
l26953_2282-2846,chromosomal_protein_mrna,_complete_cds_
u96136_4729-5233,delta-catenin_mrna,_complete_cds

Metagene 200

m24351exon_248-404,_pthlh_gene_(parathyroid_hormone-
like_protein_a)_extracted_fromparathyroid_hormon
m31210_2258-2708,endothelial_differentiation_protein_(edg-
1)_gene_mrna,_complete_cds_
m55024_2-
331,cell_surface_glycoprotein_p3.58_mrna,_partial_cds/gb=m55024/_ntype=rna
m58459_295-829,ribosomal_protein_(rps4y)_isoform_mrna,_complete_cds
m60626mrna_1283-1577,n-formylpeptide_receptor_(fmlp-r98)_mrna,_complete_cds
m60724_1847-2321,p70_ribosomal_s6_kinase_alpha-i_mrna,_complete_cds
s72024cds_13-437,_eif-
5a=eukaryotic_initiation_factor_5a_{clone_cos_9.1}_[human,_placenta,_genomic,_
u13695cds_2418-2754:in_reversesequence, 2858-
2954,homolog_of_yeast_mutl_(hpms1)_gene,_complete_cds
u38896_1411-1921,zinc_finger_protein_c2h2-171_mrna,_complete_cds_
x59434mrna_631-1129,rohu_mrna_for_rhodanese
all_x71661_2263-2768,ergic-53_mrna_
all_x96586_2898-3343,mrna_for_fan_protein

Metagene 201

reverse_ac000063_31010-31140,cosmid_clone_luca19_from_3p21.3_
hg1761-ht1778_s_at_hg1761-ht1778_tyrosine_kinase_fer_
hg2149-ht2219_at_hg2149-ht2219_mucin_
l10338_953-1360,sodium_channel_beta-1_subunit_(scn1b)_mrna,_complete_cds_
l20860_2219-2684,glycoprotein_ib_beta_mrna,_complete_cds_
m11186exon#3_20-134:not_in_gb_record,prepro-oxytocin-
neurophysin_i_(oxt)_gene,_complete_cds_
m29273_1749-2307,myelin-associated_glycoprotein_(mag)_mrna,_complete_cds_
m55040mrna_1689-2187,acetylcholinesterase_(ache)_mrna,_complete_cds
m64082_1605-2055,flavin-containing_monooxygenase_(fmo1)_mrna,_complete_cds_
m73481mrna_1227-
1641,gastrin_releasing_peptide_receptor_(grpr)_mrna,_complete_cds
m76446_1521-1977,alpha-a1-adrenergic_receptor_mrna,_complete_cds_
m86546_1284-1716,pbx1a_and_pbx1b_mrna,_complete_cds
m88282mrna_4784-5180,tactile_protein_mrna,_complete_cds

s75578_755-1286,_4-
 aminobutyrate_aminotransferase_[human,_neuroblastoma_be_cells,_mrna_partial,_13
 52
 u18991_2113-2638,retinal_pigment_epithelium-
 specific_61_kda_protein_(rpe65)_mrna,_complete_cds_
 u37251_1908-
 2328,krab_zinc_finger_protein_(znf177)_mrna,_splicing_variant,_complete_cds
 u38268cds_61-
 379,cytochrome_b_pseudogene,_partial_cds/gb=u38268_/ntype=dna_/annot=cds
 u40990_2251-2797,voltage_gated_potassium_channel_(kvlqt1)_mrna,_complete_cds
 u70663_1532-1928,zinc_finger_transcription_factor_hezf_(ezf)_mrna,_complete_cds
 u78190mrna_159-
 687,gtp_cyclohydrolase_i_feedback_regulatory_protein_gene,_complete_cds
 all_x00237_613-824,f_variable_segment_5'_to_antithrombin_iii_gene_(at_iii)_
 x07495cds_389-764:in_reversesequence,_1383-
 1449,mrna_for_cp19_homeobox_from_hox-3_locus.
 all_x51408_1626-2017,mrna_for_n-chimaerin
 all_x75308_2091-2608,mrna_for_collagenase_3
 x80062cds_1187-1268:in_reversesequence,_1430-1463,sa_mrna_

Metagene 202

d50915_7282-7750,mrna_for_kiaa0125_gene,_complete_cds
 hg2415-ht2511_at_hg2415-ht2511_transcription_factor_e2f-2
 hg3872-ht4142_at_hg3872-
 ht4142_immunoglobulin_gamma_heavy_chain,_v(6)djc_regions_
 hg4460-ht4729_at_hg4460-ht4729_immunoglobulin_heavy_chain,_vdjc_regions
 hg4462-ht4731_at_hg4462-ht4731_immunoglobulin_heavy_chain,_vdjc_regions
 j00210mrna_635-735,_ifna_gene_(interferon_alpha-
 d)_extracted_fromleukocyte_interferon_(ifn-alpha)_al
 j03068_2794-3286,dnf1552_(lung)_mrna,_complete_cds_
 l10343cds_2-308:in_reversesequence,_476-2076,_huma_elafin_gene,_complete_cds_
 l29217mrna_1299-1683,clk3_mrna,_complete_cds
 l34035_1405-1813,nadp-
 dependent_malic_enzyme_mrna,_complete_cds/gb=l34035_/ntype=rna
 l38025exon#1-3_30-
 106:not_in_gb_record,ciliary_neurotrophic_factor_alpha_receptor_gene_
 all_m21005_1803-2524,migration_inhibitory_factor-
 related_protein(mrp8)_gene,_complete_cds_
 all_u05259_4343-4740:not_in_gb_record,mb-1_gene,_complete_cds
 u16812cds_274-601:in_reversesequence,_3897-4028,bak-2_gene,_complete_cds
 u18237_231-759,atp-binding_cassette_protein_mrna_06b09_clone,_partial_cds
 u39817_3917-4373,bloom_syndrome_protein_(blm)_mrna,_complete_cds_
 u40380_961-1027,presenilin_i-374_(ad3-212)_mrna,_complete_cds
 u58837_3430-4003,cgmp-
 gated_cation_channel_beta_subunit_(cncg2)_mrna,_complete_cds_
 all_x64878_3508-3965,mrna_for_oxytocin_receptor
 x82240mrna_723-
 1251,_tcl1_gene_(t_cell_leukemia)_extracted_frommrna_for_tcell_leukemia/lymphom
 a_1_
 x83412cds_225-412:in_reversesequence,_507-539,b1_mrna_for_mucin
 z00010exon#2_75-
 158,germ_line_pseudogene_for_immunoglobulin_kappa_light_chain_leader_peptide_an
 d_var

z29574exon#3_1-
 373:in_reversesequence,_3141:not_in_gb_record,gene_for_bcma_peptide
 z49194exon#5_1962-2256,mrna_for_oct-binding_factor_

Metagene 203

d50582cds_954-1128:in_reversesequence,_1367-
 1535,gene_for_inward_rectifier_k_channel,_complete_cds_
 hg2365-ht2461_at_hg2365-ht2461_glyceraldehyde-3-phosphate_dehydrogenase
 hg4188-ht4458_at_hg4188-ht4458_n-methyl-d-
 aspartate_receptor_subunit,_splice_variant_hnr1n_
 j00146_388-718,dihydrofolate_reductase_pseudogene_(psi-hd1)
 l23808_1297-1717,metalloproteinase_(hme)_mrna,_complete_cds
 l27071_1963-2527,tyrosine_kinase_(txk)_mrna,_complete_cds
 l37378mrna_3182-3680,guanylyl_cyclase_(retgc-2)_mrna,_complete_cds
 l40380mrna_285-795,thyroid_receptor_interactor_(trip11)_mrna,_3'_end_of_cds_
 all_l48728_380-
 657:not_in_gb_record,_tcrbv10s1_gene_extracted_fromt_cell_receptor_beta_(tcrbv1
 0s1)_g
 m18079cds_85-343:in_reversesequence,_4158-
 4278,_human,_intestinal_fatty_acid_binding_protein_gene,_c
 m23234mrna_3313-3865,membrane_glycoprotein_p_(mdr3)_mrna,_complete_cds_
 m29386mrna_200-701,prolactin_mrna,_3'_end
 m94633exon_1275-
 1611,recombination_acitivating_protein_(rag2)_gene,_last_exon/gb=m94633_/ntype=
 dna_
 s77763_1132-
 1624,_nuclear_factor_erythroidisoform_f-basic_leucine_zipper_protein_{alternati
 vely_spli
 all_u07807_3319-4740:in_u07807cds_13-
 110,metallothionein_iv_(mtiv)_gene,_complete_cds_
 u10687exon#10_1056-1412,mage-4a_antigen_(mage4a)_gene,_complete_cds
 u11690_3665-4241,faciogenital_dysplasia_(fgd1)_mrna,_complete_cds
 u13948_3283-3787,zinc_finger/leucine_zipper_protein_(af10)_mrna,_complete_cds
 u19345_2258-2756,arl_protein_(ar)_mrna,_complete_cds_
 u26174_499-991,pre-granzymemrna,_complete_cds_
 u33017_1248-
 1680,signaling_lymphocytic_activation_molecule_(slam)_mrna,_complete_cds_
 u35459_629-1109,bomapin_mrna,_complete_cds/gb=u35459_/ntype=rna
 u52521_753-1131,arfaptin_1,_putative_target_protein_of_adp-
 ribosylation_factor,_mrna,_complete_cds_
 u72671_2390-2930,telencephalin_precursor_mrna,_complete_cds
 u96115_162-594,ww_domain-
 containing_protein_wwp3_mrna,_partial_cds/gb=u96115_/ntype=rna_
 x12453mrna_993-1539,mrna_for_retinal_s-antigen_(48_kda_protein)
 all_x12530_1083-1415,mrna_for_b_lymphocyte_antigen_cd20_(b1,_bp35)_
 x17648cds#2_1069-1177:in_reversesequence,_1341-1605,mrna_for_granulocyte-
 macrophage_colony-stimulati
 all_x17651_829-1412,myf-4_mrna_for_myogenic_determination_factor_
 all_x52520_2414-2673,mrna_for_tyrosine_aminotransferase_(tat)_(ec_2.6.1.5)_
 x54131mrna_5534-6026,hptp_beta_mrna_for_protein_tyrosine_phosphatase_beta
 x57303cds_1488-1866:in_reversesequence,_2022-2028,rec11_mrna
 x61615cds_2830-3160:in_reversesequence,_3482-
 3548,mrna_for_leukemia_inhibitory_factor_(lif)_receptor

x65550exon#15_2051-
 2549,mki67a_mrna_(long_type)_for_antigen_of_monoclonal_antibody_ki-67_
 all_y10032_1065-1588,mrna_for_putative_serine/threonine_protein_kinase_
 all_z29067_1423-1802,nek3_mrna_for_protein_kinase
 z30425cds_649-1009:in_reversesequence,_1299-
 1311,mrna_for_orphan_nuclear_hormone_receptor.
 z35491mrna_797-1253,mrna_for_novel_glucocorticoid_receptor-associated_protein

Metagene 204

d42040_4334-4623,mrna_for_kiaa9001_gene,_complete_cds
 u07695_3362-3770,tyrosine_kinase_(htk)_mrna,_complete_cds
 u19252_4495-5045,putative_transmembrane_protein_mrna,_complete_cds_
 u32680_1088-1664,cln3_mrna,_complete_cds_
 u80073_1289-
 1655,tip_associating_protein_(tap)_mrna,_complete_cds/gb=u80073_/ntype=rna_
 x06745mrna_4850-5288,mrna_for_dna_polymerase_alpha-subunit_
 all_x52896_1629-2195,rna_for_dermal_fibroblast_elastin_
 x53742mrna_1930-2470,mrna_for_fibulin-1_b
 x54667cds_110-326,mrna_for_kiastatin_s,mrna_for_cystatin_s_
 x59303cds_3274-3773,g7a_mrna_for_valyl-trna_synthetase_
 x64728cds_1694-1946:in_reversesequence,_2140-2278,chl1_mrna
 x79440cds_1303-1759:in_reversesequence,_1827-1851,mrna_for_nadp+-
 dependent_malic_enzyme_
 all_x97198_5010-5545,mrna_for_receptor_phosphate_pcp-2_
 all_x99975_3672-4243,mrna_for_hrtr/hgcnf_protein_
 y08612cds_1849-2197:in_reversesequence,_2257-2269,mrna_for_nup88_protein
 y10514mrna_6-270,mrna_for_cd152_protein/gb=y10514_/ntype=rna_
 all_z80788_607-1040,h4/l_gene

Metagene 205

j02973mrna_3467-
 4007,_thbd_gene_extracted_fromthrombomodulin_gene,_complete_cds_
 l36069_1283-
 1709,high_conductance_inward_rectifier_potassium_channel_alpha_subunit_mrna,_co
 mplete_cd
 u51587_4262-4772,golgi_complex_autoantigen_golgin-97_mrna,_complete_cds
 all_x55666_1222-1613,usf_mrna_for_late_upstream_transcription_factor_
 x58377mrna_1716-2232,mrna_for_adipogenesis_inhibitory_factor_

Metagene 206

m90354cds_29-301:in_reversesequence,_1165-
 1197,btf3_protein_homologue_gene,_complete_cds
 u57452_43-103,snf1-like_protein_kinase_mrna,_partial_cds/gb=u57452_/ntype=rna
 u62432_1759-
 1881,nicotinic_acetylcholine_receptor_alpha3_subunit_precursor,_mrna,_complete_
 cds_
 x87852cds_5374-5560:in_reversesequence,_5780-5966,mrna_for_sex_gene_
 all_z29678_1247-1740,mitf_mrna_

Metagene 207

hg2160-ht2230_at_hg2160-ht2230_glutamate_decarboxylase
 u68723_2126-2576,checkpoint_suppressormrna,_complete_cds
 x76059cds_1208-1424:in_reversesequence,_1709-1807,mrna_for_yrrm1

Metagene 208

d14686mrna_1554-2046,gene_for_glycine_cleavage_system_t-protein
 d14695_1259-1817,mrna_for_kiaa0025_gene,_complete_cds
 d23673_1204-
 1666,_clone_hh109_(screened_by_the_monoclonal_antibody_of_insulin_receptor_substr
 trate-1_(
 d86965_6166-6490,mrna_for_kiaa0210_gene,_complete_cds
 d89667_440-1004,mrna_for_c-myc_binding_protein,_complete_cds_
 hg2379-ht3996_s_at_hg2379-
 ht3996_serine_hydroxymethyltransferase,_cytosolic,_altsplice_2_
 hg270-ht270_at_hg270-ht270_lymphocyte_chemoattractant_factor_
 hg2868-ht3012_s_at_hg2868-ht3012_xe7,_pseudoautosomal_gene,_altsplice_2
 hg371-ht1063_s_at_hg371-ht1063_mucin_1,_epithelial,_altsplice_6
 hg3936-ht4206_at_hg3936-ht4206_interleukinreceptor
 j00287exon#1_8-248:not_in_gb_record,pepsinogen_gene_
 102867_2179-2689,62_kda_paraneoplastic_antigen_mrna,_3'_end_
 113744_2775-3345,af-9_mrna,_complete_cds_
 114927exon#7_1-159:in_reversesequence,_5382-
 5676,tear_prealbumin_(tp)_gene,_complete_cds_and_promote
 l38935mrna_564-1026,gt212_mrna
 m14218mrna_1044-1440,argininosuccinate_lyase_mrna,_complete_cds
 m38449_40-599,transforming_growth_factor-beta_mrna,_complete_cds,_clone_ptgf-
 beta-trp114_
 m57763_731-1151,adp-ribosylation_factor_(harf6)_mrna,_complete_cds_
 m60278_1771-2221,heparin-binding_egf-like_growth_factor_mrna,_complete_cds_
 m79462_3853-4333,pml-1_mrna,_complete_cds
 m91196_938-1513,dna-binding_protein_mrna,_complete_cds_
 m96326mrna_370-886,azurocidin_gene,_complete_cds
 m96739_1964-2510,nscl-1_mrna_sequence
 s72043mrna_5-68,_gif=growth_inhibitory_factor_[human,_brain,_genomic,_2015_nt]_
 s82362_1119-1690,_hrar-_beta_2=retinoic-acid-
 receptor_beta/suspected_tumor_suppressor_{5'_region,_tr
 u03494_2213-2393,transcription_factor_lsf_mrna,_complete_cds_
 u05875_1655-2105,clone_psk1_interferon_gamma_receptor_accessory_factor-1_(af-
 1)_mrna,_complete_cds_
 u40714_692-1142,tyrosyl-trna_synthetase_mrna,_complete_cds/gb=u40714_/ntype=rna
 u41068cds_2-268:in_reversesequence,_944-
 1155,retinoid_x_receptor_beta_(rxrbeta)_gene,_partial_3'_tra
 u47101_428-758,nifu-like_protein_(hnifu)_mrna,_partial_cds_
 u52112mrna#1_3929-
 4463,xq28_genomic_dna_in_the_region_of_the_l1cam_locus_containing_the_genes_for
 _ne
 u54644_1437-1806,tub_homolog_mrna,_complete_cds
 u58087_2096-2462,hs-cul-1_mrna,_complete_cds_
 u62531_3465-4029,ae2_anion_exchanger_(slc4a2)_mrna,_complete_cds_

u65785_4028-4442,150_kda_oxygen-regulated_protein_orp150_mrna,_complete_cds
 u72515_1279-1811,c3f_mrna,_complete_cds
 u79255_760-1180,x11_protein_mrna,_partial_cds
 all_x13451_84-268,mrna_for_lymphocyte_lineage-restricted_mb-
 1_membrane_glycoprotein_c-term(m-mb-1_ho
 x13973cds_996-1356:in_reversesequence,_1770-
 1896,mrna_for_ribonuclease/angiogenin_inhibitor_(rai)_
 all_x16135_1552-
 2003,mrna_for_novel_heterogeneous_nuclear_rnp_protein,_l_protein_
 x66362cds_743-1097:in_reversesequence,_1121-1217,mrna_pctaire-
 3_for_serine/threonine_protein_kinase_
 all_x80818_3601-3860,mrna_for_metabotropic_glutamate_receptor_type_4_
 x85106_2196-2712,mrna_for_ribosomal_s6_kinase

Metagene 209

all_d11139_1902-
 2407,gene_for_tissue_inhibitor_of_metalloproteinases,_partial_sequence_
 d12775_3124-3662,mrna_for_erythrocyte-specific_amp_deaminase,_complete_cds_
 d88799_43-379,mrna_for_cadherin,_partial_cds/gb=d88799_/ntype=rna_
 hg4263-ht4533_at_hg4263-ht4533_nkr-pla_protein_
 m32598cds_2214-2448:in_reversesequence,_146-
 368,muscle_glycogen_phosphorylase_(pygm)_gene_
 m80397_2847-3368,dna_polymerase_delta_catalytic_subunit_mrna,_complete_cds_
 s42457_2418-2814,_cncg=rod_photoreceptor_cgmp-
 gated_channel_[human,_retina,_mrna,_2857_nt]
 s81916_98-
 146,_phosphoglycerate_kinase_{alternatively_spliced}_[human,_phosphoglycerate_k
 inase_defic
 u40371_2129-
 2591,3',5'_cyclic_nucleotide_phosphodiesterase_(hspdelc1a)_mrna,_complete_cds_
 u41813_816-1290,i_homeoprotein_(hoxa9)_mrna,_partial_cds_
 u72514_405-837,c2f_mrna,_complete_cds
 x62055cds_1413-1767:in_reversesequence,_2028-2232,ptp1c_mrna_for_protein-
 tyrosine_phosphatase_1c_

Metagene 210

j04111exon#1_2735-3251,c-jun_proto_oncogene_(jun),_complete_cds,_clone_hcj-1_
 m19154mrna_2143-2503,transforming_growth_factor-beta-2_mrna,_complete_cds
 m55210mrna#1_7322-7844,laminin_b2_chain_(lamb2)_gene_
 m93426_7455-7845,protein_tyrosine_phosphatase_zeta-
 polypeptide_(ptprz)_mrna,_complete_cds
 u04636mrna_3882-4386,cyclooxygenase-2_(hcox-2)_gene,_complete_cds_
 u32114_756-1278,caveolin-2_mrna,_complete_cds
 u60805_3576-4146,oncostatin-
 m_specific_receptor_beta_subunit_(osmrp)_mrna,_complete_cds

Metagene 211

ab006190_705-1179,mrna_for_aquaporin_6,_complete_cds/gb=ab006190_/ntype=rna_

d13642_4248-4722,mrna_for_kiaa0017_gene,_complete_cds
 d31815_797-1295,mrna_for_smp-30_(senescence_marker_protein-30),_complete_cds_
 d31846exon#4_179-713,gene_for_aquaporin-2_water_channel,_exon1-4,_complete_cds_
 d38305_701-1181,mrna_for_tob,_complete_cds_
 d63482_1722-2226,mrna_for_kiaa0148_gene,_complete_cds
 d82070_285-843,ac1_mrna,_complete_cds
 d85527_37-349,mrna_for_lim_domain,_partial_cds/gb=d85527_/ntype=rna
 d87460_2023-2503,mrna_for_kiaa0270_gene,_partial_cds_
 d87468_2496-2886,mrna_for_kiaa0278_gene,_partial_cds_
 hg1649-ht1652_at_hg1649-ht1652_elastase_
 hg1800-ht1823_at_hg1800-ht1823_ribosomal_protein_s20_
 hg2261-ht2352_at_hg2261-ht2352_antigen,_prostate_specific,_altsplice_form_3
 hg2604-ht2700_at_hg2604-ht2700_pan-2_
 hg3432-ht3618_at_hg3432-ht3618_fibroblast_growth_factor_receptor_k-
 sam,_altsplice_1
 hg3987-ht4257_at_hg3987-ht4257_cpg-enriched_dna,_clone_e06_
 hg4036-ht4306_at_hg4036-ht4306_retinoblastoma_
 hg4051-ht4321_at_hg4051-ht4321_choline_acetyltransferase_
 hg4662-ht5075_at_hg4662-
 ht5075_omega_light_chain,_immunoglobulin_lambda_light_chain_related
 hg896-ht896_at_hg896-ht896_thrombospondin_
 hg919-ht919_at_hg919-ht919_dna_polymerase,_epsilon,_catalytic_subunit
 all_k03460_3-379,alpha-tubulin_isotype_h2-alpha_gene,_last_exon
 l20965_3164-3680,phosphodiesterase_mrna,_complete_cds
 l23852mrna_1122-1674,(clone_z146)_retinal_mrna,_3'_end_and_repeat_region
 l36720_661-1219,bystin_mrna,_complete_cds_
 l42621mrna_1775-2231,ly-9_mrna,_complete_cds
 l77561mrna_583-1093,dgs-d_mrna,_3'_end
 all_m13903_1676-2031,involucrin_mrna_
 m27749_245-323,immunoglobulin-
 related_14.1_protein_mrna,_complete_cds,immunoglobulin-related_14.1_pr
 m30185mrna_1234-1666,cholesteryl_ester_transfer_protein_mrna,_complete_cds_
 m34079_830-1298,immunodeficiency_virus_tat_transactivator_binding_protein-
 1_(tbp-1)_mrna,_complete_c
 m34182mrna#1_1112-1517,testis-specific_protein_kinase_gamma-
 subunit_mrna,_complete_cds_
 s76992_2182-
 2710,_vav2=vav_oncogene_homolog_[human,_fetal_brain,_mrna_partial,_2753_nt]_
 s78771_1149-1661,_nat=cpg_island-associated_gene_[human,_mrna,_1741_nt]_
 s81003_130-640,_l-
 ubc=ubiquitin_conjugating_enzyme_[human,_odontogenic_keratocysts,_mrna_partial,
 _68
 u01157_2506-2992,glucagon-like_peptide-
 1_receptor_mrna_with_ca_dinucleotide_repeat,_complete_cds_
 u01922_405-921,btk_region_clone_fci-12_mrna
 u08336_368-872,basic_helix-loop-helix_transcription_factor_mrna,_complete_cds
 u09210_1910-2396,vesicular_acetylcholine_transporter_mrna,_complete_cds
 u20908cds_13-193,clone_350/2_melanoma_ubiquitous_mutated_protein_(mum-
 1)_gene,_partial_cds/gb=u20908
 u31903_2052-2510,creb-rp_(creb-rp)_mrna,_complete_cds
 u34880_1699-2179,dph2l_mrna,_complete_cds
 u37673_2848-3412,neuron-
 specific_vesicle_coat_protein_and_cerebellar_degeneration_antigen_(beta-nap)
 u39576_2486-2852,butyrophilin_precursor_mrna,_complete_cds_
 u49089_2571-3075,neuroendocrine-dlg_(ne-dlg)_mrna,_complete_cds
 u52696_703-742,adrenal_creb-rp_homolog_(creb-rp),_complete_cds,_and_tenascin-
 x_(xb),_partial_cds,_mr

u59302_4047-4617,steroid_receptor_coactivator-1_f-src-1_mrna,_complete_cds_
 u62317mrna#3_1056-
 1488,_hypothetical_protein_384d8gene_extracted_from_chromosome_22q13_bac_clone_
 cit
 u66059cds#21_49-283:in_reversesequence,_207121-207343,germline_t-
 cell_receptor_beta_chain_dopamine-b
 u73328_918-1314,dlx7_(dlx7)_mrna,_complete_cds_
 u76764_2544-3054,cd97_mrna,_complete_cds_
 u78521_655-1111,immunophilin_homolog_ara9_mrna,_complete_cds
 u78678_191-
 683,thioredoxin_mrna,_nuclear_gene_encoding_mitochondrial_protein,_complete_cds
 -
 u79258_861-1407,clone_23732_mrna,_partial_cds
 u81001_2773-3039,snrpn_mrna,_3'_utr,_partial_sequence
 u90543_2445-
 2739,butyrophilin_(btfl)_mrna,_complete_cds,butyrophilin_(btfl)_mrna,_complete_
 cds
 u96629mrna#2_3194-
 3722,_2a8.2_gene_(unknown_protein_cit987sk_2a8_1)_extracted_fromchromosomebac_c
 lon
 all_x14085_1251-1422,mrna_for_beta-1,4-galactosyltransferase_(ec_2.4.1.22)_
 all_x62573_1608-2161,rna_for_fc_receptor,_tc9
 all_x66785_2930-3511,mrna_for_transacylase_(dbt)_
 all_x78817_2647-3236,partial_c1_mrna_
 all_x83368_4789-5345,mrna_for_phosphatidylinositolkinase_gamma
 x96401_1673-2186,mrna_for_rox_protein
 x96924mrna_1184-1215,gene_encoding_mitochondrial_citrate_transport_protein
 all_x99133_5342-5685:in_x99133cds_563-597:not_in_gb_record,ngal_gene_
 z31560cds_475-923:in_reversesequence,_953,sox-2_mrna_(partial)

Metagene 212

d43968_6790-
 7222,aml1_mrna_for_aml1b_protein_(alternatively_spliced_product),_complete_cds_
 d50477_1507-2066,mrna_for_membrane-
 type_matrix_metalloproteinase_3,_complete_cds_
 113286_2671-3205,mitochondrial_1,25-dihydroxyvitamin_d3_24-
 hydroxylase_mrna,_complete_cds
 m68516mrna_1662-
 2172,_pci_gene_(plasminogen_activator_inhibitor_3)_extracted_fromprotein_c_inhi
 bitor
 u72649_2206-2584,btg2_(btg2)_mrna,_complete_cds
 x17059cds_522-840:in_reversesequence,_1331-1418,nat1_gene_for_arylamine_n-
 acetyltransferase_
 x81889cds_3255-3561:in_reversesequence,_3774-3786,mrna_for_p0071_protein

Metagene 213

hg4321-ht4591_at_hg4321-ht4591_ahnak-related_sequence
 j04449_2290-2776,(clone_nf_10)_cytochrome_p-
 450_nifedipine_oxidase_mrna,_complete_cds_
 j05459mrna_695-1187,glutathione_transferase_m3_(gstm3)_mrna,_complete_cds
 117325_73-451,pre-t/nk_cell_associated_protein_(1d12a2)_mrna,_complete_cds_

132164_630-1158,zinc_finger_protein_mrna,_3'_end
 m16714exon#8_627-
 747,mhc_i_divergent_lymphocyte_antigen_gene,_complete_cds,_clone_rs5
 all_m37457_334-371,na+,k+_#name?_catalytic_subunit_alpha-
 iii_isoform_gene,na+,k+_#name?_catalytic_su
 all_m86808_2578-2977,pyruvate_dehydrogenase_complex_(pdha2)_gene,_complete_cds_
 all_x58723_1862-2049,mdr1_(multidrug_resistance)_gene_for_p-glycoprotein_
 x92368mrna_5695-6187,ncx1_gene_(exon_1)/gb=x92368_/ntype=dna_/annot=mrna_

Metagene 214

d26135_3247-3619,mrna_for_diacylglycerol_kinase_gamma,_complete_cds
 hg3105-ht3281_s_at_hg3105-ht3281_atpase,_cu2+_transporting_
 s78774_411-717,_na+/ca2+_exchanger_[human,_neuroblastoma_x_glioma_hybrid_ng108-
 15_cells,_mrna_partia
 x98225cds_31-331,mrna_for_gastrin-binding_protein/gb=x98225_/ntype=rna_

Metagene 215

d67029_4839-5355,sec14l_mrna,_complete_cds_
 m61916_5027-5582,laminin_b1_chain_mrna,_complete_cds_
 m69225mrna_8371-8845,bullous_pemphigoid_antigen_(bpag1)_mrna,_complete_cds_
 u10550_1591-2107,gem_gtpase_(gem)_mrna,_complete_cds_
 u50928_4486-
 4858,autosomal_dominant_polycystic_kidney_disease_type_ii_(pkd2)_mrna,_complete
 _cds
 u73936_5049-5523,jagged(hj1)_mrna,_complete_cds_
 u97105_4818-5364,n2a3_mrna,_complete_cds
 x05908cds_814-1012:in_reversesequence,_1110-1338,mrna_for_lipocortin
 all_x81895_791-1350,genx-5624_mrna,_3'_utr/gb=x81895_/ntype=rna

Metagene 216

101087_2189-2693,protein_kinase_c-theta_(prkct)_mrna,_complete_cds_
 m16652mrna_324-
 858,pancreatic_elastase_iaa_mrna,_complete_cds,pancreatic_elastase_iaa_mrna,_co
 mplete
 m27691_1901-2417,transactivator_protein_(creb)_mrna,_complete_cds
 m94893_989-1499,testis-specific_protein_(tspy)_mrna,_3'_end,_clone_pja923
 u30610_239-749,cd94_protein_mrna,_complete_cds_
 all_x17094_3675-4180,fur_mrna_for_furin
 x55019cds_1128-1521:in_reversesequence,_1538-
 1701,mrna_for_acetylcholine_receptor_delta_subunit.

Metagene 217

d17793_633-1161,mrna_for_kiaa0119_gene,_complete_cds_
 hg64-ht64_at_hg64-ht64_nf-kappa_b-binding_protein_kbp-1

k03474exon#5_562-829:in_reversesequence,_2817-
 2919,mullerian_inhibiting_substance_gene,_complete_cds
 100022cds_1249-1679:in_reversesequence,_1750-1816,ig_active_epsilon1_5'_ut,_v-
 d-j_region_subgroup_vh
 m31774_1858-2392,thyrotropin_receptor_(tsh)_mrna,_complete_cds_
 u58033_24-
 366,myotubularin_related_protein(mtmr2)_gene,_partial_cds/gb=u58033_/ntype=rna
 x06290cds_13307-13442:in_reversesequence,_13709-
 13913,mrna_for_apolipoprotein(a)_
 x87843cds_690-894:in_reversesequence,_1045-
 1201,mrna_for_cyclin_h_assembly_factor_
 x99350mrna_1863-2424,_hfh4_cds_gene_extracted_fromhfh4_gene,_exonand_joined_cds

Metagene 218

d89377_1587-2148,mrna_for_msx-2,_complete_cds,mrna_for_msx-2,_complete_cds
 101042_2723-
 3209,hiv1_tata_element_modulatory_factor_mrna_sequence_from_chromosome_3_
 102932_1331-1829,peroxisome_proliferator_activated_receptor_mrna,_complete_cds_
 140636_3438-
 3822,(clone_fbk_iii_16)_protein_tyrosine_kinase_(net_ptk)_mrna,_complete_cds
 177571mrna_1738-2218,dgs-a_mrna,_3'_end_
 m13207exon#2-4_6-288:in_reversesequence,_2583:not_in_gb_record,granulocyte-
 macrophage_colony-stimula
 all_m19159_3664-4193,placental_heat-stable_alkaline_phosphatase_(plap-
 1)_gene,_complete_cds
 m20681mrna#2_3326-3842,glucose_transporter-like_protein-
 iii_(glut3),_complete_cds
 m21934_at_m21934_m21934,not_in_gb_record,rearranged_and_truncated_ig_gamma_heav
 y_chain_disease_(riv)
 m22005cds_49-367,interleukingene,_clone_pattacil-
 2c/2tt,_complete_cds,_clone_pattacil-2c/2tt/gb=m220
 m28210_356-686,gtp-binding_protein_(rab3a)_mrna,_complete_cds_
 m30894_1015-1513,t-cell_receptor_ti_rearranged_gamma-chain_mrna_v-j-
 c_region,_complete_cds_
 m62800mrna_1350-1827,52-kd_ss-a/ro_autoantigen_mrna,_complete_cds
 u28833_1571-
 2075,down_syndrome_critical_region_protein_(dscr1)_mrna,_complete_cds
 u47292exon_120-564,spasmolytic_polypeptide_(sp)_gene,_5'_region_and
 u64675_1439-1853,sperm_membrane_protein_bs-63_mrna,_complete_cds_
 u66838_1138-1594,cyclin_a1_mrna,_complete_cds
 u67614_at_u67614_u67614,not_in_gb_record,sinusoidal_reduced_glutathione_transpo
 rter-associated_prote
 all_x54457_2328-2416,mrna_for_bile-salt-stimulated_lipase_(bssl)_(ec_3.1.1.3)
 all_x59656_1286-1827,crk-like_gene_crkl
 all_x76342_1484-2019,adh7_mrna_
 all_x78926_1271-1812,hzf3_mrna_for_zinc_finger_protein_
 x79568cds_1038-1314:in_reversesequence,_1399-1627,bdp1_mrna_for_protein-
 tyrosine-phosphatase_
 all_y00787_1314-1469,mrna_for_mdncf_(monocyte-
 derived_neutrophil_chemotactic_factor)_
 all_z29074_1968-2269,mrna_for_cytokeratin_9

Metagene 219

d38462exon_57-
 549, gene_for_a1_chain_of_type_xix_collagen, _exon_+3'/_gb=d38462/_ntype=dna/_ann
 ot=exon
 120433_3738-3780, octamer_binding_transcription_factor(otf1)_mrna, _complete_cds
 z68204cds_43-373, mrna_for_succinyl_coa_synthetase/gb=z68204/_ntype=rna_

Metagene 220

d13631_2795-3373, mrna_for_kiaa0006_gene, _complete_cds
 d16581_42-552, mrna_for_8-oxo-dgtpase, _complete_cds_
 d30755_1189-1633, mrna_for_kiaa0113_gene, _partial_cds_
 d38048_391-919, mrna_for_proteasome_subunit_z, _complete_cds_
 d49818_1445-1919, mrna_for_fructose_6-phosphate, 2-kinase/fructose_2,6-
 bisphosphatase, _partial_cds_
 d63487_2889-3369, mrna_for_kiaa0153_gene, _partial_cds_
 hg3989-ht4259_at_hg3989-ht4259_cpg-enriched_dna, _clone_e14_
 j04948mrna_1898-2432, alkaline_phosphatase_(alp-1)_mrna, _complete_cds_
 l16862_2289-2763, g_protein-coupled_receptor_kinase_(grk6)_mrna, _complete_cds_
 l19605_1483-1915, 56k_autoantigen_annexin_xi_gene_mrna, _complete_cds_
 l33801_860-1334, protein_kinase_mrna, _complete_cds_
 l38593mrna#1_2-200, integral_membrane_protein_(nramp1)_gene, _exon_5
 l42243exon#2_2604-
 3066, _ifnar2_gene_(interferon_receptor)_extracted_from(clone_q-
 2od3)_interferon_re
 m15796_660-1152, cyclin_protein_gene, _complete_cds_
 m25897mrna_40-359, platelet_factor(pf4)_mrna, _complete_cds_
 m28211_176-650, gtp-binding_protein_(rab4)_mrna, _complete_cds_
 all_m32639_3894-4064, salivary_statherin_gene, _5'_flank_
 m55671mrna_968-1448, protein_z_(plus_66_bp_insertion)_mrna, _complete_cds_
 m63589mrna#1_4159-4573, stem_cell_leukemia_gene_product_
 s66431_5869-6361, _rbp2=retinoblastoma_binding_protein[human, _nalm-6_pre-
 b_cell_leukemia, _mrna, _6455_
 s74221_317-
 695, _ik=ik_factor_[human, _leukemic_cells_k562, _chronic_myeloid_leukemia_patient
 , _mrna, _75
 u03634_1244-1652, p47_lbc_oncogene_mrna, _complete_cds_
 u05255_159-
 261, glycophorin_hep2_mrna, _partial_cds, glycophorin_hep2_mrna, _partial_cds
 u20499exon#10_185-
 431, thermolabile_phenol_sulfotransferase_(stm)_gene, _complete_cds_
 u27325_712-1266, thromboxane_a2_receptor_mrna, _complete_cds_
 u32315_1374-1842, syntaxin_mrna, _complete_cds_
 u43203_1561-2060, thyroid_transcription_factor(ttf-1)_mrna, _complete_cds_
 u43753exon_9-237: not_in_gb_record, frataxin_(frda)_gene, _promoter_region_and
 u56085_2568-3048, periodic_tryptophan_protein(pwp2)_mrna, _complete_cds_
 u79299_988-1462, neuronal_olfactomedin-
 related_er_localized_protein_mrna, _partial_cds.
 u82306_135-225, unknown_protein_mrna, _partial_cds/gb=u82306/_ntype=rna
 u86782_591-1077, 26s_proteasome-
 associated_pad1_homolog_(poh1)_mrna, _complete_cds/gb=u86782/_ntype=rn
 u88871_910-1312, hspex7p_(hspex7)_mrna, _complete_cds
 u89606_521-917, pyridoxal_kinase_mrna, _complete_cds.
 u96094_193-667, sarcolipin_(sln)_mrna, _complete_cds.

x56253mrna_1914-2274,mpr46_gene_for_46kd_mannose_6-phosphate_receptor_
 x61587mrna_701-1259,rhog_mrna_for_gtpase_
 all_x78549_1912-2186,brk_mrna_for_tyrosine_kinase
 x95384_435-807,mrna_for_unknown_14kda_protein
 x99720mrna_1458-1944,tprc_gene
 z18948exon#3_69-465,mrna_for_s100e_calcium_binding_protein_
 z48804mrna_1006-1528,mrna_(ocular_albinism_typerelated)_

Metagene 221

hg1763-ht1780_s_at_hg1763-ht1780_prolactin-induced_protein_
 119778_1871-2207,histone_(h2a.1b)_mrna,_complete_cds
 m35851cds_2287-2708:in_reversesequence,_200-266,androgen_receptor_gene

Metagene 222

d87444_3517-3823,mrna_for_kiaa0255_gene,_complete_cds
 d89859_2331-2841,mrna_for_zinc_fingerprotein,_complete_cds
 hg162-ht3165_at_hg162-ht3165_tyrosine_kinase,_receptor_axl,_altsplice_2
 hg33-ht33_at_hg33-ht33_ribosomal_protein_s4,_x-linked
 l06147_1586-2042,(clone_sy11)_golgin-95_mrna,_complete_cds_
 l10910_2084-2552,splicing_factor_(cc1.3)_mrna,_complete_cds_
 m18737mrna_269-
 815,_gjalpl_gene_extracted_fromhanukah_factor_serine_protease_(huhf)_mrna,_comp
 lete_c
 all_m29277_2842-
 2926,isolate_juso_muc18_glycoprotein_mrna_(3'_variant),_complete_cds,isolate_ju
 so_mu
 m33493_504-792,tryptase-iii_mrna,_3'_end_
 m83822_6791-7253,beige-like_protein_(bgl)_mrna,_partial_cds
 s52969_cds1_s_at_s52969_s52969,not_in_gb_record,_description:_alpha-
 1,3_fucosyltransferase_gene_extr
 u07620_1861-2215,map_kinase_mrna,_complete_cds_
 u48705mrna_3326-3867,receptor_tyrosine_kinase_ddr_gene,_complete_cds
 u63295_1285-1795,seven_in_absentia_homolog_mrna,_complete_cds
 u67122_469-728,ubiquitin-related_protein_sumo-1_mrna,_complete_cds.
 u70660_31-463,copper_transport_protein_hah1_(hah1)_mrna,_complete_cds
 x80907_2095-2557,mrna_for_p85_beta_subunit_of_phosphatidyl-inositol-3-kinase_
 x84707mrna_73-511,mia_gene
 x89211cds_1571-
 2129,dna_for_endogenous_retroviral_like_element/gb=x89211_/ntype=dna_/annot=cds
 _
 all_z21966_1647-2182,mpou_homeobox_protein_mrna
 z36715cds_1026-1200:in_reversesequence,_1491-
 1557,mrna_for_net_transcription_factor_

Metagene 223

all_m60749_829-1061,histone_h4_(h4)_gene,_complete_cds_
 u24577_1182-1512,ldl-phospholipase_a2_mrna,_complete_cds_

Metagene 224

hg3859-ht4129_at hg3859-ht4129_mage-4a_antigen_
u61741_25-137,clone(hl-
18),_dynein_heavy_chain_(dnahc14)_mrna,_partial_cds/gb=u61741_/ntype=rna
u67784_1106-1640,orphan_g_protein-coupled_receptor_(rdc1)_mrna,_partial_cds

Metagene 225

d21205_1715-2279,mrna_for_estrogen_responsive_finger_protein,_complete_cds_
hg2271-ht2367_s_at hg2271-ht2367_profilaggrin
hg2981-ht3125_s_at hg2981-ht3125_epican,_altsplice_1_
l17330_88-586,pre-t/nk_cell_associated_protein_(6h9a)_mrna,_complete_cds_
l76927mrna_760-1330,galactokinase_(galk1)_gene,_complete_cds
m31520mrna_2-
131,ribosomal_protein_s24_mrna,ribosomal_protein_s24_mrna,ribosomal_protein_s24_
mrna
u52111mrna#3_2176-
2659,xq28_genomic_dna_in_the_region_of_the_alu_locus_containing_the_genes_for_c
rea
u57317_2551-2989,p300/cbp-associated_factor_(p/caf)_mrna,_complete_cds_
u66468_586-1126,cell_growth_regulator_cgrr1_mrna,_complete_cds_

Metagene 226

ab001325_967-1387,aqp3_gene_for_aquaporine(water_channel),_partail_cds
all_d31784_3804-4249,mrna_for_cadherin-6_
d42087_1034-1388,mrna_for_kiaa0118_gene,_partial_cds_
d87436_5660-6116,mrna_for_kiaa0249_gene,_complete_cds
all_l32866_67-452,effector_cell_protease_receptor-1_(epr-1)_gene,_partial_cds
all_m17262_16806-
26862:in_m17262cds_1666,prothrombin_(f2)_gene,_complete_cds,_and_alu_and_kpni_r
epta
m26692exon#1_37-195,lymphocyte-
specific_protein_tyrosine_kinase_(lck)_gene,_exon_1,_and_downstream_p
m30269_4417-4849,nidogen_mrna,_complete_cds
s55606_718-1228,_betacellulin_[human,_mrna,_1271_nt]
u02019_1958-2462,au-rich_element_rna-binding_protein_auf1_mrna,_complete_cds_
u18934_4229-4311,receptor_tyrosine_kinase_(dtk)_mrna,_complete_cds_
u58034cds_38-
224,myotubularin_related_protein(mtmr3)_gene,_partial_cds/gb=u58034_/ntype=rna_
u79246_1346-1748,clone_23799_mrna_sequence_
u79289_1287-1809,clone_23695_mrna_sequence_
x71125utr#1_20-398:in_reversesequence,_985-
1093,mrna_for_glutamine_cyclotransferase_
all_x97261_25-
333,mrna_for_metallothionein_isoform_1r,mrna_for_metallothionein_isoform_1r_
x97674cds_4092-4326:in_reversesequence,_4536-
4758,mrna_for_transcriptional_intermediary_factor_2

Metagene 227

aj001047cds_485-791:in_reversesequence,_959-1013,mrna_for_matrilin-
 3/gb=aj001047_/ntype=rna
 d25216_4968-5256,mrna_for_kiaa0014_gene,_complete_cds
 d29012_230-752,mrna_for_proteasome_subunit_y,_complete_cds_
 d29954_4458-4920,mrna_for_kiaa0056_gene,_partial_cds_
 d45906_3097-3613,mrna_for_limk-2,_complete_cds_
 d50810_3494-3992,mrna_for_placental_leucine_aminopeptidase,_complete_cds_
 d50913_1494-2052,mrna_for_kiaa0123_gene,_partial_cds_
 d63160exon_6-306:in_reversesequence,_9:not_in_gb_record,dna_for_lectin_p35_
 d83703_2605-3169,mrna_for_peroxisome_assembly_factor-2,_complete_cds_
 d90042_675-1215,liver_arylamine_n-acetyltransferase_(ec_2.3.1.5)_gene
 hg2036-ht2090_at_hg2036-ht2090_stimulatory_gdp/gtp_exchange_protein_for_c-ki-
 ras_p21_and_smg_p21_
 hg2566-ht4867_at_hg2566-ht4867_microtubule-
 associated_protein_tau,_altssplice_5,_exon_4a
 hg2706-ht2802_at_hg2706-ht2802_serine/threonine_kinase_
 hg3976-ht4246_at_hg3976-ht4246_pou-domain_dna_binding_factor_pit1,_pituitary-
 specific
 hg870-ht870_at_hg870-ht870_golgin,_165_kda_polypeptide_
 hg909-ht909_at_hg909-ht909_mg81
 j02876mrna_616-1180,placental_folate_binding_protein_mrna,_complete_cds
 l05147_266-812,dual_specificity_phosphatase_tyrosine/serine_mrna,_complete_cds_
 l10405_1364-
 1910,dna_binding_protein_for_surfactant_protein_b_mrna,_complete_cds/gb=l10405_
 /ntype=rn
 l14754_3369-3813,dna-binding_protein_(smbp2)_mrna,_complete_cds
 l19058_2599-3163,glutamate_receptor_(glur5)_mrna,_complete_cds_
 l26494_1598-2084,(oct-6)_mrna,_complete_cds_
 l29433exon_53-587,factor_x_(blood_coagulation_factor)_gene_
 l36861exon#4_247-757,guanylate_cyclase_activating_protein_(gcap)_gene_exons_1-
 4,_complete_cds_
 all_l36922_938-1125,met-ase_gene,_exon_1
 l40377mrna_766-1276,cytoplasmic_antiproteinase(cap2)_mrna,_complete_cds
 l47738_2286-2856,inducible_protein_mrna,_complete_cds_
 all_m16652_714-
 760,pancreatic_elastase_ii_mrna,_complete_cds,pancreatic_elastase_ii_mrna,_co
 mplete
 m31651cds_900-1146:in_reversesequence,_5912-6098,human_sex_hormone-
 binding_globulin_(shbg)_gene,_com
 all_m34041_1414-2015,alpha-2-adrenergic_receptor_(alpha-
 2_c2)_gene,_complete_cds_
 m35878exon#4_1993-2443,insulin-like_growth_factor-binding_protein-
 3_gene,_complete_cds,_clone_hl1006
 all_m58378_75-406:in_m58378cds#1_1893-
 1930:in_m58378cds#2_2002,_syn1_gene_(synapsin_i)_extracted_fro
 m64595mrna_216-648,small_g_protein_(gx)_mrna,_3'_end_
 m76180_1461-1887,aromatic_amino_acid_decarboxylase_(ddc)_mrna,_complete_cds
 m86757_2-372,psoriasin_mrna,_complete_cds
 m91438cds_55-181:in_reversesequence,_300-540,kazal-
 type_serine_proteinase_(husi-ii)_gene,_complete_c
 m93718_3536-4034,nitric_oxide_synthase_mrna,_complete_cds
 m94077exon#2_657-1125,loricrin_gene_exonsand_2,_complete_cds
 m94547mrna_55-565,_hummlc2at;_homo_sapiens;_593_base-pairs
 m95712_2005-2407,b-raf_mrna,_complete_cds

m98045_1593-2097,folylpolyglutamate_synthetase_mrna,_complete_cds_
 all_s57887_739-
 980,(t1)=elastin_translocation_allele_{exon_28,_translocation}_[human,_genomic
 _mutan
 s67070_55-
 421,_heat_shock_protein_hsp72_homolog_[human,_thyroid_associated_ophthalmopathy
 _patient,_m
 s82198_323-827,_caldecrin=serum_calcium-
 decreasing_factor_[human,_pancreas,_mrna_partial,_894_nt]
 u06088exon_220-730,n-acetylgalactosamine_6-sulphatase_(galns)_gene_
 u08191_4687-5220,r_kappa_b_mrna,_complete_cds
 u09850_3337-3769,zinc_finger_protein_(znf143)_mrna,_complete_cds_
 u13045_2126-2690,nuclear_respiratory_factor-2_subunit_betamrna,_complete_cds
 all_u15177_2291-2724,cosmid_cri-jc2015_at_d10s289_in_10sp13
 u22526_2677-3157,2,3-oxidosqualene-lanosterol_cyclase_mrna,_complete_cds_
 u35234_6175-6290,protein_tyrosine_phosphatase_sigma_mrna,_complete_cds_
 u41763_4933-5485,muscle_specific_clathrin_heavy_chain_(cltd)_mrna,_complete_cds
 u42412_977-1535,5'_'-amp-activated_protein_kinase,_gamma-
 1_subunit_mrna,_complete_cds_
 u48408_752-1322,kidney_water_channel_(hkid)_mrna,_complete_cds_
 u49260_1284-
 1761,mevalonate_pyrophosphate_decarboxylase_(mpd)_mrna,_complete_cds_
 u49395_1361-1907,ionotropic_atp_receptor_p2x5a_mrna,_complete_cds
 u52112mrna#5_896-
 1340,xq28_genomic_dna_in_the_region_of_the_llcam_locus_containing_the_genes_for
 _neu
 u55258cds_3452-3872:in_reversesequence,_4031-4091,hbravo/nr-
 cam_precursor_(hbravo/nr-cam)_gene,_comp
 all_u57341_2-
 129,neurofilament_triplet_1_protein_mrna,_partial_cds/gb=u57341/_ntype=rna,neur
 ofilamen
 u60666_1923-
 2415,testis_specific_leucine_rich_repeat_protein_(tslrp),_complete_cds_
 u65402cds_651-915:in_reversesequence,_1437-1647,seven_transmembrane_g-
 coupled_receptor_(gpr31)_gene,
 u68485_1356-1788:not_in_gb_record,box-dependent_myc-interacting_protein-
 1_(bin1)_mrna,_complete_cds_
 u70064_6458-7030,lysosomal_trafficking_regulator_(lyst)_mrna,_partial_cds
 u72209_432-990,yy1-associated_factor(yaf2)_mrna,_complete_cds_
 u87964_1515-2094,putative_g-protein_(gp-1)_mrna,_complete_cds
 x00090cds_6-356,histone_h3_gene
 all_x00695_6073-6372,interleukin-2_(il-2)_gene_and_5'_'-flanking_region_
 x01715cds_1338-
 1537:not_in_gb_record,gene_fragment_for_the_acetylcholine_receptor_gamma_subuni
 t_prec
 x05360cds_353-785,cdc2_gene_involved_in_cell_cycle_control_
 all_x13810_1940-1986,otf-2_mrna_for_lymphoid-specific_transcription_factor_
 x51952mrna_355-
 517,_ucp_fromucp_gene_for_uncoupling_protein_exonsand/gb=x51952/_ntype=dna/_ann
 ot=exo
 all_x63717_1962-2473,mrna_for_apo-1_cell_surface_antigen_
 x66839cds_909-1335:in_reversesequence,_1407-
 1491,matu_mn_mrna_for_p54/58n_protein_
 x69950exon#1_1485-2039,dna_sequence_for_wilms'_tumor_gene
 all_x70297_1563-2020,mrna_for_neuronal_nicotinic_acetylcholine_receptor_alpha-
 7_subunit
 x77777_2210-2771,intestinal_vip_receptor_related_protein_mrna

all_x96969_1470-1759,mrna_for_urea_transporter_
 x99656cds_798-1068:in_reversesequence,_1251-
 1329,mrna_for_protein_containing_sh3_domain,_sh3gl1_
 reverse_y10871_4016-4220,twist_gene
 z25884cds_2453-2897:in_reversesequence,_3062-3068,mrna_for_clc-
 1_muscle_chloride_channel_protein
 z48475cds_1531-1795:in_reversesequence,_1918-
 2128,gckr_mrna_for_glucokinase_regulator_
 all_z69720_14484-
 15067,dna_sequence_from_cosmid_ra36_from_a_contig_from_the_tip_of_the_short_arm
 of
 all_z70220_31-266,mrna_for_5'utr_for_unknown_protein_(clone_icrfp507o0882).
 reverse_z95624_34190-
 34542,dna_sequence_from_cosmid_u237h1_contains_ras_like_gtpase_and_ests.

Metagene 228

d26535exon#15_940-
 1455,gene_for_dihydrolipoamide_succinyltransferase,_complete_cds_(exon_1-15)_
 d78577exon_853-1391,dna_for_14-3-3_protein_eta_chain_
 d86980_4616-5192,mrna_for_kiaa0227_gene,_partial_cds_
 hg2743-ht3926_s_at_hg2743-ht3926_caldesmon_1,_altsplice_6,_non-muscle
 hg4178-ht4448_at_hg4178-ht4448_af-17_
 j03060exon#11_168-666,glucocerebrosidase_(gcb)_gene
 j03077_2159-2692,co-beta_glucosidase_(proactivator)_mrna,_complete_cds_
 l12168_2032-2476,adenylyl_cyclase-associated_protein_(cap)_mrna,_complete_cds_
 m15395_2621-2736,leukocyte_adhesion_protein_(lfa-1/mac-
 1/p150,95_family)_beta_subunit_mrna_
 m22898mrna_2042-2600,phosphoprotein_p53_gene_
 m33308_4519-5071,vinculin_mrna,_complete_cds_
 m63573_370-802,secreted_cyclophilin-like_protein_(scylp)_mrna,_complete_cds_
 m80563_133-523,cap1_protein_mrna,_complete_cds_
 m94345_752-1160,macrophage_capping_protein_mrna,_complete_cds_
 s81439_2658-
 3186,_egr_alpha=early_growth_response_gene_alpha_[human,_prostate,_mrna,_3228_n
 t]_
 all_u02020_1985-2352,pre-b_cell_enhancing_factor_(pbef)_mrna,_complete_cds_
 u22055_2879-3455,100_kda_coactivator_mrna,_complete_cds_
 u25165_1579-
 2083,fragile_x_mental_retardation_proteinhomolog_fxrl_mrna,_complete_cds_
 u56637_1987-2323,capping_protein_alpha_subunit_isoformmrna,_complete_cds_
 u57721_1126-1588,l-kynurenine_hydrolase_mrna,_complete_cds_
 all_u90546_1365,butyrophilin_(btf4)_mrna,_complete_cds,butyrophilin_(btf4)_mrna
 ,_complete_cds_
 x12447mrna#13_1-241:not_in_gb_record,aldolase_a_gene_(ec_4.1.2.13)
 x62320cds_1527-1755:in_reversesequence,_1825-2095,mrna_for_epithelinand_2
 all_x74262_1725-2278,rbap48_mrna_encoding_retinoblastoma_binding_protein_
 all_x76105_1661-2208,dap-1_mrna
 all_y00281_1856-2319,mrna_for_ribophorin_i_

Metagene 229

m27160mrna_1441-1879,tyrosinase_(tyr)_mrna,_complete_cds_

m64590_3317-3737, glycine decarboxylase mrna, _complete_cds
 u26712_2910-3318, cbl-b_truncated_formlacking_leucine_zipper mrna, _complete_cds

Metagene 230

all_d29675_1092-
 1149, inducible_nitric_oxide_synthase_gene, _promoter_and_exon/gb=d29675_/ntype=dna/_a
 d29675exon_2-
 136, inducible_nitric_oxide_synthase_gene, _promoter_and_exon/gb=d29675_/ntype=dna/_annot
 hg2730-ht2827_s_at_hg2730-
 ht2827_fibrinogen, _a_alpha polypeptide, _altsplice_2, _e
 l17128_1940-2480, (clone_h4/h16)_gamma-glutamic_carboxylase mrna, _complete_cds_
 all_m10943_444-1929, metallothionein-if_gene_(hmt-if)_
 m18731_at_m18731_m18731, not_in_gb_record, galactose-1-
 phosphate_uridylyltransferase_(galt)_mrna, _comple
 m81933_1920-2394, cdc25a mrna, _complete_cds_
 s79862_1641-
 2226, _26_s_protease_subunit_5b=50_kda_subunit_[human, hela_cells, _mrna_partial, _2253_nt]
 u20734cds_709-1014:in_reversesequence, _7020-
 7258, transcription_factor_junb_(junb)_gene, _5'_region_an
 u43328_1158-1698, link_protein mrna, _complete_cds_
 u52155_1646-2168, atp-
 dependent_inwardly_rectifying_potassium_channel_kir4.1 mrna, _complete_cds_
 u77664_417-891, rnasep_protein_p38_(rpp38)_mrna, _complete_cds.
 all_x79483_1063-1556, erk6 mrna_for_extracellular_signal_regulated_kinase_
 y07829exon#2_13-
 364, _exon_fromgene_encoding_ring_finger_protein/gb=y07829_/ntype=dna/_annot=exon, _ex
 all_y08765_1854-2207, mrna_for_splicing_factor, _sf1-hl1_isoform_

Metagene 231

k02215mrna#2_1510-2026, angiotensinogen mrna, _complete_cds
 l38969cds_2517-2835:in_reversesequence, _2946-
 2964, thrombospondin(thbs3)_gene, _complete_cds
 all_u33838_62-95, nf-kappa-
 b_p65delta3 mrna, _spliced_transcript_lacking_exonsand_7, _partial_cds/gb=u3
 u79241_849-1347, clone_23759 mrna, _partial_cds

Metagene 232

all_d38024_2639-
 3228, facioscapulohumeral_muscular_dystrophy_(fshd)_gene_region, _d4z4_tandem_repeat_u
 hg2260-ht2349_s_at_hg2260-ht2349_duchenne_muscular_dystrophy_protein_(dmd)_
 hg4020-ht4290_s_at_hg4020-ht4290_transglutaminase
 m13994mrna_4482-5005, b-cell_leukemia/lymphoma(bcl-2)_proto-
 oncogene mrna_encoding_bcl-2-alpha_protei

u27516_2109-2555, recombination protein rad52 mrna, complete cds
 u82970_2601-3009, metalloendopeptidase homolog (pex) mrna, complete sequence
 x03168cds_926-1400:in_reversesequence, 1497-1509, mrna_for_s-protein
 all_x89067_751-1136, mrna_for_trpc2_transcript_(possible_pseudogene)

Metagene 233

m24283mrna_2420-2954, major_group_rhinovirus_receptor_(hrv)_mrna, complete cds
 s62027_21-320, transducin gamma subunit [human, mrna, 408_nt]
 u37546_2477-3012, iap_homolog_c_(mihc)_mrna, complete cds
 u46569mrna_1025-1241:in_reversesequence, 300-498, aquaporin-5_(aqp5)_gene

Metagene 234

u50822mrna_909-1375, neurogenic_helix-loop-helix_protein_neurod_(neurod)_gene, complete cds
 u68030_2365-2665, g_protein-coupled_receptor_(strl22)_mrna, complete cds
 all_u77827_1053-1630, orphan_g_protein-coupled_receptor_(cepr)_gene, complete cds.
 all_x77366_4160-4689, hbz17_mrna

Metagene 235

hg67-ht67_f_at_hg67-ht67_zinc_finger_protein
 m18728mrna_1932-2460, nonspecific_crossreacting_antigen_mrna, complete cds
 m29540_2616-2949, carcinoembryonic_antigen_mrna_(cea), complete cds
 m36803exon_142-352: not_in_gb_record, hemopexin_gene
 m55284_1800-2364, protein_kinase_c-l_(prkcl)_mrna, complete cds
 u13913_3871-4120, large-conductance_calcium-activated_potassium_channel_(hslo)_mrna, complete cds
 u34879mrna_1628-2073, 17-beta-hydroxysteroid_dehydrogenase_(edh17b2)_gene, complete cds
 u69140_297-846, zyginii_mrna, partial_cds

Metagene 236

m11321mrna_1193-1703, group-specific_component_vitamin_d-binding_protein_mrna, complete cds
 m58509cds#1_1114-1441:in_reversesequence, 4757-4867, fdxr_gene_(adrenodoxin_reductase)_extracted_fro
 s57153_2388-2878, rbp1=retinoblastoma_binding_proteinisoform_i_{alternatively_spliced}_[human, mrna
 s79854_1585-1963, typeiodothyronine_deiodinase=selenoenzyme_[human, placenta, mrna, 2066_nt]
]
 u34360_3316-3832, lymphoid_nuclear_protein_(laf-4)_mrna, complete cds
 all_v01515_5300-5550, gene_encoding_preproglucagonglucagon_is_a_29-amino_acid_pancreatic_hormone_whic

Metagene 237

d17427_3421-3506,mrna_for_desmocollin_type_4_
 d25278_2024-2510,mrna_for_kiaa0036_gene,_complete_cds
 d26528_1017-1515,mrna_for_rna_helicase,_complete_cds_
 d32202_2017-2263,mrna_for_alpha_1c_adrenergic_receptor_isoform_2,_complete_cds_
 d43768_663-1197,_numan_mrna_for_scm-1_(single_cysteine_motif-1),_complete_cds_
 all_d49742_2413-2984,mrna_for_hgf_activator_like_protein,_complete_cds_
 d49817_1233-1725,mrna_for_fructose_6-phosphate,2-kinase/fructose_2,6-
 biphosphatase,_complete_cds
 d49950_495-918,liver_mrna_for_interferon-
 gamma_inducing_factor(igif),_complete_cds_
 d64158_415-
 668:not_in_gb_record,mrna_for_atp_binding_protein_associated_with_cell_differen-
 tiation,_p
 d82061_357-876,b-cell_mrna_for_a_member_of_the_short-
 chain_alcohol_dehydrogenase_family,_partial_cds
 d82343_474-960,mrna_for_amy,_complete_cds
 d88270exon#2_89-293:in_reversesequence,_18899-
 19103,(lambda)_dna_for_immunoglobulin_light_chain
 hg1804-ht1829_at_hg1804-ht1829_ornithine_aminotransferase-like
 hg2367-ht2463_s_at_hg2367-ht2463_trithorax_homolog_hrx_
 hg2416-ht2512_at_hg2416-ht2512_gal_beta_1,3(4)glcnac_alpha2,3-sialyltransferase
 hg2562-ht2658_s_at_hg2562-ht2658_a-myb_
 hg2689-ht2785_at_hg2689-ht2785_mucin_5b,_tracheobronchial
 hg3364-ht3541_at_hg3364-ht3541_ribosomal_protein_l37_
 hg4102-ht4372_at_hg4102-ht4372_n-ethylmaleimide-sensitive_factor_
 hg4115-ht4385_at_hg4115-ht4385_olfactory_receptor_or17-210_
 hg4333-ht4603_at_hg4333-ht4603_zinc_finger_protein_znfpt7
 hg961-ht961_at_hg961-ht961_guanine_nucleotide_exchange_factor_
 j00073exon#2_132-255:not_in_gb_record,alpha-cardiac_actin_gene,_5'_flank_and
 j00306cds_40-304:in_reversesequence,_1168-2537,somatostatin_i_gene_and_flanks_
 l40371mrna_661-1075,thyroid_receptor_interactor_(trip4)_mrna,_3'_end_of_cds_
 l42354mrna_25-409,(clone_48es4)_mrna_fragment/gb=l42354_/ntype=rna
 l42451mrna_947-
 l397,pyruvate_dehydrogenase_kinase_isoenzyme(pdk2)_mrna,_complete_cds_
 l77559mrna_55-403,dgs-b_partial_mrna/gb=l77559_/ntype=rna_
 m12963mrna_871-
 985,i_alcohol_dehydrogenase_(adh1)_alpha_subunit_mrna,_complete_cds_
 m14091mrna_1209-1731,thyroxine-binding_globulin_mrna,_complete_cds_
 m14123cds#2_830-1280,_pol_fromendogenous_retrovirus_herv-
 k10/gb=m14123_/ntype=dna_/annot=cds,_pol_fr
 m14123cds#3_13-175,_pol_fromendogenous_retrovirus_herv-
 k10/gb=m14123_/ntype=dna_/annot=cds,_pol_from
 m25629_270-846,kallikrein_mrna,_complete_cds,_clone_clone_phkk25_
 m25809_1358-1817,endomembrane_proton_pump_subunit_mrna,_complete_cds_
 m26958_46-235,parathyroid_hormone-
 related_protein_(pthrp)_mrna,_5'_flank,_clone_pbrf52/gb=m26958_/nt
 m29194cds_1090-1408:in_reversesequence,_175-223,triglyceride_lipase_gene
 m29994exon#1_2-80,alpha-i_spectrin_gene,_exon/gb=m29994_/ntype=dna_/annot=exon_
 m31241_s_at_m31241_m31241,not_in_gb_record,complement_receptor(cr1)_gene_
 m60721mrna_1630-2182,homeobox_gene,_complete_cds_
 m62982_1795-2299,arachidonate_12-lipoxygenase_mrna,_complete_cds_
 m63603_1052-1574,phospholamban_mrna,_complete_cds

m63928_645-1161,t_cell_activation_antigen_(cd27)_mrna,_complete_cds_
 m74093_1283-1685,cyclin_mrna_
 m83664_1098-1416,mhc_ii_lymphocyte_antigen_(hla-
 dp)_beta_chain_mrna,_complete_cds
 m89914_8414-8952,neurofibromin_(nfl)_gene,_complete_cds
 m93283_898-1438,pancreatic_lipase_related_protein(plrp1)_mrna,_complete_cds_
 m99438_1768-2332,transducin-like_enhancer_protein_(tle3)_mrna,_complete_cds_
 s69115_250-808,_granulocyte_colony-
 stimulating_factor_induced_gene_[human,_cml_patient,_bone_marrow_
 s76756_510-954,_4r-map2=microtubule-
 associated_protein4r_isoform_[human,_brain,_mrna_partial,_1012_n
 u00944_1121-1619,clone_a9a2brb6_(cac)n/(gtg)n_repeat-containing_mrna_
 u04806_247-787,flt3/flk2_ligand_mrna,_complete_cds.
 u09367_1942-2449,zinc_finger_protein_znf136
 u20230exon_7-
 127,guanyl_cyclase_c_gene,_partial_cds/gb=u20230_/ntype=dna_/annot=exon_
 u23430exon_172-496:in_reversesequence,_793-
 994,cholecystokinin_type_a_receptor_(cck-a)_gene
 u33052_2643-3212,lipid-activated,_protein_kinase_prk2_mrna,_complete_cds_
 u34038_880-1390,proteinase-activated_receptor-2_mrna,_complete_cds_
 u37143_1256-1832,cytochrome_p450_monooxygenase_cyp2j2_mrna,_complete_cds_
 all_u37219_2132-2583,cyclophilin-like_protein_cyp-60_mrna,_complete_cds_
 u40223cds_660-
 1068:in_reversesequence,_1548,uridine_nucleotide_receptor_(unr)_gene,_complete_
 cds
 u47011mrna#1_581-791:in_reversesequence,_751-
 961,_fgf8_gene_(fibroblast_growth_factorprecursor)_extr
 u48707_123-597,protein_phosphatase-1_inhibitor_mrna,_complete_cds
 u50527_1493-1891,brca2_region,_mrna_sequence_cg018_
 u59286_49-439,beta-r1_mrna,_partial_cds/gb=u59286_/ntype=rna_
 u59321_1625-1967,dead-box_protein_p72_(p72)_mrna,_complete_cds_
 u60519_2965-3499,apoptotic_cysteine_protease_mch4_(mch4)_mrna,_complete_cds
 u66048mrna_2400-2838,clone_161455-2-3_b_cell_expressed_mrna_from_chromosome_x
 u66088_1895-2369,sodium_iodide_symporter_mrna,_complete_cds
 u71088_1325-1586,map_kinase_kinase_mek5c_mrna,_complete_cds
 u75272_743-1283,gastricsin_mrna,_complete_cds
 u75276_2760-3225,tfiib_related_factor_hbrf_(hbrf)_mrna,_complete_cds.
 u79115_337-886,death_adaptor_molecule_raidd_(raidd)_mrna,_complete_cds.
 u79253_734-1100,clone_23893_mrna,_complete_cds.
 u90306_13-175,iroquois-class_homeodomain_protein_irx-
 4_mrna,_partial_cds/gb=u90306_/ntype=rna
 u96629mrna#1_1142-
 1658,_2a8.2_gene_(unknown_protein_cit987sk_2a8_1)_extracted_fromchromosomebac_c
 lon
 all_x00588_5021-5514,mrna_for_precursor_of_epidermal_growth_factor_receptor
 x02612mrna#3_656-1184,gene_for_cytochrome_p(1)-450_
 all_x03663_3391-3824,mrna_for_c-fms_proto-oncogene_
 x17254cds_911-1211:in_reversesequence,_1335-
 1449,mrna_for_the_transcription_factor_eryf1
 x54673cds_1493-1775:in_reversesequence,_2015-
 2135,gat1_mrna_for_gaba_transporter
 all_x65873_3040-3551,mrna_for_kinesin_(heavy_chain)
 x65977cds_118-268:in_reversesequence,_325-499,mrna_for_corticostatin_hp-
 4_precursor_
 all_x74301_4170-4479,mrna_for_mhc_ii_transactivator
 all_x78416_369-921,alpha-s1-casein_mrna
 all_x80878_4120-4349,r_kappa_b_mrna

all_x82895_2890-3425,mrna_for_dlg2_
 x95190cds_1574-1958:in_reversesequence,_2170,mrna_for_branched_chain_acyl-
 coa_oxidase_
 x97302mrna_40-235,mrna_for_ptg-1_protein/gb=x97302_/ntype=rna
 x99393cds_292-552:in_reversesequence,_655-787,cmkbr5_gene,_non-
 functional_mutant
 y11999cds_31-358,mrna_for_inositol_1,4,5-trisphosphate_3-
 kinase/gb=y11999_/ntype=rna_
 z29090cds_2967-3183:in_reversesequence,_3201-
 3393,mrna_for_phosphatidylinositol_3-kinase
 z69923cds_1572-1818:in_reversesequence,_6905-
 7019,dna_sequence_from_cosmid_l219f9,_huntington's_dise
 z84483cds_1166-
 1676,dna_sequence_from_pac_46h23,_brca2_gene_region_chromosome_13q12-
 13_contains_klot

Metagene 238

m15856mrna#1_2984-3488,lipoprotein_lipase_mrna,_complete_cds_
 m23575_1395-1933,pregnancy-specific_beta-1_glycoprotein_mrna,_complete_cds_
 m60503cds_2942-3212:in_reversesequence,_1915-
 2047,profilaggrin_gene,_partial_cds
 s81294_4-
 160,_dcc=deleted_in_colorectal_cancer_{alternatively_spliced,_exon_1a}_[human,_
 brain_tumor,
 all_s85963_4324-4544,_hirs-1=rat_insulin_receptor_substrate-
 1_homolog_[human,_cell_line_focus,_genom

Metagene 239

ab000409_2046-2538,mrna_for_mnk1,_complete_cds_
 af000430_1941-2427,dynamin-like_protein_mrna,_complete_cds
 af009426_7540-8044,clone_22_mrna,_alternative_splice_variant_beta-
 1,_complete_cds/gb=af009426_/ntype
 d14660_739-1249,mrna_for_kiaa0104_gene,_complete_cds_
 d14878_1001-1499,mrna_for_protein_d123,_complete_cds_
 d38251_642-1149,mrna_for_rpb5_(xap4),_complete_cds_
 d50678_3909-4413,mrna_for_apolipoprotein_e_receptor_2,_complete_cds
 d87448_4763-5183,mrna_for_kiaa0259_gene,_partial_cds_
 hg1102-ht1102_at_hg1102-ht1102_ras-related_c3_botulinum_toxin_substrate
 hg3400-ht3579_at_hg3400-ht3579_nestin
 hg4120-ht4392_s_at_hg4120-ht4392_protein_kinase_pitslre,_alpha,_altsplice_1-feb
 hg944-ht944_s_at_hg944-ht944_dopamine_receptor_d4
 j03626mrna#1_1151-
 1653,_umps_gene_extracted_fromump_synthase_mrna,_complete_cds_
 102547_1290-1752,(clone_pz50-
 19)_cleavage_stimulation_factor_50kda_subunit,_complete_cds
 177864_2060-2618,stat-like_protein_(fe65)_mrna,_complete_cds_
 m29580mrna_1813-2326,zinc-finger_protein(zfp7)_mrna,_complete_cds_
 m81181_2360-2731,sodium/potassium_atpase_beta-
 2_subunit_(atpb2)_mrna,_complete_cds_
 s81221_2246-
 2546,_lanosterol_synthase_[human,_fetal_liver,_mrna_partial,_2637_nt]_

u07349_2331-
 2805,b_lymphocyte_serine/threonine_protein_kinase_mrna,_complete_cds_
 u36221_1562-1814,pancreatic_zymogen_granule_membrane_protein_gp-
 2_mrna,_complete_cds_
 u36787_491-995,putative_holocytochrome_c-type_synthetase_mrna,_complete_cds_
 u38864_1766-2186,zinc-finger_protein_c2h2-150_mrna,_complete_cds_
 u40271_3598-3999,transmembrane_receptor_precursor_(ptk7)_mrna,_complete_cds_
 u41804_882-
 1254,putative_t1/st2_receptor_binding_protein_precursor_mrna,_complete_cds_
 u51903_5202-5712,rasgap-related_protein_(iqgap2)_mrna,_complete_cds_
 u52969_19-505,pep19_(pcp4)_mrna,_complete_cds_
 u71207_1846-2224,eyes_absent_homolog_(eab1)_mrna,_complete_cds.
 u79256_655-1033,clone_23719_mrna_sequence
 all_v00594_15-75,mrna_for_metallothionein_from_cadmium-
 treated_cells,mrna_for_metallothionein_from_c
 all_x04434_4484-4971,mrna_for_insulin-like_growth_factor_i_receptor
 x07438exon#2_11-
 166,dna_for_cellular_retinol_binding_protein_(crbp)_exonsand/gb=x07438_/ntype=d
 na_/a
 x58199mrna_2491-2573,mrna_for_beta_adducin_
 all_x72304_1456-1688,mrna_for_corticotrophin_releasing_factor_receptor_
 x87344mrna#26_769-945,dma,_dmb,_hla-
 z1,_ipp2,_lmp2,_tap1,_lmp7,_tap2,_dob,_dqb2_and_ring8,_9,andgene
 all_z14093_1190-1743,mrna_for_branched_chain_decarboxylase_alpha_subunit_

Metagene 240

hg491-ht491_at_hg491-ht491_fc_receptor_iib3_for_igg,_low_affinity
 m73720mrna_1032-1584,mast_cell_carboxypeptidase_a_(mc-cpa)_gene
 m82919_1201-1579,gamma_amino_butyric_acid_(gabaa)_receptor_beta-
 3_subunit_mrna,_complete_cds_
 u27109_3633-4155,prepromultimerin_mrna,_complete_cds_

Metagene 241

d83735_1551-2085,adult_heart_mrna_for_neutral_calponin,_complete_cds_
 j04182_1914-2394,lysosomal_membrane_glycoprotein-1_(lamp1)_mrna,_complete_cds_
 all_l08895_3518-4059,mads/mef2-
 family_transcription_factor_(mef2c)_mrna,_complete_cds_
 m19267_1476-1600,tropomyosin_mrna,_complete_cds_
 all_m19481_278-651:in_m19481cds_818-921,follistatin_gene
 m21574mrna_5807-6293,platelet-
 derived_growth_factor_receptor_alpha_(pdgfra)_mrna,_complete_cds_
 m74719_1971-2475,sef2-1b_protein_(sef2-1b)_mrna,_complete_cds_
 m95787_494-1004,22kda_smooth_muscle_protein_(sm22)_mrna,_complete_cds_
 s57132_3108-
 3615,_coll16a1=type_xvi_collagen_alphachain_[human,_placenta,_mrna_partial,_3720
 _nt]
 s73591_2169-2649,_brain-expressed_hhcpa78_homolog_[human,_hl-
 60_acute_promyelocytic_leukemia_cells,_
 u26710_3398-3878,cbl-b_mrna,_complete_cds_
 u44975_791-1301,dna-binding_protein_cpbbp_(cpbbp)_mrna,_partial_cds_
 u53446_2680-3220,mitogen-responsive_phosphoprotein_doc-2_mrna,_complete_cds_

u82532_231-753,gdi-dissociation_inhibitor_rhogdigamma_mrna,_complete_cds
u90913_659-1157,clone_23665_mrna_sequence
all_x13839_768-1300,mrna_for_vascular_smooth_muscle_alpha-actin
all_x86809_1916-2367,mrna_for_major_astrocytic_phosphoprotein_pea-15_
y12670mrna_531-1011,ob-rgrp_gene/gb=y12670_/ntype=rna
all_z24727_1355-1569,tropomyosin_isoform_mrna,_complete_cds
z26248cds_178-
640:in_reversesequence,_1512,mrna_for_eosinophil_granule_major_basic_protein
all_z48923_3300-3835,mrna_for_bmpr-ii

Metagene 242

d10704_1969-2365,mrna_for_choline_kinase_
d13413mrna_578-617,mrna_for_tumor-
associated_120_kda_nuclear_protein_p120,_partial_cds(carboxyl_term
d13900_748-1234,mrna_for_mitochondrial_short-chain_enoyl-
coa_hydratase,_complete_cds_
d64108_1595-2079,mrna_for_dmcl1_homologue,_complete_cds_
hg3999-ht4269_at_hg3999-ht4269_retinoic_acid_receptor,_beta,_isoform_1_
j03071cds#3_151-604:in_reversesequence,_14327-28953,_growth_hormone_gh-
1_gene_extracted_fromgrowth_h
l13042exon#2-3_11-216:not_in_gb_record,calbindin_d-9k_gene,_5'_end_cds_
l14778_1665-2225,calmodulin-
dependent_protein_phosphatase_catalytic_subunit_(ppp3ca)_mrna,_complete_
l37043mrna_742-1294,casein_kinase_i_epsilon_mrna,_complete_cds_
l46720cds_2231-2557:in_reversesequence,_2650-2828,autotaxin-t_(atx-
t)_gene,_complete_cds_
all_m55420_605-897:in_m55420cds_109-140,ige_chain,_lastexons_
m63904mrna_1519-2029,g-alphaprotein_mrna,_complete_cds_
m65066_1903-2323,camp-dependent_protein_kinase_regulatory_subunit_ri-
beta_mrna,_3'_end_
m75099_25-493,rapamycin-_and_fk506-binding_protein,_complete_cds_
m87338_1120-1660,replication_factor_40-kda_subunit_(a1)_mrna,_complete_cds_
s68616_4005-4491,_na+/h+_exchanger_nhe-1_isoform_[human,_heart,_mrna,_4516_nt]
u20530_47-593,bone_phosphoprotein_spp-
24_precursor_mrna,_complete_cds/gb=u20530_/ntype=rna_
u22398_1030-1468,cdk-inhibitor_p57kip2_(kip2)_mrna,_complete_cds_
u33839_at_u33839_u33839,not_in_gb_record,potassium_channel_mrna,_complete_cds/g
b=u33839_/ntype=rna
u61262_4667-5195,neogenin_mrna,_complete_cds_
u66619_1165-1699,swi/snf_complex_60_kda_subunit_(baf60c)_mrna,_complete_cds_
u82313_133-439,unknown_protein_mrna,_partial_cds/gb=u82313_/ntype=rna
x69391cds_395-821,mrna_for_ribosomal_protein_l6
all_x82693_134-681,mrna_for_e48_antigen

Metagene 243

m60974_731-1304,growth_arrest_and_dna-damage-
inducible_protein_(gadd45)_mrna,_complete_cds_
all_x14894_826-1385,mrna_for_myogenic_factor_myf-5_

Metagene 244

all_m55419_2275-2470,amelogenin_(amely)_gene,_3'_end_of_cds
 s41458_3026-3200,_rod_cgmp_phosphodiesterase_beta-
 subunit_[human,_mrna,_3231_nt]
 u11036_121-553,ibd1_mrna,_partial_cds/gb=u11036_/ntype=rna_
 all_z37987_2052-2198,mrna_for_mxr7_

Metagene 245

y09912mrna_757-1315,ap-2_beta_gene

Metagene 246

hg2380-ht2476_s_at_hg2380-ht2476_adp-ribosylarginine_hydrolase_
 m35252_602-998,co-029
 u59325_2353-2815,cadherin-14_mrna,_complete_cds
 y12812cds_486-768:in_reversesequence,_914-1130,rfxap_mrna_

Metagene 247

d86983_5131-5485,mrna_for_kiaa0230_gene,_partial_cds_
 hg142-ht142_at_hg142-ht142_modulator_recognition_factor_
 hg3995-ht4265_at_hg3995-ht4265_cpg-enriched_dna,_clone_s19_
 j04599_1078-
 1630,hpgi_mrna_encoding_bone_small_proteoglycan_i_(biglycan),_complete_cds_
 j05243_7216-7732,nonerythroid_alpha-spectrin_(sptan1)_mrna,_complete_cds_
 l06139_3573-4083,receptor_protein-tyrosine_kinase_(tek)_mrna,_complete_cds_
 l41143_1635-
 2085,expressed_pseudo_tcta_mrna_at_t(1;3)_translocation_site,_complete_cds
 m13194mrna_586-
 1006,excision_repair_protein_(erccl1)_mrna,_complete_cds,_clone_pcde_
 m25079_163-230,sickle_cell_beta-globin_mrna,_complete_cds
 m57609mrna_4490-5012,dna-binding_protein_(gli3)_mrna,_complete_cds_
 x15306mrna_3269-3707,nf-h_gene,_exon(and_joined_cds)_
 x75546cds_626-926:in_reversesequence,_1204,mrna_for_fibromodulin
 z83799_15-239,mrna_for_axonemal_dynein_heavy_chain_(partial,_id_hdhc1).
 all_z84721_30317-
 34635,dna_sequence_from_cosmid_gg1_from_a_contig_from_the_tip_of_the_short_arm_
 of_c

Metagene 248

m16474mrna_1788-2223,fetal_butyrylcholinesterase_mrna,_complete_cds
 u25433_2428-
 2842:not_in_gb_record,protein_associated_with_tumorigenic_conversion_(catr1.3)_
 mrna,_com
 u59423_1481-1943,smad1_mrna,_complete_cds
 x76538_433-931,mpv17_mrna

Metagene 249

m15780cds_13-
 304,dna/endogenouspapillomavirus_type(hpv)_dna,_right_flank_and_viral_host_junc
 tion/gb=
 m22092exon_6-42,neural_cell_adhesion_molecule_(n-
 cam)_gene,_exon_sec_and_partial_cds/gb=m22092_/ntyp
 u18004_31-205,_hsu18004cdna_

Metagene 250

d00760_277-781,mrna_for_proteasome_subunit_hc3_
 d14710_1298-1808,mrna_for_atp_synthase_alpha_subunit,_complete_cds_
 d15057_162-576,mrna_for_dad-1,_complete_cds_
 d78151_2321-2825,mrna_for_26s_proteasome_subunit_p97,_complete_cds_
 d78275_959-1511,mrna_for_proteasome_subunit_p42,_complete_cds_
 hg1112-ht1112_at_hg1112-ht1112_ras-like_protein_tc4
 hg2855-ht2995_at_hg2855-ht2995_heat_shock_protein,_70_kda
 hg3214-ht3391_at_hg3214-ht3391_metallopanstimulin_
 j02683mrna_629-1066,adp/atp_carrier_protein_mrna,_complete_cds_
 j02902mrna_1694-2156,protein_phosphatase_2a_regulatory_subunit_alpha-
 isotype_(alpha-pr65)_mrna,_comp
 j04173_1114-1648,phosphoglycerate_mutase_(pgam-b)_mrna,_complete_cds_
 j04973mrna_1023-1485,cytochrome_bc-1_complex_core_protein_ii_mrna,_complete_cds_
 103532_1898-2372,m4_protein_mrna,_complete_cds_
 107633_396-870,(clone_1950.2)_interferon-gamma_ief_ssp_5111_mrna,_complete_cds_
 126247_131-617,suiliso1_mrna,_complete_cds_
 141351mrna_1269-1695,prostasin_mrna,_complete_cds_
 176159mrna_471-957,frg1_mrna,_complete_cds_
 m17733mrna_13-505,thymosin_beta-4_mrna,_complete_cds_
 m38690_584-1106,cd9_antigen_mrna,_complete_cds_
 m55265mrna_1612-2116,casein_kinase_ii_alpha_subunit_mrna,_complete_cds_
 m57730mrna_975-1437,b61_mrna,_complete_cds_
 m63488_1834-2344,replication_protein_a_70kda_subunit_mrna_complete_cds_
 m93651_1973-2519,set_gene,_complete_cds_
 s80343_1609-2077,_argrs=arginyln-trna_synthetase_[human,_ataxia-
 telangiectasia_patients,_ebv-lymphobl
 u03100_2985-3501,alpha2(e)-catenin_mrna,_complete_cds_
 u06155cds_43-
 495,chromosome_1q_subtelomeric_sequence_d1s553/gb=u06155_/ntype=dna_/annot=cds,
 chromoso
 u15008_25-433,snrnp_core_protein_sm_d2_mrna,_complete_cds_
 u18919_408-948,chromosome_17q12-21_mrna,_clone_pov-2,_partial_cds_
 u25849mrna_1717-2137,red_cell-
 type_low_molecular_weight_acid_phosphatase_(acp1)_gene,_5'_flanking_re
 u30825_528-1014,splicing_factor_srp30c_mrna,_complete_cds_
 u32944_162-540,cytoplasmic_dynein_light_chain(hdlc1)_mrna,_complete_cds_
 u38846_1294-1732,stimulator_of_tar_rna_binding_(srb)_mrna,_complete_cds_
 u39317_16-
 484,e2_ubiquitin_conjugating_enzyme_ubch5b_(ubch5b)_mrna,_complete_cds_
 u51678_276-756,small_acidic_protein_mrna,_complete_cds_

u52427mrna_239-773,rna_polymerase_ii_seventh_subunit_(rpb-7)_gene,_complete_cds.
 u60276_645-1191,hasna-i_mrna,_complete_cds_
 u73514_376-892,short-chain_alcohol_dehydrogenase_(xh98g2)_mrna,_complete_cds.
 u73824_3202-3766,p97_mrna,_complete_cds
 u77396_at_u77396_u77396,not_in_gb_record,tnf-alpha_inducible_responsive_element_mrna,_complete_cds
 x00351cds_855-1065:in_reversesequence,_1154-1376,mrna_for_beta-actin
 all_x15183_2479-2894,mrna_for_90-kda_heat-shock_protein
 all_x53331_31-590,mrna_for_matrix_gla_protein
 all_x57206_3916-4487,mrna_for_ld-myo-inositol-trisphosphate_3-kinase_b_isoenzyme_
 x57959cds_264-714,mrna_for_ribosomal_protein_l7
 x60036cds_683-1037:in_reversesequence,_1163-1223,mrna_for_mitochondrial_phosphate_carrier_protein
 x63563cds_3176-3500,mrna_for_rna_polymerase_ii_140_kda_subunit_
 x75091cds_300-653:in_reversesequence,_848-892,mrna_for_hla-dr_associated_protein_ii_(phapii)
 all_x81817_933-1240,bap31_mrna_
 x83218cds_215-539,mrna_for_atp_synthase
 all_x96752_1367-1818,mrna_for_l-3-hydroxyacyl-coa_dehydrogenase
 y12711_336-864,mrna_for_putative_progesterone_binding_protein
 z35402mrna_3912-4402,gene_encoding_e-cadherin,_exonand_joined_cds
 z50853cds_556-802:in_reversesequence,_833-1001,mrna_for_clpp

Metagene 251

j02874_63-573,adipocyte_lipid-binding_protein,_complete_cds
 m15465_1955-2384,pyruvate_kinase_type_l_mrna,_complete_cds_
 u25128_2100-2598,pth2_parathyroid_hormone_receptor_mrna,_complete_cds
 u66616_3427-3979,swi/snf_complex_170_kda_subunit_(baf170)_mrna,_complete_cds_
 x82539mrna_1313-1823,mrna_for_mage-xp
 y08417_1043-
 1558,mrna_for_nicotinic_acetylcholine_receptor_beta3_subunit_precursor_
 all_z11850_55-
 416,mrna_for_somatotropin_receptor_5'_upstream_region/gb=z11850_/ntype=rna_

Metagene 252

d10326_1427-1981,mrna_for_pyruvate_kinase
 d49372_197-755,mrna_for_eotaxin,_complete_cds
 all_d83407_2601-3184,_zaki-4_mrna_inskin_fibroblast,_complete_cds
 d87467_5371-5857,mrna_for_kiaa0277_gene,_complete_cds
 hg167-ht167_s_at_hg167-ht167_hypothetical_protein_npiiy20
 hg2810-ht2921_at_hg2810-ht2921_homeotic_protein_pl2
 hg3162-ht3339_at_hg3162-ht3339_transcription_factor_iaa
 hg3627-ht3836_at_hg3627-ht3836_calcium_channel,_voltage-gated,_betasubunit,_l_type,_altssplice_2,_ske
 hg3638-ht3993_s_at_hg3638-
 ht3993_amyloid_beta_(a4)_precursor_protein,_altssplice_4
 hg4169-ht4439_s_at_hg4169-ht4439_syntaxin_1b_
 hg830-ht830_at_hg830-ht830_potassium_channel_

j02645mrna_882-1314,translational_initiation_factor_(eif-2),_alpha_subunit_mrna,_complete_cds
 k02777_139-621,t-cell_receptor_active_alpha-chain_mrna_from_jurkat_cell_line_100354exon_7-361:not_in_gb_record,cholecystokinin_(cck)_gene
 l43821mrna_3222-3774,enhancer_of_filamentation_(hef1)_mrna,_complete_cds
 all_m15517_182-480,_ttr_gene_extracted_frommutant_prealbumin_gene_directly_linked_to_familial_amyloi
 all_m17183_531-752,parathyroid_hormone-related_protein_mrna,_complete_cds
 all_m17466_3487-4040,blood_coagulation_factor_xii_(f12)_gene
 m20642mrna_369-898,alkali_myosin_light_chainmrna,_complete_cds
 m69238_2033-2579,aryl_hydrocarbon_receptor_nuclear_translocator_(arnt)_mrna,_complete_cds
 m90299mrna_2142-2628,glucokinase_(gck)_mrna,_complete_cds
 s43646_1904-2402,_cytokeratin[human,_epidermis,_mrna,_2427_nt]_s77582_2-
 55,_hervk10/hummtv_reverse_transcriptase_homolog_{clone_rt240}_[human,_multiple_sclerosis,_s78798_1252-1687,_1-phosphatidylinositol-4-phosphate_5-kinase_isoform_c_[human,_peripheral_blood_leu
 s79219_344-902,_metastasis-associated_gene_[human,_highly_metastatic_lung_cell_subline_anip[937],_mr
 s82592_357-861,_evi-1=evi-1_protein_{3'_region,_deletion_region}_[human,_megakaryoblastoid_cell_line
 u13219_1945-2473,forkhead_protein_freac-1_mrna,_complete_cds
 u18549exon#2_1091-1571,gpr6_g_protein-coupled_receptor_gene,_complete_cds
 u40317_5400-5965,protein_tyrosine_phosphatase_ptpsigma_(ptpsigma)_mrna,_complete_cds
 u49250_2323-2851,putative_cerebral_cortex_transcriptional_regulator_t-brain-1_(tbr-1)_mrna,_complete
 u58130_2887-3301,bumetanide-sensitive_na-k-2cl_cotransporter_(nkcc2)_mrna,_complete_cds
 u67615_12883-13381,beige_protein_homolog_(chs)_mrna,_complete_cds
 u77846mrna_979-1356,elastin_gene,_partial_cds_and_partial_3'_utr,elastin_gene,_partial_cds_and_parti
 u79277_986-1520,clone_23548_mrna_sequence
 u89995_3040-3460,dna_binding_protein_fkhl15_(fkhl15)_mrna,_complete_cds
 u92015_605-1031,clone_143789_defective_mariner_transposon_hsmar2_mrna_sequence_all_x07876_1706-2205,mrna_for_irp_protein_(int-1_related_protein)
 x16706cds_541-931:in_reversesequence,_970,fra-2_mrna
 x54380mrna_4050-4590,mrna_for_pregnancy_zone_protein_all_x64269_2501-2754,gene_mttf1_for_mitochondrial_transcription_factor_1_x68561cds_2234-2324:in_reversesequence,_2547-2943,spr-1_mrna_for_gt_box_binding_protein
 all_x69920_2736-3249,mrna_for_calcitonin_receptor
 all_x73079_2348-2919,encoding_polymeric_immunoglobulin_receptor_all_x77737_992-
 1431,mrna_for_red_cell_anion_exchanger_(epb3,_ae1,_band_3)_3'_non-coding_region
 all_x78342_1655-1857,pisslre_mrna
 x78711cds_1553-1638:in_reversesequence,_1665-1735,mrna_for_glycerol_kinase_testis_specific_1
 x87871cds_939-1367:in_reversesequence,_1472-1588,mrna_for_hepatocyte_nuclear_factor_4b
 all_x90846_2935-3407,mrna_for_mixed_lineage_kinase_2,mrna_for_mixed_lineage_kinase_2

x91220_3940-4165,mrna_for_na-cl_electroneutral_thiazide-sensitive_cotransporter
 all_z11502_886-1451,mrna_for_intestine-specific_annexin
 z48051mrna_1733-2303,gene_for_myelin_oligodendrocyte_glycoprotein_(mog)_
 all_z70218_2-333,mrna_for_mnl_protein_(clone_icrfp507i0498)
 all_z73903_5001-5554,mrna_for_trpc1a.
 z96810cds_482-968,dna_sequence_from_pac_452h17_on_chromosome_x_contains_sodium-
 and_chloride-dependen

Metagene 253

ab002356_5330-5807,mrna_for_kiaa0358_gene,_complete_cds/gb=ab002356_/ntype=rna_
 l11701_2320-2609,phospholipase_d_mrna,_complete_cds
 l42374mrna_1836-2389,pp2a_b56-beta_mrna,_complete_cds_
 m19508exon#1_2-98,_mpo_frommyeloperoxidase_gene,_exons_1-
 4/gb=m19508_/ntype=dna_/annot=exon_
 all_m32879_690-1129,steroid_11-beta-hydroxylase_(cyp11b1)_gene,steroid_11-beta-
 hydroxylase_(cyp11b1)
 m81182_2831-3314,peroxisomal_70_kd_membrane_protein_mrna,_complete_cds
 u25975_1675-1795,serine_kinase_(hpak65)_mrna,_partial_cds
 u47686_2174-
 2747,signal_transducer_and_activator_of_transcription_stat5b_mrna,_complete_cds
 all_u67092_1093-1868:not_in_gb_record,ataxia-
 telangiectasia_locus_protein_(atm)_gene,_exons_1a,_1b,_
 all_x16609_6641-7241,mrna_for_ankyrin_(variant_2.1)
 x51953exon#1-2_37-
 64:not_in_gb_record,ucp_gene_for_uncoupling_protein_exonsand/gb=x51953_/ntype=d
 na_
 all_x52228_1631-2103,mrna_for_secreted_epithelial_tumour_mucin_antigen_
 x58528mrna_2689-3193,pmp70_mrna_for_a_peroxisomal_membrane_protein_
 x95808mrna_5503-
 6037,mrna_for_protein_encoded_by_a_candidate_gene,_dxs6673e,_for_mental_retarda
 tion
 z11899cds_446-706:in_reversesequence,_989-
 1074,otf3_mrna_encoding_octamer_binding_protein_3b
 z22951mrna_717-
 1231,of_p65_gene_encoding_p65_subunit_of_transcription_factor_nf-kappab_
 reverse_z68280_34936-
 35175,dna_sequence_from_cosmid_l25a3,_huntington's_disease_region,_chromosome_4

Metagene 254

d28118_1807-2263,mrna_for_db1,_complete_cds
 d45370mrna_13-
 337,apm2_mrna_for_gs2374_(unknown_product_specific_to_adipose_tissue),_complete
 _cds
 hg2465-ht4871_at_hg2465-ht4871_dna-binding_protein_ap-2,_altsplice_3_
 m31682mrna_2130-2526,testicular_inhibin_beta-b-subunit_mrna,_3'_end
 m86933_220-
 681,amelogenin_(amely)_mrna,_complete_cds,amelogenin_(amely)_mrna,_complete_cds
 u28249_919-1405,11kd_protein_mrna,_complete_cds
 u68031_91-301,g_protein-
 coupled_receptor_(strl22)_mrna,_alternatively_spliced_5'_utr_sequence/gb=u68

x76732cds_975-1221:in_reversesequence,_1464-
1518:not_in_gb_record,nefa_protein_mrna,_complete_cds_(d

Metagene 255

d10922_1288-1808,mrna_for_fm1p-related_receptor_(hm63)_
m11567mrna_188-
620,angiogenin_gene,_complete_cds,_and_three_alu_repetitive_sequences

Metagene 256

hg210-ht210_s_at_hg210-ht210_galactokinase
j02923_2574-3132,65-kilodalton_phosphoprotein_(p65)_mrna,_complete_cds_
104270_1613-
2111,(clone_cd18)_tumor_necrosis_factor_receptorrelated_protein_mrna,_complete_
cds_
106633_1153-1669,transcription_factor_mrna,_complete_cds_
m14219_1375-
1753,chondroitin/dermatan_sulfate_proteoglycan_(pg40)_core_protein_mrna,_comple
te_cds
m21624mrna_603-1149,t-cell_receptor_delta_chain_mrna_(vjc-region),_complete_cds
m76766_679-1129,transcription_factor_(tfiib)_mrna,_complete_cds
u88964_130-568,hem45_mrna,_complete_cds

Metagene 257

ac002115cds#4_474-750:in_reversesequence,_100047-
100269,_cox6b_gene_(coxg)_extracted_fromdna_from_ov
af001620_1478-2000,trabecular_meshwork-
induced_glucocorticoid_response_protein_(tigr)_mrna,_complete
hg4185-ht4455_at_hg4185-ht4455_estrogen_sulfotransferase,_ste
hg537-ht537_at_hg537-ht537_collagen,_type_viii,_alpha_2
l19183mrna_1533-1959,mac30_mrna,_3'_end
l27584cds_1093-1400:in_reversesequence,_1464-
1677,ca_channel_b3_subunit_(cal_bet_3)_mrna,_complete_c
l39009mrna_109-
475,iv_alcohol_dehydrogenase(adh7)_gene,_5'_flanking_region/gb=l39009/_ntype=dn
a/_ann
m10058mrna_706-1252,asialoglycoprotein_receptor_h1_mrna,_complete_cds
m18700cds_288-784,elastase_iii_a_gene,_exon_8
m24122mrna_309-774,myosin_alkali_light_chain_(ventricular)_mrna,_complete_cds
m26679exon#2_505-925,homeobox_protein_(hox-1.3)_gene,_complete_cds
m73047_4025-4565,tripectidyl_peptidase_ii_mrna,_complete_cds
s67156_876-1368,_asp=aspartoacylase_[human,_kidney,_mrna,_1435_nt]
u07225_1430-1958,p2u_nucleotide_receptor_mrna,_complete_cds
u18288_2804-3314,clone_ciita-10_mhc_ii_transactivator_ciita_mrna,_complete_cds_
u19878_1137-1647,transmembrane_protein_mrna,_complete_cds
x52479cds_1689-1995:in_reversesequence,_2040-
2202,pkc_alpha_mrna_for_protein_kinase_c_alpha_
x99802_1983-2463,mrna_for_zyg_homologue
z33642mrna_2763-3291,v7_mrna_for_leukocyte_surface_protein_

Metagene 258

ab000816_783-1357,mrna_for_bmal1d,_partial_cds/gb=ab000816_/ntype=rna
d17716_1820-2390,mrna_for_n-
acetylglucosaminyltransferase_v,_complete_cds/gb=d17716_/ntype=rna_
d25539_3997-4375,mrna_for_kiaa0040_gene,_complete_cds
hg742-ht742_at_hg742-ht742_latent_membrane_protein_lmp1
107597_2496-3036,ribosomal_protein_s6_kinase(rps6ka2)_mrna,_complete_cds_
m10014cds#1_1048-1264:in_reversesequence,_9512-
9722,fibrinogen_gamma_chain_and_gamma-prime_chain_gen
m28825_1513-2047,thymocyte_antigen_cd1a_mrna,_complete_cds_
u03274_1497-1941,biotinidase_mrna,_complete_cds
u51241cds_717-1029:in_reversesequence,_1257-
1497,eosinophil_eotaxin_receptor_(cmkbr3)_gene,_complete
all_x63755_579-994,mrna_for_high-sulphur_keratin_
x80343cds_435-807:in_reversesequence,_1006-
1036,p35_mrna_for_regulatory_subunit_of_cdk5_kinase
all_x83929_2707-3257,mrna_for_typedesmocollin_

Metagene 259

m57471exon_13-
59,urate_oxidase_(uox)_gene,_exon/gb=m57471_/ntype=dna_/annot=exon_
m99439_1082-1385,transducin-like_enhancer_protein_(tle4)_mrna,_3'_end
u46024_2801-3377,myotubularin_(mtm1)_mrna,_partial_cds_
all_u57341_2-
129,neurofilament_triplet_1_protein_mrna,_partial_cds/gb=u57341_/ntype=rna,neur
ofilamen
u82468_1566-2091,tubby_related_protein(tulp1)_mrna,_complete_cds
x56741cds_85-595:in_reversesequence,_617,mrna_for_rab8_gene_
x74328mrna_1175-
1745,_cb2_(peripheral)_cannabinoid_receptor_gene_extracted_frommrna_for_cb2_(pe
riphe

Metagene 260

d29833_194-680,mrna_for_salivary_proline_rich_peptide_p-b,_complete_cds
d87433_6272-6752,mrna_for_kiaa0246_gene,_partial_cds_
u31384_57-591,g_protein_gamma-11_subunit_mrna,_complete_cds
u62801_935-1481,protease_m_mrna,_complete_cds

Metagene 261

hg274-ht274_s_at_hg274-ht274_gamma-glutamyltransferase
u49379_2051-2537,diacylglycerol_kinase_epsilon_dgk_mrna,_complete_cds
u81607_6007-6535,gravin_mrna,_complete_cds_
all_x81479_2655-3118,mrna_for_emr1_hormone_receptor
x86816mrna_4-193,estrogen_receptor_cdna,_5'_splice_variant/gb=x86816_/ntype=rna

Metagene 262

d90070_1329-1828,atl-derived_pma-responsive_(apr)_peptide_mrna_
 m69181_6995-7523,nonmuscle_myosin_heavy_chain-b_(myh10)_mrna,_partial_cds
 u02680_2435-2837,protein_tyrosine_kinase_mrna,_complete_cds

Metagene 263

ab003698_2634-3138,mrna_for_cdc7-related_kinase,_complete_cds
 m77140_91-409,pro-galanin_mrna,_3'_end_
 m98447mrna_2256-2670,keratinocyte_transglutaminase_gene,_complete_cds_
 u23752_1679-1919,sox-11_mrna,_complete_cds

Metagene 264

d21239_3475-3997,mrna_for_c3g_protein,_complete_cds
 d49958_1830-2346,fetus_brain_mrna_for_membrane_glycoprotein_m6,_complete_cds_
 d88613_1068-1518,mrna_for_hgcma,_complete_cds
 d88667_1298-1652,mrna_for_cerebroside_sulfotransferase,_complete_cds_
 hg1098-ht1098_at_hg1098-ht1098_cystatin_d
 hg2161-ht2231_at_hg2161-ht2231_translocation-
 associated_notch_(drosophila)_homolog
 hg2191-ht2261_at_hg2191-ht2261_crystallin,_beta_b3_
 hg3477-ht3670_at_hg3477-ht3670_cd4_antigen_
 hg3928-ht4198_at_hg3928-ht4198_surfactant_protein_sp-a1_delta_
 hg4336-ht4606_at_hg4336-ht4606_bactericidal_bpi'gene_
 hg4535-ht4940_s_at_hg4535-ht4940_dematin_
 j02888_453-915,quinone_oxidoreductase_(nqo2)_mrna,_complete_cds
 k03008cds_90-118:not_in_gb_record,_gamma-g2-psi_gene_extracted_fromgamma-c-
 crystallin_(gamma-3)_gene
 l11372_497-
 893,protocadherin_43_mrna,_3'_end_of_cds_for_alternative_splicing_pc43-12_
 l17327_16-196,pre-t/nk_cell_associated_protein_(3b3)_mrna,_3'_end
 l40904mrna_1228-
 1656,hsapiens_peroxisome_proliferator_activated_receptor_gamma,_complete_cds_
 m12625mrna_893-1259:in_reversesequence,_1599-1683,lecithin-
 cholesterol_acyltransferase_mrna,_complet
 m14123cds#1_263-665,_pol_fromendogenous_retrovirus_herv-
 k10/gb=m14123_/ntype=dna_/annot=cds,_pol_fro
 all_m16707_590-
 631,histone_h4_gene,_complete_cds,_clone_fo108,histone_h4_gene,_complete_cds,_c
 lone_f
 m21302_402-514,small_proline_rich_protein_(sprii)_mrna,_clone_174n_
 m21904cds_1189-1549:in_reversesequence,_372-
 378,4f2_glycosylated_heavy_chain_(4f2hc)_antigen_gene_
 m61733_2454-2934,erythroid_membrane_protein_4.1_mrna,_complete_cds
 m90366_1683-2175,zona_pellucida_glycoprotein(zp2)_mrna,_complete_cds
 m91585_3719-4175,br140_mrna,_complete_cds
 s80267_1304-1872,_p72syk_{g_insertion_nucleotide_92}_[human,_jurkat_e6-
 1_j.cam1_cells,_mrna_partial_

u01120_2484-2982,glucose-6-phosphatase_mrna,_complete_cds
 u04270_3505-3973,putative_potassium_channel_subunit_(h-erg)_mrna,_complete_cds_
 u07856cds#5_1300-
 1846,endogenous_retrovirus_in_complement_c4a_gene,_a3_allele,_herv-
 k(c4)_(gag),_(po
 u11090_733-1243,hydroxyindole-o-methyltransferase_promoter_a-
 derived_(hiomt)_mrna,_complete_cds
 u13666cds_671-989:in_reversesequence,_1329-1413,g_protein-
 coupled_receptor_(gpr1)_gene,_complete_cds
 u18244_1166-1640,excitatory_amino_acid_transporter_mrna,_complete_cds
 u18543_1853-2339,zinc-finger_protein_mrna,_complete_cds
 all_u19107_3423-3658,znf127_(znf127)_gene,_complete_cds_
 u19977_735-1227,preprocarboxypeptidase_a2_(procpa2)_mrna,_complete_cds_
 u20582_1180-1690,actin-like_peptide_mrna,_partial_cds
 u20657_2439-2890:not_in_gb_record,ubiquitin_protease_(unph)_proto-
 oncogene_mrna,_complete_cds_
 u31342mrna_1173-1629,nucleobindin_gene_
 u33317mrna_25-421,defensin(hd-6)_gene,_complete_cds
 u33761_1017-1557,cyclin_a/cdk2-associated_p45_(skp2)_mrna,_complete_cds
 u36501_1704-2148,sp100-b_(sp100-b)_mrna,_complete_cds
 u43148_6015-6483,patched_homolog_(ptc)_mrna,_complete_cds
 u48263_627-1173,pre-pro-orphanin_fq_(ofq)_mrna,_complete_cds_
 u49973cds#1_764-
 1340,_orf1;_mer37;_putative_transposase_similar_to_pogo_element_fromtiger1_tra
 nspos
 u59878_469-895,low-mr_gtp-binding_protein_(rab32)_mrna,_partial_cds
 u76010_1520-1964,putative_zinc_transporter_znt-3_(znt-3)_mrna,_complete_cds
 u77845_1515-1905,htrip_(htrip)_mrna,_complete_cds
 u78793_6-29,folate_receptor_alpha_(hfr)_mrna,_partial_cds/gb=u78793_/ntype=rna_
 u86759_1374-1856,netrin-2_like_protein_(ntn2l)_mrna,_complete_cds
 all_u90543_2501-
 2545,butyrophilin_(btfl)_mrna,_complete_cds,butyrophilin_(btfl)_mrna,_complete_
 cds
 u95019_2358-2862,voltage-dependent_calcium_channel_beta-
 2c_subunit_mrna,_complete_cds
 all_x04297_3519-4090,mrna_for_na,k-atpase_alpha-subunit
 all_x05246_1045-1556,testis-specific_pgk-
 2_gene_for_phosphoglycerate_kinase_(atp:3-phospho-d-glycera
 all_x53800_377-961,mrna_for_macrophage_inflammatory_protein-2beta_(mip2beta)_
 x76942cds_24-420:in_reversesequence,_487-527,mrna_for_72.1_protein
 x92518mrna_4077-4127,mrna_for_hmgi-c_protein_
 x96783mrna_1442-2015,syt_v_gene_(genomic_and_cdna_sequence)_
 all_x97058_1042-1565,mrna_for_p2y6_receptor
 y08200_1496-2006,mrna_for_rab_geranylgeranyl_transferase,_alpha-subunit
 all_z71460_2546-3033,mrna_for_vacuolar-type_h(+)-atpase_115_kda_subunit

Metagene 265

d84110_1113-1515,mrna_for_werner_syndrome-1/type_4,_complete_cds_
 d86982_5824-6286,mrna_for_kiaa0229_gene,_partial_cds_
 hg4518-ht4921_at_hg4518-ht4921_transcription_factor_btfl3_homolog_
 x04085mrna_1684-
 2236,gene_for_catalase_(ec_1.11.1.6)_5'_flank_and_exonmapping_to_chromosome_11,
 _band
 x67098exon#8_40-454,rtf_alpha_mrna_containing_four_open_reading_frames_

Metagene 266

u18467_1436-1946, pregnancy-specific beta 1-glycoprotein (psg7) _mrna, _complete_cds
 u65918_1248-1820, putative_rna_binding_protein_(dazh) _mrna, _complete_cds
 z78290_44-109, mrna_(clone_1d7) .

Metagene 267

hg544-ht544_at_hg544-ht544_endothelial_cell_growth_factor_105072exon#10_375-907, interferon_regulatory_factorgene, _complete_cds_107261mrna_283-505, alpha_adducin_mrna, _partial_cds_including_alternate_exons_a_and_b_(trimmed_to_889137360_146-698, (clone_hehk1-1)_ehk1_receptor_tyrosine_kinase_ligand_(efl-2)_mrna, _complete_cds177567mrna_947-1231, mitochondrial_citrate_transport_protein_(ctp)_mrna, _3'_end_m25667_1086-1200, neuronal_growth_protein_43_(gap-43)_mrna, _complete_cds_m32886_351-843, sorcin_cp-22_mrna, _complete_cds_u07151_395-869, gtp_binding_protein_(arl3)_mrna, _complete_cds_u29175_5199-5223, transcriptional_activator_(brg1)_mrna, _complete_cds_u30827_1253-1817, splicing_factor_srp40-3_(srp40)_mrna, _complete_cds_u30999_25-379, (memc)_mrna, _3'_utr/gb=u30999_/ntype=rna_u51432_1557-2079, nuclear_protein_skip_mrna, _complete_cds_u53830_1469-1835, interferon_regulatory_factor_7a_mrna, _complete_cds_u60873_115-439, clone_137308_mrna, _partial_cds_u79261_883-1422, clone_23959_mrna, _partial_cds_all_x14813_1077-1618, liver_mrna_for_3-oxoacyl-coa_thiolase_x64177cds_8-147:in_reversesequence, _2-277, mrna_for_metallothionein_x94333_1617-2157, mrna_for_tgn46_protein_x97074cds_182-398:in_reversesequence, _704-782, mrns_for_clathrin-associated_protein_z46376mrna_4703-5249, hk2_mrna_for_hexokinase_ii_

Metagene 268

d63483_2777-3304, mrna_for_kiaa0149_gene, _complete_cds104510_2769-3285, nucleotide_binding_protein_mrna, _complete_cds_m25322mrna_2577-3039, granule_membrane_protein-140_mrna, _complete_cds_s76978_29-224, _prostate-specific_membrane_antigen_{alternatively_spliced}_[human, _primary_prostatic_u33429_2481-2994, k+_channel_betasubunit_mrna, _complete_cds

Metagene 269

hg3985-ht4255_at_hg3985-ht4255_cpg-enriched_dna, _clone_e04_m16967_6338-6806, coagulation_factor_v_mrna, _complete_cds_m59941_2557-2965, gm-csf_receptor_beta_chain_mrna, _complete_cds_

u00672_3067-3577,interleukin-10_receptor_mrna,_complete_cds
 u79526_1787-2327,orphan_g-
 protein_coupled_receptor_dez_isoform_a_mrna,_complete_cds
 reverse_z49208_20545-
 20696,dna_from_cosmid_l161a8,_huntington_disease_region,_chromosome_4p16.3

Metagene 270

d45917_634-1120,mrna_for_timp-3,_partial_cds_(c-terminus_region)_
 d83174_1524-1896,mrna_for_collagen_binding_protein_2,_complete_cds_
 d86479_2250-2814,mrna_for_aebp1_gene,_complete_cds_
 d87258_1489-1999,cancellous_bone_osteoblast_mrna_for_serin_protease_with_igf-
 binding_motif,_complete
 hg2197-ht2267_s_at_hg2197-ht2267_collage,_type_vii,_alpha_1
 hg3543-ht3739_at_hg3543-ht3739_insulin-like_growth_factor_
 hg987-ht987_at_hg987-ht987_mac25_
 j02611mrna_208-766,apolipoprotein_d_mrna,_complete_cds_
 j03040_1508-2000,sparc/osteonectin_mrna,_complete_cds_
 j03278_5029-5485,platelet-
 derived_growth_factor_(pdgf)_receptor_mrna,_complete_cds_
 l32137_1910-2309,germline_oligomeric_matrix_protein_(comp)_mrna,_complete_cds_
 l36033_2929-3343,pre-
 b_cell_stimulating_factor_homologue_(sdf1b)_mrna,_complete_cds_
 m11718_716-1274,alpha-2_type_v_collagen_gene,_3'_end_
 m16279mrna_757-1153,mic2_mrna,_complete_cds_
 m25269_1791-2211,tyrosine_kinase_(elk1)_oncogene_mrna,_complete_cds_
 m55593mrna#1_2600-2936,collagenase_type_iv_(clg4)_gene_
 m85289_14032-14302,heparan_sulfate_proteoglycan_(hspg2)_mrna,_complete_cds_
 m96233exon#8_114-
 467,glutathione_transferase_mu_number(gstm4)_gene,_complete_cds_
 all_u14394_4004-4533,tissue_inhibitor_of_metalloproteinases-
 3_mrna,_complete_cds_
 u16306_10722-11142,chondroitin_sulfate_proteoglycan_versican_v0_splice-
 variant_precursor_peptide_mrn
 u24389cds_1495-1696:in_reversesequence,_207-339:not_in_gb_record,lysyl_oxidase-
 like_protein_gene_
 u60115_1863-2211,skeletal_muscle_lim-protein_slim1_mrna,_complete_cds_
 u77846mrna_979-
 1356,elastin_gene,_partial_cds_and_partial_3'_utr,elastin_gene,_partial_cds_and
 _parti
 all_x15880_1690-2273,mrna_for_collagen_vi_alpha-1_c-terminal_globular_domain_
 x15882cds_984-1230:in_reversesequence,_1272-1554,mrna_for_collagen_vi_alpha-
 2_c-terminal_globular_do
 x79683cds_4908-5361:in_reversesequence,_5594-5620,lamb2_mrna_for_beta2_laminin
 x86693mrna_2171-2675,mrna_for_hevin_like_protein_
 z48199exon#4_1510-2026,syndecan-1_gene_(exons_2-5)_
 z49269exon#1-3_76-199:not_in_gb_record,gene_for_chemokine_hcc-1_

Metagene 271

m10901mrna_4325-4655,glucocorticoid_receptor_alpha_mrna,_complete_cds
 m88338_1465-1867,serum_constituent_protein_(mse55)_mrna,_complete_cds
 u03891_90-576,phorbolin_i_mrna,_partial_cds

u77643_1462-1972,k12_protein_precursor_mrna,_complete_cds
 x74795cds_1923-2181:in_reversesequence,_2272-2488,p1-cdc46_mrna_
 all_x78669_1114-1643,erc-55_mrna_

Metagene 272

m86917_2402-2972,oxysterol-binding_protein_(osbp)_mrna,_complete_cds_
 u19142_69-510,gage-1_protein_mrna,_complete_cds
 u30872_9600-10116,mitosin_mrna,_complete_cds_
 all_u66061_134531-176445,germline_t-
 cell_receptor_beta_chain_tcrbv17s1alt,_tcrbv2s1,_tcrbv10s1p,_tcr
 u79297_1095-1575,clone_23589_mrna_sequence_
 u90268_1427-1703,krit1_mrna,_complete_cds
 all_x07024_4938-5257,x_chromosome_mrna_for_ccg1_protein_invin_cell_proliferation
 x16504cds_781-1266:in_reversesequence,_1283-1354,eno3_mrna_for_beta-
 enolase_(ec_4.2.1.11).

Metagene 273

d13666_2630-3072,mrna_for_osteoblast_specific_factor(osf-2os)
 d21255_3362-3812,mrna_for_ob-cadherin-2,_complete_cds
 hg1140-ht4817_s_at_hg1140-ht4817_collagen,_type_vi,_alpha_2,_altsplice_2_
 hg3044-ht3742_s_at_hg3044-ht3742_fibronectin,_altsplice_1
 hg3431-ht3616_s_at_hg3431-ht3616_decorin,_altsplice_1
 j04177_5773-6133,alpha-1_type_xi_collagen_(col11a1)_mrna,_complete_cds_
 all_l16895_1511-2016,lysyl_oxidase_(lox)_gene,_exon_7
 m24486mrna_2110-2684,prolyl_4-
 hydroxylase_alpha_subunit_mrna,_complete_cds,_clone_pa-11
 m65292_667-1202,factor_h_homologue_mrna,_complete_cds
 u21128_1254-1632,lumican_mrna,_complete_cds
 u37283_370-868,microfibril-associated_glycoprotein-2_magp-2_mrna,_complete_cds_
 all_x02761_7082-7646,mrna_for_fibronectin_(fn_precursor)_
 all_x06700_1946-2466,mrna_3'_region_for_pro-alpha1(iii)_collagen_
 all_x14787_5124-5701,mrna_for_thrombospondin_
 x52022_9941-10349,rna_for_type_vi_collagen_alpha3_chain
 x57766mrna_1658-2168,stromelysin-3_mrna
 all_x82153_1128-1615,mrna_for_cathepsin_o
 all_z74615_5320-5852,mrna_for_prepro-alpha1(i)_collagen
 all_z74616_4470-4992,mrna_for_prepro-alpha2(i)_collagen

Metagene 274

af015910_41-433,unknown_protein_mrna,_partial_cds/gb=af015910_/ntype=rna
 l13800mrna_4-397,liver_expressed_protein_gene,_3'_end/gb=l13800_/ntype=rna
 l14269_1369-1729,synaptic_vesicle_amine_transporter_(svat)_mrna,_complete_cds_
 m74447mrna_2012-2510,psf-2_mrna,_complete_cds
 u10693exon#2_1196-1553,mage-8_antigen_(mage8)_gene,_complete_cds_
 u11821_363-907,fas_ligand_(fasl)_mrna,_complete_cds
 x51985cds_1083-1479:in_reversesequence,_1787-1829,lag-3_mrna_for_cd4-
 related_protein_involved_in_lym
 x63454cds_327-567:in_reversesequence,_659-719,hst-2_(fgf-6)_mrna

y08564cds_1238-1688,galnac-t4_gene/gb=y08564_/ntype=dna_/annot=cds_

Metagene 275

j04168_1867-2263,leukosialin_mrna,_complete_cds
 105515_2108-2594,camp_response_element-binding_protein_(cre-
 bp1)_mrna,_complete_cds_
 109190mrna_6480-6930,trichohyalin_(trhy)_gene,_complete_cds_
 m26602_181-469,defensinprotein_mrna,_complete_cds_
 u79245_1139-1541,clone_23586_mrna_sequence_
 u82668mrna#2_1298-
 1820,_shox_gene_(shoxb)_extracted_fromshox_gene,_alternatively_spliced_products
 ,_c
 z18954exon#1-4_126-240:in_reversesequence,_246-
 264,mrna_for_s100d_calcium_binding_protein_

Metagene 276

hg1067-ht1067_r_at_hg1067-ht1067_mucin_
 u43292_706-1252,mds1b_(mds1)_mrna,_complete_cds
 all_x83492_418-500,mrna_for_fas/apo-1_(clone_pcrtm11-
 fasdelta(4,7))/gb=x83492_/ntype=rna,mrna_for_fa
 x95826cds_203-773,art4_gene/gb=x95826_/ntype=dna_/annot=cds
 x99894_936-1482,mrna_coding_for_insulin_promoter_factor_1

Metagene 277

ac000066cds_2985-3237:in_reversesequence,_48519-
 48663,bac_clone_rg293f11_from_7q21-7q22_
 af000560_1220-1697,ttf-i_interacting_peptidemrna,_partial_cds.
 d86958_6175-6430,mrna_for_kiaa0203_gene,_complete_cds
 hg3369-ht3546_at_hg3369-ht3546_potassium_channel,_voltage-gated,_isk-
 related_family,_member_1
 l43575mrna_1021-1106,(clone_48a8)_mrna
 m15841_492-945,u2_small_nuclear_rna-associated_b''_antigen_mrna,_complete_cds
 m27878_2656-3172,dna_binding_protein_(hpf2)_mrna,_complete_cds_
 m31516mrna_1492-2002,decay-accelerating_factor_mrna,_complete_cds
 m34309_4410-4836,epidermal_growth_factor_receptor_(her3)_mrna,_complete_cds
 m99436_1808-2246,transducin-like_enhancer_protein_(tle2)_mrna,_complete_cds
 u18242_761-
 1265,calcium_modulating_cyclophilin_ligand_(camlg)_mrna,_complete_cds_
 u51334_1840-2068,putative_rna_binding_protein_(rbp56)_mrna,_complete_cds_
 u60205_1192-1726,methyl_sterol_oxidase_(erg25)_mrna,_complete_cds
 u65928_711-1125,jun_activation_domain_binding_protein_mrna,_complete_cds_
 u82279_1505-2069,immunoglobulin-like_transcriptmrna,_complete_cds_
 u91521_2098-2470,peroxin(hspex12)_mrna,_complete_cds.
 all_x79353_1624-2189,xap-4_mrna_for_gdp-dissociation_inhibitor_
 all_x80754_1279-1862,mrna_for_gtp-binding_protein
 x81851cds_26-326,_hsapiens_il-4_gene_splice_variant/gb=x81851_/ntype=rna
 all_x83543_7066-7427,apxl_mrna_
 x90999cds_390-726:in_reversesequence,_828-942,mrna_for_glyoxalase_ii

all_x99584_197-630,mrna_for_smt3a_protein
 all_y00291_2443-2888,hap_mrna_encoding_a_dna-binding_hormone_receptor
 all_y07566_951-1066,mrna_for_rit_protein_

Metagene 278

d00654exon_127-196:not_in_gb_record,enteric_smooth_muscle_gamma-
 actin_gene,_5'_flank_and
 d42085_2200-2572,mrna_for_kiaa0095_gene,_complete_cds
 d76435_2639-3065,mrna_for_zic_protein,_complete_cds
 m37712mrna_3280-
 3760,p58/gta_(galactosyltransferase_associated_protein_kinase)_mrna,_complete_c
 ds
 u06681_1348-1774,clone_cca12_mrna_containing_cca_trinucleotide_repeat
 u15552_1831-2311,acidic_82_kda_protein_mrna,_complete_cds
 u66198_215-713,fibroblast_growth_factor_homologous_factor(fhf-
 2)_mrna,_complete_cds/gb=u66198_/ntype
 all_x13293_2056-2549,mrna_for_b-myb_gene_
 x13334cds_659-1049:in_reversesequence,_1234,cd14_mrna_for_myelid_cell-
 specific_leucine-rich_glycopro
 all_x87159_2076-2527,mrna_for_beta_subunit_of_epithelial_amiloride-
 sensitive_sodium_channel

Metagene 279

all_l10381_2086-2579,2-5a-dependent_rnase_gene,_complete_cds_
 m57703_129-629,melanin_concentrating_hormone_(mch)_mrna,_complete_cds
 u66359_1205-1583,t54_protein_(t54)_mrna,_complete_cds

Metagene 280

u60665_1603-2149,testis_specific_basic_protein_(tsbp),_complete_cds

Metagene 281

d28235exon#10_1923-2282,ptgs2_gene_for_prostaglandin_endoperoxide_synthase-
 2,_complete_cds_
 all_k02545_752-1044,_tcrb_gene_extracted_fromt-cell_receptor_germline_beta-
 chain_j-beta-1_gene_clust
 all_x98330_15142-15731,mrna_for_ryanodine_receptor_2_

Metagene 282

aj001421cds_117-567:in_reversesequence,_585-
 600,mrna_for_rer1_protein/gb=aj001421_/ntype=rna_
 d86981_5936-6410,mrna_for_kiaa0228_gene,_partial_cds_

142452mrna_1100-
 1520,pyruvate_dehydrogenase_kinase_isoenzyme (pdk3)_mrna,_complete_cds
 m22632mrna_1744-
 2284,mitochondrial_aspartate_aminotransferase_mrna,_complete_cds_
 m87503_1085-1535,ifn-responsive_transcription_factor_subunit_mrna,_complete_cds
 u01923_1649-2090,btk_region_clone_ftp-3_mrna_
 u02081_1642-
 2026,guanine_nucleotide_regulatory_protein_(net1)_mrna,_complete_cds_
 u04285utr#1_689-
 1148,lysosomal_acid_lipase,_cholesteryl_ester_hydrolase_(lipa)_gene
 u16799_865-1419,na,k-atpase_beta-1_subunit_mrna,_complete_cds
 u40038_1236-1425,gtp-binding_protein_alpha_q_subunit_(gnaq)_mrna,_complete_cds_
 u53445_2442-
 2928,ovarian_cancer_downregulated_myosin_heavy_chain_homolog_(doc1)_mrna,_compl
 ete_cds_
 u58046_4637-5176,p167_mrna,_complete_cds_
 u76421_4572-4962,dsrna_adenosine_deaminase_drada2b_(drada2b)_mrna,_complete_cds
 u77718_2100-2592,desmosome_associated_protein_pinin_mrna,_complete_cds_
 u81006_1886-2348,p76_mrna,_complete_cds
 u89505_1087-1537,hlark_mrna,_complete_cds
 u94586_145-445,nadh:ubiquinone_oxidoreductase_mlrq_subunit_mrna,_complete_cds
 all_x01060_4427-4986,mrna_for_transferrin_receptor_
 all_x13916_14416-14876,mrna_for_ldl-receptor_related_protein_
 x53586mrna_4766-
 5306,_integrin_alpha(or_alpha_e)_protein_gene_extracted_frommrna_for_integrin_a
 lpha_
 all_x68560_2909-3480,spr-2_mrna_for_gt_box_binding_protein_
 x69978cds_3218-3494:in_reversesequence,_3769-3781,mrna_for_xp-g_factor
 all_x71490_1059-1552,mrna_for_vacuolar_proton_atpase,_subunit_d
 all_x72790_30-1461,endogenous_retrovirus_mrna_for_orf/gb=x72790_/ntype=rna_
 x77909cds_888-1122:in_reversesequence,_1202-1406,ikbl_mrna
 x82676_3333-3873,mrna_for_tyrosine_phosphatase_
 all_y00757_629-1134,mrna_for_polypeptide_7b2_
 all_z34975_2303-2862,ldlc_mrna_
 z49989cds_779-1079:in_reversesequence,_1540,mrna_for_smoothelin_

Metagene 283

d26070mrna_8922-9492,mrna_for_typeinositol_1,4,5-
 trisphosphate_receptor,_complete_cds_
 l08044_8-358,intestinal_trefoil_factor_mrna,_complete_cds
 l38608_1950-2478,cd6_ligand_(alcam)_mrna,_complete_cds
 m12174_28-493,ras-related_rho_mrna_(clone_6),_partial_cds
 m23263_3498-3648,androgen_receptor_mrna,_complete_cds
 m31627_1191-1725,x_box_binding_protein-1_(xbp-1)_mrna,_complete_cds
 s37730cds_625-916:in_reversesequence,_496-635,_insulin-
 like_growth_factor_binding_protein-2_[human,_
 u09770_61-391,cysteine-rich_heart_protein_(hcrhp)_mrna,_complete_cds_
 u39840_2313-2823,hepatocyte_nuclear_factor-3_alpha_(hnf-
 3_alpha)_mrna,_complete_cds
 u52522_1047-1581,arfaptin_2,_putative_target_protein_of_adp-
 ribosylation_factor,_mrna,_complete_cds
 u94831_1555-
 1933,multispanning_membrane_protein_mrna,_complete_cds/gb=u94831_/ntype=rna
 all_x06614_2300-2889,mrna_for_receptor_of_retinoic_acid

x12876mrna_144-670,mrna_fragment_for_cytokeratin_18
 x52003cds_63-213:in_reversesequence,_289-445,ps2_protein_gene
 x53002cds_2049-2356:in_reversesequence,_2724-2849,mrna_for_integrin_beta-5_subunit
 all_x76180_2760-3115,mrna_for_lung_amiloride_sensitive_na+_channel_protein_
 all_z11793_1553-2001,mrna_for_selenoprotein_p

Metagene 284

k03021exon#14_343-853,tissue_plasminogen_activator_(plat)_gene,_complete_cds_
 all_m55998_2-265,alpha-1_collagen_type_i_gene,_3'_end
 m88461_993-1538,neuropeptide_y_peptide_yy_receptor_mrna,_complete_cds
 u32907_1401-1923,p37nb_mrna,_complete_cds
 u62325_2343-2805,fe65-like_protein_(hfe65l)_mrna,_partial_cds
 all_x52947_2497-2942,mrna_for_cardiac_gap_junction_protein_
 all_x54667_676-706,mrna_for_cystatin_s,mrna_for_cystatin_s
 all_x57351_294-891,1-8d_gene_from_interferon-inducible_gene_family,1-8d_gene_from_interferon-inducib
 all_x69111_662-1185,hlh_1r21_mrna_for_helix-loop-helix_protein_
 all_z29083_1644-2023,5t4_gene_for_5t4_oncofetal_antigen

Metagene 285

d37931_395-911,mrna_for_rnase_4,_complete_cds
 hg3731-ht4001_at_hg3731-ht4001_immunoglobulin_heavy_chain,_vdjrc_regions_
 hg4668-ht5083_s_at_hg4668-ht5083_transcription_factor_mef2,_altsplice_2
 l23333_725-1305,corticotropin_releasing_factor_receptor_mrna,_complete_cds.
 l38503_531-993,glutathione_s-transferase_theta(gstt2)_mrna,_complete_cds_
 m13981_1253-1300,inhibin_a-subunit_mrna,_complete_cds
 all_m35093_2155-2456,secreted_epithelial_tumor_mucin_antigen_(muc1)_gene,_complete_cds_
 u15932_1928-2294,dual-specificity_protein_phosphatase_mrna,_complete_cds_
 u79249_873-1359,clone_23839_mrna_sequence
 x65727cds#1_199-591,_gstalpha_locus_gene_(glutathione_s-transferase)_extracted_fromgstalpha_gene_for
 all_x77166_798-1183,gene_for_kunitz-type_protease_inhibitor,_hkib9_
 x95097mrna_924-1503,mrna_for_vip2_receptor
 all_z46261_490-899,dna_for_histone_h3a_

Metagene 286

d14446_794-1166,hfrep-1_mrna_for_unknown_protein,_complete_cds_
 d21262_3210-3663,mrna_for_kiaa0035_gene,_partial_cds_
 d28383_4-37,mrna_for_atp_synthase_b_chain,_5'_utr_(sequence_from_the_5'_cap_to_the_start_codon)/gb=d
 d42063_9590-9962,mrna_for_ranbp2_(ran-binding_protein_2),_complete_cds_
 d87453_2046-2586,mrna_for_kiaa0264_gene,_partial_cds_
 hg3088-ht3263_at_hg3088-ht3263_splicing_factor_sc35,_alt_splice_form_3_
 l48692_581-1067,(clone_p5-23-3)_mrna
 m74558_4849-5170,sil_mrna,_complete_cds

u28251exon_1192-1642,krueppel-
 type_zinc_finger_protein_(znf169)_gene,_partial_cds_
 u33632_1401-1839,two_p-domain_k+_channel_twik-1_mrna,_complete_cds_
 u41745_296-794,pdgf_associated_protein_mrna,_complete_cds
 u96131_1638-
 2130,hpv16_e1_protein_binding_protein_mrna,_complete_cds/gb=u96131_/ntype=rna_
 x82206cds_769-1107:in_reversesequence,_1192-1410,mrna_for_alpha-centractin
 z15005cds_7614-7968:in_reversesequence,_8076-8184,cenp-e_mrna_

Metagene 287

d17525mrna_3966-4446,mrna_for_precursor_of_p100_serine_protease_of_ra-
 reactive_factor,_complete_cds
 d28483_944-1466,scr3_mrna_for_rna_binding_protein_scr3,_complete_cds_
 d28532_1223-1763,mrna_for_renal_na+-
 dependent_phosphate_cotransporter,_complete_cds
 d31628cds_781-1132,gene_for_4-
 hydroxyphenylpyruvic_acid_dioxygenase_(hpd),_complete_cds_
 hg2707-ht2803_at_hg2707-ht2803_serine/threonine_kinase_
 j04990cds_371-683:in_reversesequence,_2929-2989,cathepsin_g_gene,_complete_cds
 j05257_1239-
 1713,(clones_mdp4,_mdp7)_microsomal_dipeptidase_(mdp)_mrna,_complete_cds
 l02321_1089-1509,glutathione_s-transferase_(gstm5)_mrna,_complete_cds
 l08485_1759-2257,gaba-benzodiazepine_receptor_alpha-5-
 subunit_(gabra5)_mrna,_complete_cds
 m34065mrna_1526-1952,cdc25hs_mrna,_complete_cds
 s68287_662-
 1124,_chlordecone_reductase_{clone_hakra}_[human,_liver,_mrna,_1167_nt]
 u64863_1556-2030,hpd-1_(hpd-1)_mrna,_complete_cds

Metagene 288

l07919_1386-1779,homeodomain_protein_dlx-2_mrna,_3'_end
 u17032_4391-4961,p190-b_(p190-b)_mrna,_complete_cds

Metagene 289

all_d29992_987-1132,mrna_for_placental_protein(pp5),_complete_cds_
 m86849_1747-2179,connexin_26_(gjb2)_mrna_
 all_m96132_32-66,mhc_ii_hla-dr-beta-1*09012_(hla-drb1*09012)_gene,_3'_end_cds

Metagene 290

d13540_1948-2500,mrna_for_protein-tyrosine_phosphatase_
 s83325_1796-2275,_aspartyl(asparaginy1)beta-
 hydroxylase_[human,_hepatoblastoma_cell_line_hepg2,_mrna
 all_x53296_1099-1657,mrna_for_irap_
 all_x95237_1357-1868,mrna_for_cysteine-rich_secretory_protein-1

Metagene 291

af006609_5-189,rgs3_mrna,_5'_utr/gb=af006609_/ntype=rna_
d38491_298-808,mrna_for_kiaa0117_gene,_partial_cds_
d50924_3807-4083,mrna_for_kiaa0134_gene,_complete_cds
m86826_1501-2023,igf_binding_protein_complex_acid-
labile_subunit_a_mrna,_complete_cds
m97252_5809-6271,kallmann_syndrome_(kal)_mrna,_complete_cds_
u27768_235-709,rgp4_mrna,_complete_cds_
u51127_1706-2084,interferon_regulatory_factor(humirf5)_mrna,_complete_cds_
u62961_2749-3241,succinyl_coa:3-
oxoacid_coa_transferase_precursor_(oxct)_mrna,_complete_cds

Metagene 292

l20814_2826-3306,glutamate_receptor(hbgr2)_mrna,_complete_cds_
u79260_1035-1341,clone_23745_mrna,_complete_cds

Metagene 293

l02320_1463-1997,radixin_mrna,_complete_cds
m86868_1189-1585,gamma_amino_butyric_acid_(gaba_rho2)_gene_mrna,_complete_cds

Metagene 294

a28102cds_986-1442:in_reversesequence,_1546-1582,gabaa_receptor_alpha-
3_subunit.
m17446mrna_648-
1186,kaposi_sarcoma_oncogene_fibroblast_growth_factor_mrna,_complete_cds
m98528utr#1_543-1101,neuron-specific_protein_gene,_last_exon,_clone_d4s234
u20816mrna#1_258-795,nuclear_factor_kappa-b2_(nf-
kb2)_gene,_partial_cds/gb=u20816_/ntype=dna_/annot=
all_u31799_528-683:in_u31799cds_1746-1777,melanocyte_protein_pmelgene_
all_x87870_2045-2289,mrna_for_hepatocyte_nuclear_factor_4a_

Metagene 295

u78551_838-1396,gallbladder_mucin_muc5b_mrna,_partial_cds_

Metagene 296

m69177_1992-2436,monoamine_oxidase_b_(maob)_mrna,_complete_cds_
m94151_3127-3631,cadherin-associated_protein-related_(cap-r)_mrna,_complete_cds

u01102exon#1-3_4-
 109: not_in_gb_record, lung_clara_cellskda_secretory_protein_(cc10)_gene, _satelli
 te_a
 u49835_832-1361, ykl-39_precursor_mrna, _complete_cds
 u88898_561-757, endogenous_retroviral_h_protease/integrase-
 derived_orf1_mrna, _complete_cds, _and_putat

Metagene 297

141690_906-1332, tnfr_receptor-1_associated_protein_(tradd)_mrna, _3'_end_of_cds_
 s78693_2-40, _alpha_creb-1=cyclic_amp_response_element-binding_protein-
 1_alpha_isoform_{alternatively
 x05153mrna_264-678, _alpha-lactalbumin_precursor_gene_extracted_fromalpha-
 lactalbumin_gene_
 all_x06956_5299-5359, halpha44_gene_for_alpha-tubulin, _exons_3-jan

Metagene 298

d64110_615-1161, mrna_for_tob_family, _complete_cds
 hg2564-ht2660_s_at_hg2564-ht2660_gamma-
 aminobutyric_acid_(gaba)_a_receptor, _alpha_subunit
 j04056_746-1118, carbonyl_reductase_mrna, _complete_cds
 m64174_3012-3468, protein-tyrosine_kinase_(jak1)_mrna, _complete_cds_
 u82319_470-980, clone_ydd19_mrna_sequence_
 x67594cds_507-909:in_reversesequence, _1119-1221, mrna_for_msh_receptor_

Metagene 299

s75881_234-719, _a-myb=dna-binding_transactivator_{3'_region}_[human, _ccrf-
 cem_t-leukemia_line, _mrna_
 z21707cds_552-912:in_reversesequence, _954-984, p18_mrna

Metagene 300

d15050_4757-5231, mrna_for_transcription_factor_areb6, _complete_cds_
 hg3748-ht4018_at_hg3748-ht4018_basic_transcription_factor, _44_kda_subunit
 s82472cds_3-
 73, _beta_#name?_polymerase_beta_{exon_alpha_to_exon_vii_region}_[human, _genomic
 , _124_nt,

Metagene 301

113698_2227-2791, gas1_gene, _complete_cds_
 l24203_2423-2891, ataxia-telangiectasia_group_d-
 associated_protein_mrna, _complete_cds
 m18533mrna_13566-13926, dystrophin_(dmd)_mrna, _complete_cds

m24485cds_109-604:in_reversesequence,_3966,(clone_phgst-pi)_glutathione_s-transferase_pi_(gstp1)_gen
 all_m98539_46-209:not_in_gb_record,prostaglandin_d2_synthase_gene_
 u03057_2172-2724,actin_bundling_protein_(hsn)_mrna,_complete_cds_
 u33849_2850-3366,lymphoma_proprotein_convertase_(lpc)_mrna,_complete_cds_
 u45955_834-1362,neuronal_membrane_glycoprotein_m6b_mrna,_partial_cds_
 all_x66534_2622-2953,soluble_guanylate_cyclase_large_subunit_mrna
 all_x87212_1273-1772,mrna_for_cathepsin_c
 x96381mrna_3518-4028,erm_gene,_exon_2,3,4,5_(and_joined_cds)

Metagene 302

ab002332_5132-5666,mrna_for_kiaa0334_gene,_complete_cds/gb=ab002332_/ntype=rna_
 k03008_cds1_at_k03008_k03008,not_in_gb_record,_gamma-g2-
 psi_gene_extracted_fromgamma-c-crystallin_(g
 107044_1420-1762,calcium/calmodulin-
 dependent_protein_kinase_(camk)_isoform_b_mrna_sequence_
 l36844mrna_292-
 808,(clone_pl5ink4b/ha5)_cdk_inhibitory_protein_mrna,_complete_cds_
 u35407mrna_77-
 193,peroxisomal_targeting_signal_import_receptor_(pxr1)_gene,_allele_5,_partial
 _cds/gb
 y07846exon#7_92-587,mrna_for_gar22_protein_
 all_y09616_1443-1948,mrna_for_putative_carboxylesterase

Metagene 303

d43682_1584-2115,mrna_for_very-long-chain_acyl-coa_dehydrogenase_(vlcad),_complete_cds_
 j05633_2714-3008,integrin_beta-5_subunit_mrna,_complete_cds
 l07615mrna_2289-2727,neuropeptide_y_receptor_y1_(npyy1)_mrna,_exon_3-
 feb_and_complete_cds/gb=l07615_
 l07807_2600-3147,dynamin_mrna,_alternative_exons_and_complete_cds
 l27841_6012-6498,autoantigen_pericentriol_material(pcm-1)_mrna,_complete_cds
 m15182mrna_1686-2106,beta-glucuronidase_mrna,_complete_cds_
 m19309mrna_382-939,slow_skeletal_muscle_troponin_t_mrna,_clone_h22h
 m29877mrna_1434-1932,alpha-l-fucosidase,_complete_cds
 m36205cds_73-319:in_reversesequence,_26-
 56:not_in_gb_record,synaptobrevin(syb2)_gene
 m62403_1343-1924,insulin-
 like_growth_factor_binding_protein(igfbp4)_mrna,_complete_cds
 m74715_1574-2080,alpha-l-iduronidas_(idua)_mrna,_complete_cds
 m97815exon#3_21-405,retinoic_acid-binding_protein_ii_(crabp-ii)_gene_
 s80437_1601-
 2185,_fatty_acid_synthase_{3'_region}_[human,_breast_and_hepg2_cells,_mrna_part
 ial,_2237
 s81914_760-1180,_iex-1=radiation-inducible_immediate-
 early_gene_[human,_placenta,_mrna_partial,_1223
 u26726_1548-1842,11-beta-hydroxysteroid_dehydrogenase_typemrna,_complete_cds
 u28369_2474-2894,semaphorin_v_mrna,_complete_cds_
 u49278_2752-3262,putative_dna-binding_protein_mrna,_partial_cds
 u53225_1409-1949,sorting_nexin(snx1)_mrna,_complete_cds_
 all_u57316_1593-1996,gcn5_(hgc5)_gene,_complete_cds_

u72066_2672-3212,ctbp_interacting_protein_ctip_(ctip)_mrna,_complete_cds_
 x13238cds_19-199:in_reversesequence,_272-
 386,mrna_for_cytochrome_c_oxidase_subunit_vic
 x54232mrna_3259-3643,mrna_for_heparan_sulfate_proteoglycan_(glypican)
 x57129cds_373-583:in_reversesequence,_1216-1366,h1.2_gene_for_histone_h1
 all_x82456_3287-3834,mln50_mrna
 y00503cds_799-1165:in_reversesequence,_1221-1227,mrna_for_keratin_19
 all_z68228_2878-3328,mrna_for_plakoglobin

Metagene 304

d13639_5889-6345,mrna_for_kiak0002_gene,_complete_cds
 d89077_2160-2592,mrna_for_src-like_adapter_protein,_complete_cds_
 hg1872-ht1907_at_hg1872-ht1907_major_histocompatibility_complex,_dg
 hg3576-ht3779_f_at_hg3576-ht3779_major_histocompatibility_complex,_ii_beta_w52_
 all_j00123_539-1020,enkephalin_gene
 j03909_461-995,gamma-interferon-inducible_protein_(ip-30)_mrna,_complete_cds_
 j04130mrna_87-634,activation_(act-2)_mrna,_complete_cds
 all_k02405_5550-7761:in_k02405cds_778,mhc_ii_hla-dc-3-beta_gene_(dr3,3)_
 m12529mrna_562-1132,apolipoprotein_e_mrna,_complete_cds
 m12886_950-1091,t-cell_receptor_active_beta-chain_mrna,_complete_cds_
 m13560exon_3-562:not_in_gb_record,ia-associated_invariant_gamma-chain_gene
 m20902cds_2-200:in_reversesequence,_517-5083,apolipoprotein_c-
 i_(vldl)_gene,_complete_cds_
 m21119_137-591,lysozyme_mrna,_complete_cds_
 m26062_3505-3871,interleukinreceptor_beta_chain_(p70-75)_mrna,_complete_cds_
 m34996_448-699,mhc_cell_surface_glycoprotein_(hla-dqa)_mrna,_3'_end
 m57466mrna_514-1036,mhc_ii_hla-dp_light_chain_mrna,_complete_cds_
 m59807mrna_369-933,nk4_mrna,_complete_cds
 m63835mrna_896-1388,igg_fc_receptor_i_gene_
 u15085_821-1289,hla-dmb_mrna,_complete_cds_
 u19713_18-374,allograft-inflammatory_factor-1_mrna,_complete_cds_
 u20158_1551-1911,76_kda_tyrosine_phosphoprotein_slp-76_mrna,_complete_cds
 u51240_1679-2171,lysosomal-
 associated_multitransmembrane_protein_(laptm5)_mrna,_complete_cds_
 u89922_267-
 773,lymphotoxin_beta_isoform_variant,_alternatively_spliced_mrna,_complete_cds
 x00274exon#5_1-337:not_in_gb_record,gene_for_hla-
 dr_alpha_heavy_chain_a_ii_antigen_(immune_response_
 x03068_f_at_x03068_x03068,_40_in_x03068cds_600-750:_29_in_reversesequence,_867-
 1167,mrna_for_hla-d_i
 x03100mrna_908-1124:in_reversesequence,_10629-10851,_hla-
 sb_alpha_gene_(class_ii_antigen)_extracted_
 all_x07743_2156-2679,mrna_for_pleckstrin_(p47)_
 all_x16663_1397-1872,hs1_gene_for_hematopoietic_lineage_cell_specific_protein_
 all_x59892_2163-2542,mrna_for_ifn-inducible_gamma2_protein_
 x62744cds_469-745:in_reversesequence,_814-
 1018,ring6_mrna_for_hla_ii_alpha_chain-like_product_
 x66401cds#1_327-615:in_fullsequence,_45931-
 47208:not_in_gb_record,_lmp2_gene_extracted_fromgenes_tap
 x68090cds_5-61,fc-gamma-
 riia_gene_for_igg_fc_receptor_ii_a_(5'_flank)/gb=x68090_/ntype=dna_/annot=cds
 all_x72755_2106-2479,humig_mrna
 x89109cds_860-1326:in_reversesequence,_1457-1488,mrna_for_coronin_

z36531cds_934-1294:in_reversesequence,_1345-1453,mrna_for_fibrinogen-like_protein_(pt49_protein)

Metagene 305

d17357exon_25-295,activin_beta-
a_gene,_regulatory_sequence_of_5'_upstream_region/gb=d17357_/ntype=dn
d28124_1346-1886,mrna_for_unknown_product,_complete_cds
d86425_4224-4776,osteoblast_mrna_for_osteonidogen,_complete_cds
l12350mrna_5247-5721,thrombospondin(thbs2)_mrna,_complete_cds_
l13923_9109-9601,fibrillin_mrna,_complete_cds_
m12125mrna_671-1013,fibroblast_muscle-type_tropomyosin_mrna,_complete_cds
m83186_103-
316,cytochrome_c_oxidase_subunit_viia_(cox7a)_muscle_isoform_mrna,_complete_cds_
m92934mrna_1492-2026,connective_tissue_growth_factor,_complete_cds_
u09278_2285-2735,fibroblast_activation_protein_mrna,_complete_cds
u19718_479-947,microfibril-associated_glycoprotein_(mfap2)_mrna,_complete_cds
u30521_1621-1951,p311_hum_-3.1_mrna,_complete_cds
u89942_2867-3383,lysyl_oxidase-related_protein_(ws9-14)_mrna,_complete_cds_
x02419mrna_1754-2210,upa_gene_
x57579exon_545-840:in_reversesequence,_1392-1555,activin_beta-
a_subunit_(exon_2)
all_x63759_1241-1752,htnp2_gene_for_transition_protein_2_

Metagene 306

hg3238-ht4861_s_at_hg3238-ht4861_prostaglandin_ep3_receptor,_altsplice_8_
s72904_1884-
2322,_apk1_antigen=mab_ki_recognized_[human,_ovarian_carcinoma_cell_line_ovcar-
3,_mrna,_
u45285_2099-2579,specific_116-kda_vacuolar_proton_pump_subunit_(oc-
116kda)_mrna,_complete_cds
u80017mrna#1_412-
673,_btf2p44_gene_(basic_transcription_factorp44)_extracted_frombasic_transcrip-
tion
x01057mrna_1492-1738,mrna_for_interleukin-2_receptor_
x95592_558-1122,mrna_for_cld_protein_
x97301mrna_13-148,mrna_for_ptg-11_protein/gb=x97301_/ntype=rna_

Metagene 307

d84454_2031-2577,mrna_for_udp-galactose_translocator,_complete_cds_
l09708mrna_2255-2795,complement_component(c2)_gene_allele_b_
u41315mrna#1_3083-3653,ring_zinc-finger_protein_(znf127-
xp)_gene_and_5'_flanking_sequence_
x58529mrna_1754-
2276,rearranged_immunoglobulin_mrna_for_mu_heavy_chain_enhancer_and_constant_re-
gion
x72475cds_111-
343,mrna_for_rearranged_ig_kappa_light_chain_variable_region_(i.114)_

Metagene 308

u14518_859-1315,centromere_protein-a_(cenp-a)_mrna,_complete_cds_
 u31116_1448-2012,beta-sarcoglycan_a3b_mrna,_complete_cds_
 all_u58675_25626-39844,_or17-
 228_gene_extracted_fromolfactory_receptor_gene_cluster_on_chromosome_17
 u64573exon_58-
 164,connexin43_gap_junction_protein_(connexin43)_gene,_exonand_promoter_region/
 gb=u645
 all_x99142_1281-1702,mrna_for_hair_keratin,_hnb6_

Metagene 309

d88146_1156-1408,mrna_for_udp-galactose_transporter_2,_complete_cds
 hg2175-ht2245_s_at_hg2175-ht2245_myosin,_heavy_polypeptide_10,_non-muscle
 hg3991-ht4261_at_hg3991-ht4261_cpg-enriched_dna,_clone_e18_
 all_m19989_804-1279,platelet-
 derived_growth_factor_(pdgfa)_a_chain_gene,platelet-derived_growth_fact
 u30313_372-
 756,diadenosine_tetraphosphatase_mrna,_complete_cds/gb=u30313_/ntype=rna
 u66077_1401-1822,daz_mrna,_3'_utr
 u79272_699-1179,clone_23720_mrna_sequence
 x98337cds_643-971:in_reversesequence,_1061-1256,mrna_for_complement_factor_h-
 related_protein_4

Metagene 310

hg3319-ht3496_s_at_hg3319-ht3496_split_geneenhancer,_tup1-like
 hg4480-ht4833_at_hg4480-ht4833_collagen,_type_vi,_alpha_2,_n-terminal_domain_
 l32163_1998-2380,zinc_finger_protein_mrna,_3'_end_
 l34219exon#7_26-452:not_in_gb_record,retinaldehyde-
 binding_protein_(cralbp)_gene,_complete_cds_
 m34181_2356-2872,testis-specific_camp-
 dependent_protein_kinase_catalytic_subunit_(c-beta_isoform)_mr
 u17195_1567-2143,a-kinase_anchor_protein_(akap100)_mrna,_complete_cds
 u20647_232-736,zinc_finger_protein_(znf151)_mrna,_partial_cds
 u22815_3771-3923,lar-interacting_protein_1a_mrna,_complete_cds_
 u25265_1758-2052,mek5_mrna,_complete_cds_
 all_u48405_1076-1650,g_protein_coupled_receptor_ogr1_gene,_complete_cds
 u48730_2629-2690,transcription_factor_stat5b_(stat5b)_mrna,_complete_cds.
 u79280_795-1359,clone_23575_mrna,_partial_cds
 u82320_546-1050,unknown_protein_mrna,_partial_cds/gb=u82320_/ntype=rna_
 u89717_635-1151,9-cis-retinol_specific_dehydrogenase_mrna,_complete_cds
 u89896_1184-1688,casein_kinase_i_gammamrna,_complete_cds
 x56654mrna_3221-3641,dsg1_mrna_for_desmoglein_type_1_
 all_x96849_49-323,5'_mrna_of_pecam-1_molecule/gb=x96849_/ntype=rna_

Metagene 311

d13305_1572-1992,mrna_for_brain_cholecystokinin_receptor_
d55640_110-635,monocyte_pabl_(pseudoautosomal_boundary-
like_sequence)_mrna,_clone_mo2/gb=d55640_/nty
l19063exon_79-451,glial-
derived_neurotrophic_factor_gene,_complete_cds/gb=l19063_/ntype=dna_/annot=e
l39211_1877-
2399,mitochondrial_carnitine_palmitoyltransferase_i_mrna,_complete_cds
m10051_4111-4651,insulin_receptor_mrna,_complete_cds_
m69203cds_4-254:in_reversesequence,_122-144,cytokine_(scya2)_gene_
u03644_1050-1452,recepin_mrna,_complete_cds
u17566_2214-2754,65_kda_hydrophobic_protein_mrna,_complete_cds_
u78628_7-
199,leukemia_inhibitory_factor_receptor_mrna,_5'_untranslated_region/gb=u78628_
/ntype=rna_
x66363cds_1279-1459:in_reversesequence,_1594-1702,mrna_pctaire-
1_for_serine/threonine_protein_kinase
x85785mrna_1060-1498,darc_gene
x99076mrna_736-1234,nrgn_gene,_exons_2,3_&(joined_cds)_
y00451cds_1461-1890:in_reversesequence,_2009-2037,mrna_for_5-
aminolevulinate_synthase_

Metagene 312

d31716_4264-4831,mrna_for_gc_box_bindig_protein,_complete_cds
l14430_at_l14430_l14430,not_in_gb_record,udp-
glucose_pyrophosphorylase_mrna,_complete_cds_and_flanki
u26591_1640-
2108,clone_is10_diabetes_mellitus_type_i_autoantigen_(icap69)_mrna,_complete_cd
s_
u33837_13803-14343,glycoprotein_receptor_gp330_precursor,_mrna,_complete_cds_
u33880mrna_189-
240,betaintegrin_isoform_d_(itgb1)_gene,_partial_cds/gb=u33880_/ntype=dna_/anno
t=exon
u62434_1665-
1787,nicotinic_acetylcholine_receptor_alpha5_subunit_precursor,_mrna,_complete_
cds_
all_x56199_1025-1614,xist,_coding_sequence_a_mrna_(locus_dxs399e)
x60382mrna_2717-3149,col10a1_gene_for_collagen_(alpha-1_type_x)_
z48520exon#5_1-98:in_reversesequence,_154-
163,xg_mrna_(clone_race6)/gb=z48520_/ntype=rna

Metagene 313

ac002045mrna#1_643-838,_a-589h1.1_fromchromosomebac_clone_cit987-ska-
589h1_-complete_genomic_sequenc
aj000099_1243-1750,mrna_for_lyosomal_hyaluronidase/gb=aj000099_/ntype=rna
d83260_604-1150,hxc-26_mrna,_complete_cds
j04823mrna_61-391,cytochrome_c_oxidase_subunit_viii_(cox8)_mrna,_complete_cds_
l11066_2272-2770,mrna_sequence_
l13939_3297-3791,beta_adaptin_protein_mrna,_complete_cds_
l25878_1092-1657,p33/heh_epoxide_hydrolase_(ephx)_mrna,_complete_cds
m34668_3044-3590,protein_tyrosine_phosphatase_(ptpase-alpha)_mrna

m64929_1572-2100,protein_phosphatase_2a_alpha_subunit_mrna,_complete_cds_
 m74491_3066-3552,adp-ribosylation_factor_mrna,_complete_cds
 m88279_1591-2131,immunophilin_(fkbp52)_mrna,_complete_cds
 m94046_1788-2346,zinc_finger_protein_(maz)_mrna
 s82470_1398-1836,_bb1=malignant_cell_expression-
 enhanced_gene/tumor_progression-enhanced_gene_[human
 u04241_979-
 1264,homolog_of_drosophila_enhancer_of_split_m9/m10_mrna,_complete_cds
 u13991_335-713,tata-
 binding_protein_associated_factor_30_kda_subunit_(tafi30)_mrna,_complete_cds
 u18937_1840-2344,histidyl-trna_synthetase_homolog_(ho3)_mrna,_complete_cds_
 u32986_3609-4126,xeroderma_pigmentosum_group_e_uv-
 damaged_dna_binding_factor_mrna,_complete_cds
 u37146_5411-
 5927,silencing_mediator_of_retinoid_and_thyroid_hormone_action_(smrt)_mrna,_com
 plete_cds
 u41635_2207-2651,os-9_precursor_mrna,_complete_cds
 u60644_1537-1957,hu-k4_mrna,_complete_cds
 u65579_138-648,mitochondrial_nadh_dehydrogenase-ubiquinone_fe-
 s_protein_8,_23_kda_subunit_precursor_
 u67171_229-697,selenoprotein_w_(selw)_mrna,_complete_cds/gb=u67171_/ntype=rna
 u78735_5872-6424,abc3_mrna,_complete_cds.
 u79287_813-1305,clone_23867_mrna_sequence
 u82108_987-1464,sip-1_mrna,_complete_cds_
 u83246_1364-1904,copine_i_mrna,_complete_cds_
 u95040_2366-2876,transcriptional_corepressor_hkap1/tif1b_mrna,_complete_cds
 all_x04106_907-1478,mrna_for_calcium_dependent_protease_(small_subunit)
 x57346cds_308-674:in_reversesequence,_1118-1154,mrna_for_hsl_protein
 x70649_2231-2663,cl.1042_mrna_of_dead_box_protein_family_
 all_x72964_606-1027,mrna_for_caltractin
 all_x73358_355-815,haes-1_mrna
 x92896exon#2-3_39-222:in_reversesequence,_295-301,mrna_for_itba2_protein
 x98801cds_3489-3729:in_reversesequence,_3771-4017,mrna_for_dynactin_
 x99728exon_13-247,ndufv3_gene,_exon/gb=x99728_/ntype=dna_/annot=exon
 y07604cds_291-483:in_reversesequence,_572-776,mrna_for_nucleoside-
 diphosphate_kinase_
 z14244cds_31-169:in_reversesequence,_43-
 409,coxviib_mrna_for_cytochrome_c_oxidase_subunit_viib
 z56281cds_772-1222:in_reversesequence,_1334-
 1382,mrna_for_interferon_regulatory_factor_3
 all_z69881_3952-4535,mrna_for_adenosine_triphosphatase,_calcium

Metagene 314

104656_370-856,carbonic_anhydrase_related_protein_(carp)_mrna,_complete_cds_
 l49209exon_25-
 92,retinoblastoma_susceptibility_protein_(rb1)_i66dbp_deletion_mutant_(resultin
 g_in_pr
 m84605_4280-4766,putative_opioid_receptor_mrna,_complete_cds_
 u14747_410-944,visinin-like_peptidehomolog_mrna,_complete_cds_
 u21556_709-1204,membrane_protein-
 like_protein_mrna,_partial_cds/gb=u21556_/ntype=rna_
 u50929_1910-2330,betaine:homocysteine_methyltransferase_mrna,_complete_cds_
 u83326cds_538-1010,cc_chemokine_receptor-5_(ccr5)_gene,_complete_cds.

Metagene 315

d83018_2645-3149,mrna_for_nel-related_protein_2,_complete_cds
 all_131860_2084-2589,glycophorin_mn-types_(gypa)_mrna,_complete_cds_
 m16961_937-1477,alpha-2-hs-glycoprotein_alpha_and_beta_chain_mrna,_complete_cds
 all_u01317_19502-63478,_epsilon-
 globin_gene_extracted_frombeta_globin_region_on_chromosome_11,_epsil
 u01877_8517-8997,p300_protein_mrna,_complete_cds_

Metagene 316

hg172-ht3924_at_hg172-ht3924_spermidine/spermine_n1-
 acetyltransferase,_altsplince_2_
 s79267_2828-3398,_cd4_receptor_{exonsand_2}_[human,_t-
 lymphocyte,_mrna,_3429_nt]_
 u10868_2267-2765,aldehyde_dehydrogenase_aldh7_mrna,_complete_cds_
 u31449_773-1337,intestinal_and_liver_tetraspan_membrane_protein_(il-
 tmp)_mrna,_complete_cds
 u57911_1693-2203,fetal_brain_(239fb)_mrna,_from_the_wagr_region,_complete_cds
 u67934cds_375-501:in_reversesequence,_549-
 765,44.9_kda_protein_c18b11_homolog_gene,_partial_cds
 x58022mrna_803-1223,mrna_for_corticotropin-
 releasing_factor_binding_protein_(crf-bp)_

Metagene 317

j03242_1155-1324,insulin-lke_growth_factor_ii_mrna,_complete_cds_
 j05068_984-1494,transcobalamin_i_mrna,_complete_cds
 m32578_1131-1191,mhc_ii_hla-dr_beta-1_mrna_(dr2.3),_5'_end_
 all_x79981_3411-3946,ve-cadherin_mrna

Metagene 318

hg3111-ht3287_at_hg3111-ht3287_autoantigen_
 m57230_2652-3000,membrane_glycoprotein_gp130_mrna,_complete_cds
 all_x68487_1174-1667,mrna_for_a2b_adenosine_receptor_
 all_x89430_1828-2333,mrna_for_methyl_cpg_binding_protein_2_
 z18951cds_311-509:in_reversesequence,_627-813,mrna_for_caveolin_

Metagene 319

d42072_2020-2542,mrna_for_nf1_n-isoform-exon11,_complete_cds_
 hg3998-ht4268_at_hg3998-ht4268_l-glycerol-3-phosphate:nad+_oxidoreductase
 m28170_1894-1987,cell_surface_protein_cd19_(cd19)_gene,_complete_cds_
 m62843_906-
 1404,brain_protein_recognized_by_the_sera_of_patients_with_paraneoplastic_senso
 ry_neurono

s67247_365-
 821,smooth_muscle_myosin_heavy_chain_isoform_smemb_[human,umbilical_cord,_fet
 al_aorta,_
 u08006exon#1_78-567,complementalpha_subunit_(c8a)_gene
 u09411_1794-2343,zinc_finger_protein_znf132_mrna,_complete_cds_
 u40343_657-1119,cdk_inhibitor_p19ink4d_mrna,_complete_cds
 u52827_1022-1508,cri-du-chat_region_mrna,_clone_nibb11_
 u66052mrna_7-271,clone_w2-6_mrna_from_chromosome_x/gb=u66052/_ntype=rna
 x07173cds_2503-2803:in_reversesequence,_2956-
 3028,mrna_for_second_protein_of_inter-alpha-trypsin_inh
 x16316cds_2109-2355:in_reversesequence,_2483-2693,mrna_for_vav_oncogene_
 x63578mrna_31-535,gene_for_parvalbumin

Metagene 320

d17400_196-622,mrna_for_6-pyruvoyl-tetrahydropterin_synthase,_complete_cds_
 d38498_37-
 604,pms5_mrna_(yeast_mismatch_repair_gene_pms1_homologue),_partial_cds_(c-
 terminal_region).
 hg3991-ht4261_r_at_hg3991-ht4261_cpg-enriched_dna,_clone_e18_
 j05500mrna#1_6200-6740,beta-spectrin_(sptb)_mrna,_complete_cds_
 l13689mrna_2674-3076,prot-oncogene_(bmi-1)_mrna,_complete_cds
 u18291_1439-1973,cdc16hs_mrna,_complete_cds
 u22662_1017-1473,nuclear_orphan_receptor_lxr-alpha_mrna,_complete_cds
 u35100_330-915,complexin_ii_mrna,_complete_cds.
 x05855cds_12-
 65:not_in_gb_record,histone_h3.3_gene_exon_2,histone_h3.3_gene_exon_2_
 all_x63597_5486-5979,si_mrna_for_sucrase-isomaltase
 all_x68486_2465-2934,mrna_for_a2a_adenosine_receptor_
 all_z23091_6853-7358,gpv_gene_encoding_platelet_glycoprotein_v_precursor

Metagene 321

all_d13315_1488-1975,mrna_for_lactoyl_glutathione_lyase
 d14812_1345-1747,mrna_for_kiaa0026_gene,_complete_cds
 d16469_2264-2738,mrna_for_orf_xq_terminal_portion_
 d23662_61-565,mrna_for_ubiquitin-like_protein,_complete_cds
 d30756_4053-4611,mrna_for_kiaa0049_gene,_complete_cds
 d31767_1338-1812,mrna_for_kiaa0058_gene,_complete_cds
 d50495mrna_493-1033,mrna_for_transcription_elongation_factor_s-ii,_hs-ii-
 t1,_complete_cds
 d86985_5502-5946,mrna_for_kiaa0232_gene,_complete_cds
 d87438_3322-3808,mrna_for_kiaa0251_gene,_partial_cds_
 hg1595-ht4788_s_at_hg1595-
 ht4788_heterogeneous_nuclear_ribonucleoprotein_i,_altssplice_2,_ptb-1_
 hg4683-ht5108_s_at_hg4683-
 ht5108_tumor_necrosis_factor_receptorassociated_protein_trap3_
 hg998-ht998_s_at_hg998-ht998_sulfotransferase,_phenol-preferring_
 j03805_926-1491,phosphatase_2a_mrna,_partial_cds_
 l19686mrna_61-
 493,macrophage_migration_inhibitory_factor_(mif)_gene,_complete_cds
 l36151_2433-2907,phosphatidylinositol_4-kinase_mrna,_complete_cds_
 l38810mrna_706-1246,thyroid_receptor_interactor_(trip1)_mrna,_complete_cds

l40391mrna_889-1435,(clone_s153)_mrna_fragment
 l43964_1671-2211,(clone_f-t03796)_stm-2_mrna,_complete_cds
 l77213mrna_479-959,phosphomevalonate_kinase_mrna,_complete_cds
 m34175mrna_5100-5670,beta_adaptin_mrna,_complete_cds_
 m62762_681-1083,vacuolar_h+_atpase_proton_channel_subunit_mrna,_complete_cds_
 m63959_1030-1444,alpha-2-macroglobulin_receptor-
 associated_protein_mrna,_complete_cds
 m69023_524-1088,globin_gene
 m98343_2695-3163,amplaxin_(ems1)_mrna,_complete_cds_
 u02556_1579-2101,rp3_mrna,_complete_cds
 u17969exon#6_165-663,initiation_factor_eif-5a_gene,_complete_cds_
 u19796_406-760,melanoma_antigen_p15_mrna,_complete_cds_
 u22897_1798-2338,nuclear_domainprotein_(ndp52)_mrna,_complete_cds_
 u25435_3227-3737,transcriptional_repressor_(ctcf)_mrna,_complete_cds_
 u31930_411-963,deoxyuridine_nucleotidohydrolase_mrna,_complete_cds_
 u36341mrna#1_3376-
 3862,_slc6a8_gene_(creatine_transporter)_extracted_fromxq28_cosmid,_creatine_tr
 ans
 u49869mrna_785-887,ubiquitin_gene,_complete_cds_
 u64444_633-1113,ubiquitin_fusion-degradation_protein_(ufd1l)_mrna,_complete_cds
 u72342mrna_5025-
 5499,platelet_activating_factor_acetylhydrolase,_brain_isoform,_45_kda_subunit_
 (lis1
 u78095_942-1434,placental_bikunin_mrna,_complete_cds_
 u80017mrna#2_5760-
 6039,_btf2p44_gene_(basic_transcription_factorp44)_extracted_frombasic_transcri
 pti
 u81556_1541-1925,hypothetical_protein_a4_mrna,_complete_cds
 all_x04526_2577-2968,liver_mrna_for_beta-
 subunit_signal_transducing_proteins_gs/gi_(beta-g)
 x13546mrna_657-1137,_puthmg-17_protein_gene_extracted_fromhmg-17_gene_for_non-
 histone_chromosomal_pr
 x15341cds_13-235:in_reversesequence,_374-500,cox_via-
 l_mrna_for_cytochrome_c_oxidase_liver-specific_
 all_x55330_1609-2120,mrna_for_aspartylglucosaminidase
 x56681mrna_1311-1835,jund_mrna_
 all_x64330_3792-4243,mrna_for_atp-citrate_lyase
 all_x64364_1014-1561,mrna_for_m6_antigen_
 all_x75593_679-1202,mrna_for_rab_13
 x82103cds_660-840:in_reversesequence,_954-1128,mrna_for_beta-cop
 all_x84709_1088-1683,mrna_for_mediator_of_receptor-induced_toxicity
 z35093cds_674-842:in_reversesequence,_898-976,mrna_for_surf-1_

Metagene 322

hg2229-ht2306_at_hg2229-ht2306_paired_box_hup1_
 m54914exon_1099-1666,follicle-stimulating_hormone_beta-subunit_gene

Metagene 323

l49229cds_2-
 87,retinoblastoma_susceptibility_protein_(rb1)_gene,_with_abp_deletion_in_exon_
 22_(11191

y09305cds_267-675:in_reversesequence,_711-
 771,mrna_for_protein_kinase,_dyrk4,_partial_
 y10517mrna_252-606,mrna_for_cd108_protein/gb=y10517_/ntype=rna_

Metagene 324

d29810_835-1363,mrna_for_unknown_product,_partial_cds
 l76224_3424-3970,nmda_receptor_mrna,_complete_cds_
 all_m24349_838-1316,parathyroid_hormone-
 like_protein_(plp)_gene,_exon_4,_clones_lambda-plpg(1,3,7-2)
 s81944_1173-1689,_gamma-
 aminobutyric_acid_type_a_receptor_alphasubunit_[human,_cerebellum,_mrna_part
 all_u03642_1060-1565,g_protein-coupled_receptor_apj_gene,_complete_cds_
 all_u06155_512-
 660,chromosome_1q_subtelomeric_sequence_d1s553/gb=u06155_/ntype=dna_/annot=cds,
 chromo
 u19557_998-1104,squamous_cell_carcinoma_antigen(scca2)_mrna,_complete_cds_
 u32659_1393-1825,il-17_mrna,_complete_cds
 u43519_2976-3474,dystrophin-related_protein(drp2)_mrna,_complete_cds
 u88902_cds1_f_at_u88902_u88902,_40_in_u88902cds#1_19-
 247:_21_in_reversesequence,_289-499,_integrase_
 x80915mrna_1908-2322,gdf5_gene
 y10205mrna_146-548,mrna_for_cd88_protein/gb=y10205_/ntype=rna

Metagene 325

d86096_cds1_s_at_d86096_d86096,not_in_gb_record,_ep3-
 iv_gene_extracted_fromdna_for_prostaglandin_e_r
 d86096_cds3_at_d86096_d86096,not_in_gb_record,_ep3-
 iv_gene_extracted_fromdna_for_prostaglandin_e_rec
 s74720_1889-1995,_dax-1=dss-
 ahc_critical_region_on_x_chromosome,_gene[human,_adrenal_hypoplasia_cong
 all_x17098_1278-1357,psg10_mrna_for_pregnancy_specific_glycoprotein_10_

Metagene 326

l10035_162-666:in_reversesequence,_684-690,crystallin_beta-
 b2_mrna,_complete_cds
 m16594_790-904,glutathione_s-transferase_ha_subunit(gst)_mrna,_complete_cds_
 u81523_1378-1870,endometrial_bleeding_associated_factor_mrna,_complete_cds.
 all_y10375_1179-1706,mrna_for_sirp-alpha1

Metagene 327

hg4167-ht4437_at_hg4167-ht4437_nuclear_factor_1,_a_type
 hg855-ht855_s_at_hg855-ht855_dna_excision_repair_protein_ercc6_
 j05037_918-1368,serine_dehydratase_mrna,_complete_cds
 j05401_1158-
 1554,sarcomeric_mitochondrial_creatine_kinase_(mtck)_gene,_complete_cds

146353mrna_6579-7077,high-mobility_group_phosphoprotein_(hmgi-c)_gene,_exons_3-jan
 u10886_4762-5068,density_enhanced_phosphatase-1_mrna,_complete_cds_
 u22233_1659-2166,methylthioadenosine_phosphorylase_(mtap)_mrna,_complete_cds_
 all_x03350_1973-2514,mrna_for_alcohol_dehydrogenase_beta-1-subunit_(adh1-2_allele)_
 z94753exon_92-444:in_fullsequence,_1246-
 1265,dna_sequence_from_pac_465g10_on_chromosome_x_contains_m

Metagene 328

d25274_727-1177,randomly_sequenced_mrna
 d49396_948-1446,mrna_for_apo1(mer5(aop1-mouse)-like_protein),_complete_cds
 l04731_13654-14152,translocation_t(4:11)_of_all-1_gene_to_chromosome_4
 l25081_595-1015,gtpase_(rhoc)_mrna,_complete_cds_
 m22538_286-778,nuclear-encoded_mitochondrial_nadh-ubiquinone_reductase_24kd_subunit_mrna,_complete_c
 m31951exon#2_671-
 1061:in_reversesequence,_6169,perforin_(prf1)_gene,_complete_cds_
 m63138mrna_1545-2007,cathepsin_d_(catd)_gene_
 s65738_1061-
 1373,_actin_depolymerizing_factor_[human,_fetal_brain,_mrna,_1452_ntl]
 u09848_2904-3474,zinc_finger_protein_(znf139)_mrna,_partial_cds
 u43901mrna#1_429-
 557,37_kd_laminin_receptor_precursor/p40_ribosome_associated_protein_gene,_complete
 u83908cds_941-1295:in_reversesequence,_1589-
 1649,nuclear_antigen_h731_mrna,_complete_cds
 u90878_693-1179,lim_domain_protein_clp-36_mrna,_complete_cds.
 u90902_939-1407,clone_23612_mrna_sequence
 u94855_696-1176,translation_initiation_factor47_kda_subunit_mrna,_complete_cds
 all_x16416_4998-5497,c-abl_mrna_encoding_p150_protein
 all_x51466_2702-3057,mrna_for_elongation_factor_2
 x70218_771-1203,_hsapiens_mrna_for_protein_phosphatase_x
 all_x74929_1365-1706,krt8_mrna_for_keratin_8_
 all_x76228_677-1242,mrna_for_vacuolar_h+atpase_e_subunit
 x78136cds_688-1060:in_reversesequence,_1130-1244,hnrnp-e2_mrna
 x82207cds_876-1098:in_reversesequence,_1166-1412,mrna_for_beta-centractin_(pc3)
 y08999cds_583-1045:in_reversesequence,_1132,mrna_for_sop2p-like_protein_
 all_z14000_958-1463,ring1_gene_
 all_z49835_1354-1805,mrna_for_protein_disulfide_isomerase

Metagene 329

m27968mrna_3289-3658,basic_fibroblast_growth_factor_(fgf)_mrna,_complete_cds_
 all_m31994_117-538,cytosolic_aldehyde_dehydrogenase_(aldh1)_gene_
 m73780_3266-3746,integrin_beta-8_subunit_mrna,_complete_cds
 u20860exon#3_1889-2279,angiotensin_ii_typerceptor_gene,_complete_cds_
 u65002_6724-7240,zinc_finger_protein_plagl_mrna,_complete_cds
 all_x04688_227-798,mrna_for_t-cell_replacing_factor_(interleukin-5)

Metagene 330

d10040_3243-3489,mrna_for_long-chain_acyl-coa_synthetase_
 d55654_786-1224,mrna_for_cytosolic_malate_dehydrogenase,_complete_cds
 d63874_865-1153,mrna_for_hmg-1,_complete_cds
 d63878_2850-3408,mrna_for_kiaa0158_gene,_complete_cds
 d63880_4952-5504,mrna_for_kiaa0159_gene,_complete_cds
 d79205_5-319:in_reversesequence,_323-
 325,mrna_for_ribosomal_protein_l39,_complete_cds
 d79996_1759-2305,mrna_for_kiaa0174_gene,_complete_cds
 d90209_1420-1972,mrna_for_dna_binding_protein_taxreb67_
 hg1116-ht1116_at_hg1116-ht1116_proliferating-cell_nucleolar_antigen,_120_kda_
 hg4312-ht4582_s_at_hg4312-ht4582_transcription_factor_iiia_
 hg4334-ht4604_s_at_hg4334-ht4604_glycogenin
 j05032_1721-2153,aspartyl-trna_synthetase_alpha-2_subunit_mrna,_complete_cds_
 l08069_909-1347,heat_shock_protein,_ecoli_dna_j_homologue_mrna,_complete_cds
 l13761mrna_3838-4270,dihydrolipoamide_dehydrogenase_gene,_exon_14_
 l20941_615-1143,ferritin_heavy_chain_mrna,_complete_cds
 l25931_3127-3607,lamin_b_receptor_(lbr)_mrna,_complete_cds_
 l33881_1822-2206,protein_kinase_c_iota_isoform,_complete_cds_
 l76200_268-796,guanylate_kinase_(guk1)_mrna,_complete_cds
 m15990_3916-4390,c-yes-1_mrna
 all_m19283_2724-3319,cytoskeletal_gamma-actin_gene,_complete_cds_
 m22382mrna_1758-
 2184,mitochondrial_matrix_protein_p1_(nuclear_encoded)_mrna,_complete_cds
 m26880_2206-2246,ubiquitin_mrna,_complete_cds
 m29064_1225-1657,hnrnp_b1_protein_mrna_
 m33521exon#2_2706-3144:in_reversesequence,_4118-4148,hla-b-
 associated_transcript(bat3)_gene,_5'_end
 m55531mrna_1647-2175,glucose_transport-like(glut5)_mrna,_complete_cds_
 m60858mrna_2193-2481,nucleolin_gene,_complete_cds_
 m84739_1366-1876,autoantigen_calreticulin_mrna,_complete_cds_
 m85169_2712-3276,homologue_of_yeast_sec7_mrna,_complete_cds
 m94556_171-
 567,mitochondrial_specific_single_stranded_dna_binding_protein_mrna,_complete_c
 ds_
 m96843_668-
 1112,striated_muscle_contraction_regulatory_protein_(id2b)_mrna,_complete_cds_
 m96982_483-801,u2_snrnp_auxiliary_factor_small_subunit,_complete_cds
 s63912_2442-3018,d10s102=fbrnp_[human,_fetal_brain,_mrna,_3043_nt]_
 u05227_1078-1564,rar_protein_mrna,_complete_cds
 u07550_139-493,chaperoninmrna,_complete_cds
 u09587_2261-2330,glycyl-trna_synthetase_mrna,_complete_cds.
 u19247mrna_1469-1939,interferon-gamma_receptor_alpha_chain_gene_
 u24576_1467-2013,breast_tumor_autoantigen_mrna,_complete_sequence
 u40369mrna_851-995,spermidine/spermine_n1-
 acetyltransferase_(ssat)_gene,_complete_cds_
 u41816_614-1004,c-1_mrna,_complete_cds_
 u47635_1921-2353,d13s824e_locus_mrna,_complete_cds_
 u51478_856-1282,sodium/potassium-transporting_atpase_beta-
 3_subunit_mrna,_complete_cds_
 u63743_2187-2715,mitotic_centromere-associated_kinesin_mrna,_complete_cds
 u69126_1831-2345,fuse_binding_protein(fbp2)_mrna,_partial_cds_
 u75308_3654-4092,tbp-associated_factor_(htafii130)_mrna,_partial_cds_
 u90552_2814-
 3377,butyrophilin_(btf5)_mrna,_complete_cds,butyrophilin_(btf5)_mrna,_complete_
 cds

all_x14684_629-1150,mrna_for_la_protein_c-terminal_region
 all_x51755_8272-8537,_ig_light-chain,_partial_ke-oz-_polypeptide;_author-
 given_protein_sequence_is_i
 x56494mrna#1_1894-2398,m_gene_for_m1-type_and_m2-type_pyruvate_kinase
 all_x59812_1586-2025,cyp_27_mrna_for_vitamin_d3_25-hydroxylase_
 all_x60221_635-1044,mrna_for_h+-atp_synthase_subunit_b_
 all_x78627_2163-2674,mrna_for_translin_
 all_x99325_1482-1927,mrna_for_ste20-like_kinase
 all_z29064_3656-4251,af-1p_mrna
 z50022mrna_2064-2478,mrna_for_surface_glycoprotein_
 z74792mrna_1470-1917,mrna_for_ccaat_transcription_binding_factor_subunit_gamma.

Metagene 331

ac002045mrna#2_625-908,_a-589h1.1_fromchromosomebac_clone_cit987-ska-
 589h1_-complete_genomic_sequenc
 d10523_3533-4079,mrna_for_2-oxoglutarate_dehydrogenase,_complete_cds_
 d31840_3679-4148,drpla_mrna_for_orf,_complete_cds
 d50912_2685-3183,mrna_for_kiaa0122_gene,_partial_cds_
 d80008_2695-3205,mrna_for_kiaa0186_gene,_complete_cds
 d86963_4563-5097,mrna_for_kiaa0208_gene,_complete_cds
 d87078_4798-5296,mrna_for_kiaa0235_gene,_partial_cds_
 hg1612-ht1612_at_hg1612-ht1612_macmarcks_
 hg2525-ht2621_at_hg2525-ht2621_helix-loop-helix_protein_delta_max,_altsplice_1_
 hg3635-ht3845_f_at_hg3635-ht3845_zinc_finger_protein,_kruppel-like_
 l07648_1955-2321,mx11_mrna,_complete_cds_
 l76702mrna_2447-3005,b56-delta_mrna,_complete_cds_
 m13452_1927-2435,lamin_a_mrna,_3'_end
 m91670_301-787,ubiquitin_carrier_protein_(e2-epf)_mrna,_complete_cds_
 s49592_1868-2425,_transcription_factor_e2f_like_protein_[human,_mrna,_2492_nt]
 u09820_5579-6058,helicase_ii_(rad54l)_mrna,_complete_cds.
 u22963_752-1238,i_histocompatibility_antigen-like_protein_mrna,_complete_cds.
 u34044_1143-1647,selenium_donor_protein_(seld)_mrna,_complete_cds
 u37012_3868-
 4372,cleavage_and_polyadenylation_specificity_factor_mrna,_complete_cds
 u52426_3469-3997,gok_(gok)_mrna,_complete_cds
 u54778_1131-1671,14-3-3_epsilon_mrna,_complete_cds_
 u57342_967-
 1459,myelodysplasia/myeloid_leukemia_factor(mlf2)_mrna,_complete_cds_
 u72761_2753-3233,karyopherin_betamrna,_complete_cds/gb=u72761_/ntype=rna
 u81984_2277-2739,endothelial_pas_domain_protein(epas1)_mrna,_complete_cds_
 all_x06323_1105-
 1520,mrl3_mrna_for_ribosomal_protein_l3_homologue_(mrl3=_mammalian_ribosome_l
 3_)_
 x71428mrna_1284-1788,fus_mrna
 x75755mrna#1_1337-1471,pr264_gene_
 all_x76717_3-268,mt-1l_mrna
 all_x83928_456-919,mrna_for_transcription_factor_tfiid_subunit_tafii28_
 all_x90824_828-1337,mrna_for_usf2a_&_usf2b,_clone_p9dh_
 x97160mrna_2016-
 2532,_tfe3_transcription_factor_gene_extracted_fromtfe3_gene,_exons_1,2,3_(and_
 joine
 y07595cds_948-
 1344:in_reversesequence,_1501,mrna_for_52_kd_subunit_of_transcription_factor_tf
 iih

y13247_3077-3581,fb19_mrna
 y13620_5732-6182,mrna_for_bcl9_gene/gb=y13620_/ntype=rna
 z37166cds_1006-1252:in_reversesequence,_1432-
 1570,bat1_mrna_for_nuclear_rna_helicase_(dead_family)

Metagene 332

l37362_1009-1579,(clone_d2-
 115)_kappa_opioid_receptor_(oprk1)_mrna,_complete_cds
 all_m28879_3325-4444,granzyme_b_(ctla-1)_gene,_complete_cds
 u34070cds_744-1053:in_reversesequence,_1731-
 1763,ccaat/enhancer_binding_protein_alpha_gene,_complete
 u57592_3563-4043,jumonji_putative_protein_(jumonji)_mrna,_complete_cds_
 u93867_1248-
 1764,rna_polymerase_iii_subunit_(rpc62)_mrna,_complete_cds/gb=u93867_/ntype=rna
 all_z28339_2084-2649,mrna_for_delta_4-3-oxosteroidbeta-reductase

Metagene 333

u96191_19-439,trophoblast_hypoxia-regulated_factor-5_(hrf-
 5)_mrna,_3'_end/gb=u96191_/ntype=rna_
 all_x13955_675-827,mrna_for_myosin_alkali_light_chain
 x64877cds_417-762:in_reversesequence,_889-
 894,mrna_for_serum_protein,mrna_for_serum_protein

Metagene 334

d13146mrna#1_2083-2551,_2'_,_3'_-cyclic-nucleotide_3'_-
 phosphodiesterase_gene_extracted_from2'_,_3'_-c
 d21235_1418-1673,mrna_for_hhr23a_protein,_complete_cds_
 d83702_2392-2902,brain_mrna_for_photolyase_homolog,_complete_cds_
 d87452_3950-4418,mrna_for_kiaa0263_gene,_complete_cds
 d87459_2144-2564,mrna_for_kiaa0269_gene,_complete_cds
 l13848_3675-4161,rna_helicase_a_mrna,_complete_cds_
 l20591exon_1-295:not_in_gb_record,annexin_iii_(anx3)_gene,_alternative
 m22348_3-494,mitochondrial_ubiquinone-binding_protein_mrna,_complete_cds_
 s74017_1721-2213,_nrf2=nf-e2-
 like_basic_leucine_zipper_transcriptional_activator_[human,_hemin-induc
 s75313_1197-
 l387,_mjd1=mjd1_protein_{cag_repeats}_[human,_brain,_mrna,_1776_nt]_
 u19765exon#5_630-1194,nucleic_acid_binding_protein_gene,_complete_cds
 u64105_2540-3104,guanine_nucleotide_exchange_factor_p115-
 rhogef_mrna,_partial_cds
 u67156_4641-5151,mitogen-
 activated_kinase_kinase_kinase(mapkkk5)_mrna,_complete_cds_
 all_x06318_2381-2541,mrna_for_protein_kinase_c_(pkc)_type_beta_i_
 x55740mrna_2940-3516,placental_cdna_coding_for_5'_nucleotidase_(ec_3.1.3.5)
 all_x76648_338-777,mrna_for_glutaredoxin_
 z78291_28-223,mrna_(clone_ld8).

Metagene 335

k02882cds_660-1098,ighd_gene_(immunoglobulin_delta-chain)_extracted_fromgermline_igd_chain_gene,_c-m61199_1227-1689,cleavage_signalprotein_mrna,_complete_cds

Metagene 336

u08021_447-909,nicotinamide_n-methyltransferase_(nnmt)_mrna,_complete_cds
all_x83107_1867-2348,bmx_mrna_for_cytoplasmic_tyrosine_kinase

Metagene 337

d87469_8413-8899,mrna_for_kiaa0279_gene,_partial_cds_
l21934_3401-3905,acyl_coenzyme_a:cholesterol_acyltransferase_mrna,_complete_cds
s60415_2937-
3333,_myasthenic_syndrome_antigen_b_[human,_fetal_brain,_mrna,_3477_nt]_
u09716_1621-2124,mannose-specific_lectin_(mr60)_mrna,_complete_cds_
u48250_1490-2030,protein_kinase_c-binding_protein_rack17_mrna,_partial_cds_
all_x94612_2745-3328,mrna_for_type_ii_cgmp-dependent_protein_kinase
y11709mrna_169-709,mrna_for_extracellular_matrix_protein_collagen_type_xiv,_n-terminus/gb=y11709_/nt

Metagene 338

d50370_2047-2581,mrna_for_nucleosome_assembly_protein,_complete_cds
l43576_709-1009,(clone_est02946)_mrna_
m36118_491-828,cytotoxin_serine_protease-c_mrna,_complete_cds
s81419_25-
349,_dystrophin,_dystrophin_{purkinje_promoter,_alternatively_spliced}_[human,_cortical_br
u04735_1728-
2184,microsomal_stress_70_protein_atpase_core_(stch)_mrna,_complete_cds
u45255mrna_1576-1952,paired-box_protein_pax2_(pax2)_gene_
u58331_762-1041,placental_delta_sarcoglycan_mrna,_complete_cds_
u63139_5305-5779,rad50_(rad50)_mrna,_complete_cds
x92110mrna_714-1242,mrna_for_hcgviil_protein_
z47553mrna_1761-2247,mrna_for_flavin-containing_monooxygenase(fmo5)_

Metagene 339

d42045_3927-4419,mrna_for_kiaa0086_gene,_complete_cds
all_m86933_669-
706,amelogenin_(amely)_mrna,_complete_cds,amelogenin_(amely)_mrna,_complete_cds
m96980_2034-2598,myelin_transcription_factor(mtf1)_mrna,_3'_end
all_x16282_710-1185,mrna_for_zinc_finger_protein_(clone_647)_
x89960cds_21-327:in_reversesequence,_458-
698,mrna_for_mitochondrial_capsule_selenoprotein

Metagene 340

l34838_40-586,early_placenta_insulin-
like_peptide_epil_(insl4)_mrna,_complete_cds_
all_u05255_159-
188,glycophorin_hep2_mrna,_partial_cds,glycophorin_hep2_mrna,_partial_cds
u31501_2359-
2773,fragile_x_mental_retardation_syndrome_related_protein_(fxr2)_mrna,_complet
e_cds_
u37689_344-752,rna_polymerase_ii_subunit_(hsrpb8)_mrna,_complete_cds_
x15943mrna_884-1220:in_reversesequence,_7046-7076,_huamn_calcitonin/alpha-
cgrp_gene

Metagene 341

u17033_5092-5578,180_kda_transmembrane_pla2_receptor_mrna,_complete_cds
u77949_2079-2622,cdc6-related_protein_(hscdc6)_mrna,_complete_cds

Metagene 342

j00139cds_68-506,dihydrofolate_reductase_gene
s76942_5-
311,_dopamine_d4_receptor_{exon_1}_[human,_brain_tumor_tissue,_mrna_partial_mut
ant,_386_nt]
u09477_2707-3175,clone_53bp1_p53-binding_protein_mrna,_partial_cds_
u56102_1973-2537,adhesion_molecule_dnam-1_mrna,_complete_cds_
all_x04706_1122-1295,homeobox_gene_(clone_hho.c13)_
x69398cds_898-927,mrna_for_oa3_antigenic_surface_determinant_
all_x83301_1254-1471,sma5_mrna.
x83705mrna_67-535,mrna_for_c-sis_proto-oncogene

Metagene 343

d25217_2864-3410,mrna_for_kiaa0027_gene,_partial_cds_
d45371mrna_4040-4464,apml_mrna_for_gs3109_(novel_adipose_specific_collagen-
like_factor),_complete_cd
d85815cds_282-564:in_reversesequence,_753-879,dna_for_rhohp1,_complete_cds
hg1205-ht1205_at_hg1205-ht1205_collagen,_type_iv,_alpha_2,_n-terminus
hg4157-ht4427_at_hg4157-ht4427_glycinamide_ribonucleotide_synthetase_
hg732-ht732_at_hg732-ht732_serum_amyloid_al
j03600_2058-2364,lipoxygenase_mrna,_complete_cds_
k01911mrna_85-481,neuropeptide_y_(npv)_mrna,_complete_cds
l05148_1890-2388,protein_tyrosine_kinase_related_mrna_sequence_
l05779_1535-2069,cytosolic_epoxide_hydrolase_mrna,_complete_cds
l10123_3572-4100,surfactant_protein_a_mrna,_complete_cds
l19297_602-1034,nuclear-
encoded_mitochondrial_carbonic_anhydrase_(ca5)_mrna,_complete_cds
l29277_2204-2762,dna-binding_protein_(aprf)_mrna,_complete_cds

138707mrna_2405-2951,diacylglycerol_kinase_(dagk)_mrna,_complete_cds.
 141668_887-1433,udp-galactoseepimerase_(gale)_gene,_complete_cds
 148516_473-1013,paraaxonase(pon3)_mrna,_3'_end_of_cds
 m13829_603-1029,putative_raf_related_protein_(pks/a-raf)_mrna,_partial_cds_
 m14565mrna_1262-1712,cholesterol_side-
 chain_cleavage_enzyme_p450scc_mrna,_complete_cds_
 m20777_434-956,_homo_sapiens,_alpha-2_(vi)_collagen_
 m29696_1063-1597,interleukin-7_receptor_(il-7)_mrna,_complete_cds
 m37271cds_361-672:in_reversesequence,_2722-2909,cd7_antigen_gene,_exons_4-jan_
 m54951mrna_438-852,atrial_natriuretic_factor_gene
 all_m59829_2774-3117,mhc_iii_hsp70-hom_gene_(hla),_complete_cds
 m60298_2117-
 2615,erythrocyte_membrane_protein_band_4.2_(epb42)_mrna,_complete_cds
 m68519mrna_1542-1916,pulmonary_surfactant-associated_protein_sp-
 a_(sftpl)_gene,_complete_cds
 m69197mrna#1_611-1184,_hpr_fromhaptoglobin_and_haptoglobin-
 related_protein_(hp_and_hpr)_genes,_compl
 m74091_925-1453,cyclin_mrna
 m80629_1678-2170,cdc2-related_protein_kinase_(ched)_mrna,_complete_cds_
 m89957_675-
 1095,immunoglobulin_superfamily_member_b_cell_receptor_complex_cell_surface_gly
 coprotein_
 m93405_888-1374,methylmalonate_semialdehyde_dehydrogenase_gene,_complete_cds_
 m93650_1119-1599,paired_box_gene_(pax6)_homologue,_complete_cds
 m99701_627-1137,(pp21)_mrna,_complete_cds_
 s69265_1402-1943,_neuron-specific_rna_recognition_motifs_(rrms)-
 containing_protein_[human,_hippocamp
 s75989_1492-1948,_gamma-
 aminobutyric_acid_transporter_type[human,_fetal_brain,_mrna,_1991_nt]
 s76475_2144-2659,_trkc_[human,_brain,_mrna,_2715_nt]
 u07358_2794-3310,protein_kinase_(zpk)_mrna,_complete_cds_
 u09877_3381-3849,helicase-like_protein_(hlp)_mrna,_complete_cds
 u10991_6267-6789,g2_protein_mrna,_partial_cds
 u16031_2451-2943,transcription_factor_il-4_stat_mrna,_complete_cds_
 u26398_2628-3168,inositol_polyphosphate_4-phosphatase_mrna,_complete_cds_
 u26403_991-1495,receptor_tyrosine_kinase_ligand_lerk-
 7_precursor_(eplg7)_mrna,_complete_cds
 u30930_1877-2423,udp-
 galactose_ceramide_galactosyl_transferase_(cgt)_mrna,_complete_cds
 u43431_3166-3712,dna_topoisomerase_iii_mrna,_complete_cds
 u52840_7503-7755,cri-du-chat_region_mrna,_clone_csa1_
 u64998cds_61-
 361,ribonuclease_k6_precursor_gene,_complete_cds/gb=u64998_/ntype=dna_/annot=cd
 s
 u82535_1485-2019,fatty_acid_amide_hydrolase_mrna,_complete_cds.
 all_v00565_2218-
 2422,gene_for_preproinsulin,_from_chromosomeincludes_a_highly_polymorphic_regio
 n_ups
 x04445mrna_521-1075,inha_gene_exon(and_joined_cds)_
 x06985mrna_943-1393,mrna_for_heme_oxygenase
 x07732mrna#2_991-1543,hepatoma_mrna_for_serine_protease_hepsin_
 all_x52773_1343-1866,mrna_for_retinoic_acid_receptor-like_protein
 x60188mrna_1360-1741,erk1_mrna_for_protein_serine/threonine_kinase_
 x60957cds_3066-3378:in_reversesequence,_3432-
 3678,tie_mrna_for_putative_receptor_tyrosine_kinase_
 x86779cds_1174-1606:in_reversesequence,_1741,mrna_for_fast_kinase_
 x99961cds_55-409,mrna_for_novel_protein/gb=x99961_/ntype=rna_

z26317cds_2904-3324:in_reversesequence,_3443-3491,mrna_for_desmoglein_2_

Metagene 344

m57293mrna#1_4-289,parathyroid_hormone-
related_peptide_(pthrp)_gene,_exons_1a,_1b,_1c,_and/gb=m57293
m85276exon#2-5_5-
92:in_reversesequence,_5295:not_in_gb_record,nkg5_gene,_complete_cds_
all_x69116_2-434,znf37a_gene_for_zinc_finger_protein_
z80345mrna_4931-5457,scad_gene,_5'_utr_exonand(and_joined_cds)

Metagene 345

d00632_1032-
1470,plasma_(extracellular)_mrna_for_glutathione_peroxidase,_complete_cds
d38145_1418-1952,mrna_for_prostacyclin_synthase,_complete_cds
s77812_148-
211,_flt=vascular_endothelial_growth_factor_receptor/vegf_receptor/cell_surface
tyrosine
u05861exon_50-243:not_in_gb_record,hepatic_dihydrodiol_dehydrogenase_gene_

Metagene 346

u45974_1007-1517,phosphatidylinositol_(4,5)_bisphosphate_5-
phosphatase_homolog_mrna,_partial_cds_
u79304_1102-1630,clone_23909_mrna,_partial_cds.
x05839mrna_2298-
2467,_transforming_growth_factor_betaprecursor_gene_extracted_fromtransforming_
growt

Metagene 347

d50840_1048-1474,mrna_for_ceramide_glucosyltransferase,_complete_cds_
hg3125-ht3301_s_at_hg3125-ht3301_estrogen_receptor_
140401mrna_572-992,(clone_zap128)_mrna,_3'_end_of_cds_
m14745_5435-5981,bcl-2_mrna
s68805_1972-2305,_l-
arginine:glycine_amidinotransferase_[human,_kidney_carcinoma_cells,_mrna,_2330_
n
u21931mrna_965-1373,fructose-1,6-biphosphatase_(fbp1)_gene_
u22376exon#20_757-1256,_c-myb_gene_extracted_from(c-
myb)_gene,_complete_primary_cds,_and_five_comple
u41060_2936-3416,breast_cancer,_estrogen_regulated_liv-1_protein_(liv-
1)_mrna,_partial_cds_
u67963_590-1148,lysophospholipase_homolog_(hu-k5)_mrna,_complete_cds_
u72661_650-1196,ninjurin1_mrna,_complete_cds.
u79293_1221-1749,clone_23948_mrna_sequence_
u82987_1140-1614,bcl-2_binding_component(bbc3)_mrna,_partial_cds

u96113_1463-2003,nedd-4-like_ubiquitin-
protein_ligase_wwp1_mrna,_partial_cds/gb=u96113_/ntype=rna_
all_x03635_5885-6402,mrna_for_oestrogen_receptor_
x55037mrna_863-1448,gata-3_mrna
x58072mrna_1793-2309,hgata3_mrna_for_trans-acting_t-
cell_specific_transcription_factor_
all_x83425_1831-2390,lu_gene_for_lutheran_blood_group_glycoprotein_

Metagene 348

ab005535_1056-1635,mrna_for_clock,_partial_cds/gb=ab005535_/ntype=rna_
ad000684cds#1_934-1252:in_reversesequence,_16809-17037,_lisch7_gene_(liver-
specific_bhlh-zip_transcr
d26068_2056-2398,mrna_for_kiaa0038_gene,_partial_cds_
d26362_2475-2985,mrna_for_kiaa0043_gene,_complete_cds
d26561cds#4_3-
237:in_reversesequence,_4010:not_in_gb_record,_orf_for_ll_protein_gene_extracte
d_fromp
d29013_664-1234,mrna_for_dna_polymerase_beta,_complete_cds_
d31886_3076-3592,mrna_for_kiaa0066_gene,_partial_cds_
d38293_2926-3400,mrna_for_clathrin-like_protein,_complete_cds
d44466_2575-3115,mrna_for_proteasome_subunit_p112,_complete_cds
d50525mrna_3316-3886,mrna_for_ti-227h/gb=d50525_/ntype=rna_
d63486_5877-6267,mrna_for_kiaa0152_gene,_complete_cds
d63881_3840-4278,mrna_for_kiaa0160_gene,_partial_cds_
d64154_786-1254,mrna_for_mr_110,000_antigen,_complete_cds
d78156cds_888-1140:in_reversesequence,_2058-
2292,mrna_for_rasgtpase_activating_protein,_partial_cds_
d80002_4430-4938,mrna_for_kiaa0180_gene,_partial_cds_
d82348_1479-1947,mrna_for_5-aminoimidazole-4-carboxamide-1-beta-d-
ribonucleoti_de_transformylase/ino
d85758_214-748,mrna_forprotein_homologous_to_droer_protein,_complete_cds
d86979_5308-5842,mrna_for_kiaa0226_gene,_complete_cds
d90084exon#10-8_36-
41,pyruvate_dehydrogenase_(ec_1.2.4.1)_alpha_subunit_gene,_exons_11-jan_
hg110-ht110_s_at_hg110-ht110_heterogeneous_nuclear_ribonucleoprotein_a/b_
hg1869-ht1904_at_hg1869-ht1904_male_enhanced_antigen_
hg2274-ht2370_at_hg2274-ht2370_rna_polymerase_ii,_14.5_kda_subunit_
hg662-ht662_at_hg662-ht662_epstein-barr_virus_small_rna-associated_protein_
j04611_1533-2061,lupus_p70_(ku)_autoantigen_protein_mrna,_complete_cds_
k03515mrna_1392-1938,neuroleukin_mrna,_complete_cds
l02426_1040-1556,26s_protease_(s4)_regulatory_subunit_mrna,_complete_cds_
l16896_1717-2257,zinc_finger_protein_mrna,_complete_cds
l20773_1025-1517,mrna_in_the_region_near_the_btk_gene_involved_in_a-gamma-
globulinemia
l25851_3332-3812,integrin_alpha_e_mrna,_complete_cds
l37127mrna_73-553,(clone_mf.18)_rna_polymerase_ii_mrna,_complete_cds
m24398mrna_522-970,parathymosin_mrna,_complete_cds_
m25077mrna_1310-1712:in_reversesequence,_1760-1826,ss-
a/ro_ribonucleoprotein_autoantigen_60_kd_subun
m58028mrna_2999-3401,ubiquitin-activating_enzyme_e1_(ubel)_mrna,_complete_cds
m84332exon#4_764-1226:in_reversesequence,_2337-2397,adp-ribosylation_factorgene
u12465_19-367,ribosomal_protein_l35_mrna,_complete_cds_
u21090_1109-1541,dna_polymerase_delta_small_subunit_mrna,_complete_cds_
u56418_785-1313,lysophosphatidic_acid_acyltransferase-beta_mrna,_complete_cds

u79716_11015-11537, reelin_(reln)_mrna, _complete_cds
 u81554_431-839, cam_kinase_ii_isoform_mrna, _complete_cds/gb=u81554_/ntype=rna_
 u86602_772-1240, nucleolar_protein_p40_mrna, _complete_cds_
 u90426_959-1439, nuclear_rna_helicase, _complete_cds_
 u90915_122-674, clone_23600_cytochrome_c_oxidase_subunit_iv_mrna, _complete_cds
 all_x14346_1969-2534, mrna_for_eosinophil_peroxidase
 x52851mrna_152-
 692, _peptidylprolyl_isomerase_gene_extracted_fromcyclophilin_gene_for_cyclophil
 in_(ec
 x58401mrna_356-900, 12-
 9_transcript_of_unrearranged_immunoglobulin_v(h)5_pseudogene.
 x59543mrna_2500-3016, mrna_for_m1_subunit_of_ribonucleotide_reductase_
 all_x60486_394-737, h4/g_gene_for_h4_histone
 all_x69141_1444-1997, mrna_for_squalene_synthase
 z21507cds_424-802:in_reversesequence, _901-955, ef-
 1delta_gene_encodingelongation_factor-1-delta_

Metagene 349

j02943mrna_869-1373, corticosteroid_binding_globulin_mrna, _complete_cds_
 m96789_1026-1548, connexin_37_(gja4)_mrna, _complete_cds
 z81326cds_913-1189:in_reversesequence, _1348-
 1486, mrna_for_protease_inhibitor(pi12;_neuroserpin).

Metagene 350

d14497_2222-2726, mrna_for_proto-oncogene_protein, _complete_cds_
 d64015_1126-1222, mrna_for_t-
 cluster_binding_protein, _complete_cds/gb=d64015_/ntype=rna
 100352exon_1952-2492, low_density_lipoprotein_receptor_gene_
 107493_193-631, replication_protein_a_14kda_subunit_(rpa)_mrna, _complete_cds_
 u20980_1596-2118, chromatin_assembly_factor-i_p60_subunit_mrna, _complete_cds
 u34962_1074-1560, transcription_factor_hcsx_(hcsx)_mrna, _complete_cds_
 u46571_1183-1687, tetratricopeptide_repeat_protein_(tpr2)_mrna, _complete_cds
 x56088mrna_2240-2794, mrna_for_cholesterol_7-alpha-hydroxylase

Metagene 351

d38503_915-
 1455, pms8_mrna_(yeast_mismatch_repair_gene_pms1_homologue), _partial_cds_(c-
 terminal_regio
 hg3313-ht3490_at_hg3313-ht3490_thyroid_hormone_receptor, _beta-2
 hg3996-ht4266_at_hg3996-ht4266_cpg-enriched_dna, _clone_s21_

Metagene 352

ac000115cds#1_546-684:in_reversesequence, _35138-
 35366, _wugsc:h_gs188p18.1a_gene_extracted_frombac_cl
 d31887_4050-4512, mrna_for_kiaa0062_gene, _partial_cds_

d79992_6597-6897,mrna_for_kiaa0170_gene,_complete_cds_
 d79994_4227-4749,mrna_for_kiaa0172_gene,_partial_cds_
 l06419_2544-3066,lysyl_hydroxylase_(plod)_mrna,_complete_cds_
 l13391exon#5_265-808,helix-loop-
 helix_basic_phosphoprotein_(g0s8)_gene,_complete_cds_
 l19493exon_1931-2064,fmr1_gene,_3'_end_
 m11313mrna_3966-4522,alpha-2-macroglobulin_mrna,_complete_cds_
 m86699_3355-3787,kinase_(ttk)_mrna,_complete_cds_
 s56151_672-1186,_hmfg=milk_fat_globule_protein_[human,_mrna_partial,_1270_nt]_
 s69231_1444-1981,_tyrp2=tyrosinase-related-protein-
 2_[human,_melanocytic_cell_line_sk-mel-19,_mrna,_
 u07919_2973-3399,aldehyde_dehydrogenasemrna,_complete_cds_
 u20391mrna#1_720-1080,folate_receptor_(folr1)_gene,_complete_cds_
 u26727_512-938,p16ink4/mts1_mrna,_complete_cds_
 u38847_4574-5000,tar_rna_loop_binding_protein_(trp-185)_mrna,_complete_cds_
 u58516_1860-1893,breast_epithelial_antigen_ba46_mrna,_complete_cds_
 u66075_2349-2793,transcription_factor_hgata-6_mrna,_complete_cds.
 u72621_2581-3145,lot1_mrna,_complete_cds_
 u78313_963-1515,myogenic_repressor_i-mf_(mdfi)_mrna,_complete_cds_
 u85193_1817-2399,nuclear_factor_i-b2_(nfib2)_mrna,_complete_cds_
 all_x16354_2895-
 3400,mrna_for_transmembrane_carcinoembryonic_antigen_bgpa_(formerly_tm1-cea)_
 all_x81420_1150-1601,mrna_for_hhkbl1_protein
 all_x87241_14353-14738,mrna_for_hfat_protein_
 all_y07909_2383-2774,mrna_for_progression_associated_protein_
 z75190cds_1747-2070:in_reversesequence,_2087-
 2276,mrna_for_apolipoprotein_e_receptor_2

Metagene 353

d14520_718-1258,mrna_for_gc-box_binding_protein_bteb2,_complete_cds_
 d90097cds_983-1499,amy2b_gene_for_alpha-amylase
 l33798_5571-6129,dihydropyridine-sensitive_l-type_calcium_channel_alpha-
 1_subunit_(cacn1a3)_mrna,_c
 m12959_1035-1486,t-cell_receptor_active_alpha-
 chain_mrna_from_jm_cell_line,_complete_cds_
 m16750_1699-2210,pim-1_oncogene_mrna,_complete_cds_
 m32334cds_461-737:in_reversesequence,_186-
 348,intercellular_adhesion_molecule(icam-2)_gene_
 m37766_475-955,mem-102_glycoprotein_mrna,_complete_cds_
 m81695_4051-4597,leukocyte_adhesion_glycoprotein_p150,95_mrna,_complete_cds_
 u48959_5397-5793,myosin_light_chain_kinase_(mlck)_mrna,_complete_cds_
 u82979_785-1371,immunoglobulin-like_transcript-3_mrna,_complete_cds_
 u91903_1323-1815,fritz_mrna,_complete_cds_
 all_x00437_966-1143,mrna_for_t-cell_specific_protein_
 x02910exon#4_604-1132,gene_for_tumor_necrosis_factor_(tnf-alpha)_
 all_x63629_2582-3126,mrna_for_p_cadherin_
 all_x74039_805-1058,mrna_for_urokinase_plasminogen_activator_receptor_
 all_x76383_376-821,mrna_for_he3(alpha)_
 z35278mrna_3328-3760,pebp2ac1_acute_myeloid_leukaemia_mrna_

Metagene 354

aj000480cds_116-650,mrna_for_c8fw_phosphoprotein/gb=aj000480_/ntype=rna_
 d2124lexon#2_2-72,_ovary-_and_prostate-specific_exonfromcytochrome_p-
 450_aromatase_gene,_multiple_ex
 d30742_1211-1697,mrna_for_calmodulin-dependent_protein_kinase_iv,_complete_cds_
 d80011_4259-4793,mrna_for_kiaa0189_gene,_complete_cds
 hg1980-ht2023_at_hg1980-ht2023_tubulin,_beta_2_
 hg2264-ht2360_at_hg2264-
 ht2360_atpase,_ca2+_transporting,_plasma_membrane_1,_altsplice_6_
 hg273-ht273_at_hg273-ht273_lymphocyte_antigen_hla-g3_
 hg3517-ht3711_at_hg3517-ht3711_alpha-1-antitrypsin,_5'_end_
 hg620-ht620_at_hg620-ht620_tyrosine_phosphatase,_epsilon_
 l05424_cds2_at_l05424_l05424,not_in_gb_record,_cd44_gene_(cell_surface_glycopro
 tein_cd44)_extracted_
 l10844_1646-2213,cellular_growth-regulating_protein_mrna,_complete_cds_
 l14848_802-1181,mhc_i-related_protein_mrna,_complete_cds_
 l28957_685-1231,ctp:phosphocholine_cytidyltransferase_mrna,_complete_cds
 all_m23178_2889-3818,homologue-
 1_of_gene_encoding_alpha_subunit_of_murine_cytokine_(mip1/sci),_compl
 m27436mrna_1638-
 1979,tissue_factor_gene,_complete_cds,_with_a_alu_repetitive_sequence_in_the_3'
 _untr
 m27819_3060-3426,anion_exchange_protein(ae1,_band_3)_mrna,_complete_cds_
 m33318mrna_1538-1583,cytochrome_p450iia3_(cyp2a3)_mrna,_complete_cds_
 m62324_1584-2052,modulator_recognition_factor_i_(mrf-1)_mrna,_3'_end_
 u30888_1892-2420,trna-guanine_transglycosylase_mrna,_complete_cds
 u40571_1695-2073,alpha1-syntrophin_(snt_a1)_mrna,_complete_cds_
 u82310_19-229,unknown_protein_mrna,_partial_cds/gb=u82310_/ntype=rna_
 u82818_1005-1058,ucp3s_mrna,_complete_cds/gb=u82818_/ntype=rna
 u84551_cds2_at_u84551_u84551,not_in_gb_record,dystrobrevin_(dtn)_gene_
 x03934cds_255-423:in_reversesequence,_3890-4112,t-
 cell_antigen_receptor_gene_t3-delta_
 all_x07619_658-1162,mrna_for_cytochrome_p450_db1_variant_b_
 x12458mrna_1566-2046,_p3_protein_(aa_1-1382)_gene_extracted_fromp3_gene_
 all_x13967_3247-3806,mrna_for_leukaemia_inhibitory_factor_(lif/hilda)
 x16901cds_411-711:in_reversesequence,_866-
 1094,mrna_for_rap30_subunit_of_transcription_initiation_fa
 x52599cds_295-649,mrna_for_beta_nerve_growth_factor
 x94563mrna#1_109-
 123,_exon_1b;_used_only_in_typetranscripts_fromdbi/acbp_gene_exon&/gb=x94563_/n
 type
 y10506mrna_251-593,mrna_for_cd110_protein/gb=y10506_/ntype=rna_
 y10615cds_115-535,cyrn2_gene/gb=y10615_/ntype=dna_/annot=cds_
 all_z46632_2953-3206,hspde4c1_gene_for_3'_5'_-
 cyclic_amp_phosphodiesterase,hspde4c1_gene_for_3'_5'

Metagene 355

all_x85750_1935-
 2500,mrna_for_transcript_associated_with_monocyte_to_macrophage_differentiation
 y09306cds_308-812,mrna_for_protein_kinase,_dyrk6,_partial/gb=y09306_/ntype=rna_

Metagene 356

d26156_4588-5166,mrna_for_transcriptional_activator_hsnf2b,_complete_cds_
 d86964_5449-5995,mrna_for_kiaa0209_gene,_partial_cds_
 hg3141-ht3317_f_at_hg3141-ht3317_nadh-ubiquinone_oxidoreductase,_39_kda_subunit
 k03494cds_557-
 1062:in_reversesequence,_115,green_cone_photoreceptor_pigment_gene_1
 l19437_857-
 l211,transaldolase_mrna_containing_transposable_element,_complete_cds_
 l24783_78-624,mrna_fragment/gb=l24783_/ntype=rna
 l28010_1292-1748,hnrnp_f_protein_mrna,_complete_cds_
 m80254_492-840,cyclophilin_isoform_(hcyp3)_mrna,_complete_cds
 m88108_2156-2636,p62_mrna,_complete_cds
 u19251_s_at_u19251_u19251,not_in_gb_record,neuronal_apoptosis_inhibitory_protei
 n_mrna,_complete_cds
 u24166_2107-2395,eb1_mrna,_complete_cds
 u33936_578-1050,adenosine_kinase_mrna,_complete_cds/gb=u33936_/ntype=rna_
 u51990_867-1269,hprp18_mrna,_complete_cds
 u60521_1398-1860,protease_promch6_(mch6)_mrna,_complete_cds
 u62389_31-409,putative_cytosolic_nadp-
 dependent_isocitrate_dehydrogenase_mrna,_partial_cds/gb=u62389
 u72511_440-596,b-cell_receptor_associated_protein_(hbap)_mrna,_partial_cds_
 x05196exon#9_2-458:in_reversesequence,_3199:not_in_gb_record,aldolase_c_gene_
 all_x12953_859-1130,rab2_mrna,_ypt1-related_and_member_of_ras_family_
 all_x17644_1976-2559,gst1-hs_mrna_for_gtp-binding_protein
 x57152mrna#1_536-962,gene_for_casein_kinase_ii_subunit_beta_(ec_2.7.1.37)_
 x78338mrna_5278-
 5824,_synthetic_adenovirus_transformedretina_cell_line,_mrp_mrna_
 all_x91247_3261-3700,mrna_for_thioredoxin_reductase
 x97065cds_1852-2260:in_reversesequence,_2389-
 2395,mrna_for_sec23b_isoform,_2450bp_
 x98411cds_2016-2256:in_reversesequence,_2340-2490,mrna_for_myosin-ie
 x99209_1549-2053,mrna_for_arginine_methyltransferase_
 all_z11695_2189-2736,40_kda_protein_kinase_related_to_rat_erk2_
 z29481cds_624-792:in_reversesequence,_898-1186,mrna_for_3-
 hydroxyanthranilic_acid_dioxygenase

Metagene 357

hg3432-ht3620_s_at_hg3432-ht3620_fibroblast_growth_factor_receptor_k-
 sam,_altsplice_3,_k-sam_iii_
 s79048_61-421,_lprp=phl_elf1_[human,_lacrimal_gland,_mrna_partial,_507_nt]
 u39657_2341-2863,map_kinase_kinase(mkk6)_mrna,_complete_cds_
 u97188_3602-4010,putative_rna_binding_protein_koc_(koc)_mrna,_complete_cds
 x66417cds_230-524:in_reversesequence,_658-766,cask_mrna_for_kappa-casein

Metagene 358

hg2841-ht2970_at_hg2841-ht2970_albumin,_altsplice_5
 u12259cds_492-808:in_reversesequence,_16275-
 16368,paired_box_homeotic_protein_(pax3)_gene
 all_y07701_3290-3651,mrna_for_aminopeptidase_

Metagene 359

d86975_5570-5978,mrna_for_kiaa0222_gene,_complete_cds
 105514cds_20-116:in_reversesequence,_1789-
 1815:not_in_gb_record,histatin(his2)_gene_
 all_x83857_1431-1809,mrna_for_prostaglandin_e_receptor_(ep3a1)_

Metagene 360

d28137_395-743,mrna_for_bst-2,_complete_cds
 j04164_366-804,interferon-inducible_protein_27-sep_mrna,_complete_cds
 l22342_672-810,nuclear_phosphoprotein_mrna,_complete_cds_
 m13755mrna_33-591,interferon-induced_17-kda/15-kda_protein_mrna,_complete_cds
 m31724mrna_2694-3168,phosphotyrosyl-protein_phosphatase_(ptp-
 1b)_mrna,_complete_cds
 m62505_1952-2240,c5a_anaphylatoxin_receptor_mrna,_complete_cds_
 u12255_905-1391,igg_fc_receptor_hfcrn_mrna,_complete_cds_
 u50648mrna_2211-2751,interferon-inducible_rna-
 dependent_protein_kinase_(pkr)_gene
 u72882_448-1009,interferon-
 induced_leucine_zipper_protein_(ifp35)_mrna,_partial_cds
 u95006_114-654,d9_splice_variant_a_mrna,_complete_cds
 x00371mrna_495-1011,myoglobin_gene_(exon_1)_(and_joined_cds)
 all_x02874_1063-1298,mrna_for_(2'-5')_oligo_a_synthetase_e_(1,6_kb_rna)
 all_x02875_158-628,mrna_(3'-fragment)_for_(2'-
 5')_oligo_a_synthetase_e_(1,8_kb_rna)_
 all_x57351_294-891,1-8d_gene_from_interferon-inducible_gene_family,1-
 8d_gene_from_interferon-inducib
 x79882cds_2116-2656:in_reversesequence,_2773,lrp_mrna_
 x85116_rnal_s_at_x85116_x85116,not_in_gb_record,epb72_gene_exon_1_

Metagene 361

m16364_749-1311,creatine_kinase-b_mrna,_complete_cds_
 m64554mrna_1602-
 1962,_f13a1_gene_(coagulation_factor_xiiib)_extracted_fromfactor_xiii_b_subunit
 _gene
 u07794_cds2_at_u07794_u07794,not_in_gb_record,tyrosine_kinase_(txk)_gene

Metagene 362

s74445_152-662,_cellular_retinoic_acid-
 binding_protein_[human,_skin,_mrna,_735_nt]
 u84487_2776-
 3238,cx3c_chemokine_precursor,_mrna,_alternatively_spliced,_complete_cds_
 x82554mrna_103-571,sphar_gene_for_cyclin-related_protein

Metagene 363

hg1496-ht1496_s_at_hg1496-ht1496_adrenal-specific_protein_pg2
 s73205_2183-
 2573, insulin_activator_factor_[human, pancreatic_insulinoma, mrna_partial, _262
 2_nt]/gb=
 u00930_2705-3191, clone_c4e_1.63_(cac)n/(gtg)n_repeat-containing_mrna_
 x59131_2735-
 3119: not_in_gb_record, d13s106_mrna_for_a_highly_charged_amino_acid_sequene

Metagene 364

131573_1849-2347, sulfite_oxidase_mrna, complete_cds
 m11973_cds1_at_m11973_m11973, not_in_gb_record, gamma-b-crystallin_gene_(gamma_1-
 2)_
 m29474mrna_5986-6490, recombination_activating_protein_(rag-
 1)_gene, complete_cds_
 u08471_492-780, folate_receptormrna, complete_cds
 u57352_2094-2646, sodium_channel(hbnac1)_mrna, complete_cds
 u76388_1630-1842, steroidogenic_factor_mrna, complete_cds_
 all_z22536_1732-2333, alk-4_mrna, complete_cds_

Metagene 365

ad001527cds#1_317-575: in_reversesequence, _3640-3802, _comment_for_location_3447-
 3655: blastx_gi|10329
 m31423cds_322-640: in_reversesequence, _1200-1320, cerebellar-degeneration-
 related_antigen_(cdr34)_gene
 u44060_2395-2845, homeodomain_protein_(prox_1)_mrna, complete_cds_
 u57093_501-969, small_gtp-binding_protein_rab27b_mrna, complete_cds_

Metagene 366

ad000092cds#7_730-1062: in_reversesequence, _99587-99822, _hypotheticalserine-
 threonine_protein_kinase_
 d50405_1628-2054, mrna_for_rpd3_protein, complete_cds_
 d50925_3408-3918, mrna_for_kiaa0135_gene, partial_cds_
 d87442_2204-2684, mrna_for_kiaa0253_gene, partial_cds_
 l04490_954-1362, (clone_cc6)_nadh-
 ubiquinone_oxidoreductase_subunit_mrna, _3'_end_cds_
 l37033_1039-1480, fk-506_binding_protein_homologue_(fkbp38)_mrna, complete_cds
 m92269cds_6175-6626: in_reversesequence, _6958-7053, l-
 type_calcium_channel_hfcc_mrna, complete_cds
 u94585_1810-2308, requiem_homolog_(hsreq)_mrna, complete_cds.
 all_x02596_4186-
 4733, mrna_for_bcr_(breakpoint_cluster_region)_gene_in_philadelphia_chromosome
 all_x69550_1266-1801, mrna_for_rho_gdp-dissociation_inhibitor_1_
 x80200_1428-1866, mln62_mrna
 all_x80497_3995-4428, phkla_mrna
 z21488cds_2749-3016: in_reversesequence, _3179-3326, contactin_mrna
 all_z48054_2544-3067, mrna_for_peroxisomal_targeting_signal(skl_type)_receptor_

Metagene 367

hg4236-ht4506_f_at_hg4236-ht4506_zinc_finger_protein_znf138
 132606_1862-2196,homeobox-like_mrna
 m61826exon_72-568,alpha-spectrin_gene
 u09279_1375-1777,type_xix_collagen_(col19a1)_mrna,_partial_cds_
 u38964cds_1096-1146:in_reversesequence,_1291-
 1359,pms2_related_(hpmsr2)_gene,_complete_cds_
 u79301_999-1509,clone_23842_mrna_sequence
 x00540_at_x00540_x00540,not_in_gb_record,gene_encoding_prolactin,_exonand_joine
 d_cds_
 all_x15088_1146-1276,gnat1_mrna_for_transducin_alpha-chain_

Metagene 368

d87447_5712-6258,mrna_for_kiaa0258_gene,_complete_cds
 all_j03589_2962-3443,ubiquitin-like_protein_(gdx)_gene,_complete_cds_
 l18960_679-1177,protein_synthesis_factor_(eif-4c)_mrna,_complete_cds_
 m60784mrna_595-950:in_reversesequence,_701-886,u1_snrnp-
 specific_protein_a_gene_
 m68864_598-1078,orf_mrna,_complete_cds_
 m74002_2243-2681,arginine-rich_nuclear_protein_mrna,_complete_cds_
 u09510_1878-2425,glycyl-trna_synthetase_mrna,_complete_cds_
 u12387_1468-1722,thiopurine_methyltransferase_(tpmt)_mrna,_complete_cds_
 u33821_1229-1661,tax1-binding_protein_txbp151_mrna,_complete_cds_
 u41163exon#9_36-266:in_reversesequence,_2625-
 2862:not_in_gb_record,creatine_transporter_(slc6a10)_ge
 u52111mrna#4_1182-
 1671,xq28_genomic_dna_in_the_region_of_the_ald_locus_containing_the_genes_for_c
 rea
 u59309_1200-
 1710,fumarase_precursor_(fh)_mrna,_nuclear_gene_encoding_mitochondrial_protein,
 _complete
 u90716_1825-2299,cell_surface_protein_hcar_mrna,_complete_cds
 all_x51521_2653-3026,mrna_for_ezrin
 x87237cds_2133-2487:in_reversesequence,_2661-2787,mrna_for_processing_a-
 glucosidase_i_
 all_x98296_7705-8096,mrna_for_ubiquitin_hydrolase
 z49099mrna_1011-1521,mrna_for_spermine_synthase

Metagene 369

d86966_4491-5031,mrna_for_kiaa0211_gene,_complete_cds
 d87074_6650-7184,mrna_for_kiaa0237_gene,_complete_cds
 hg1862-ht1897_at_hg1862-ht1897_calmodulin_type_i_
 hg825-ht825_at_hg825-ht825_guanine_nucleotide-binding_protein,_alpha_12
 108424_1124-1586,achaete_scute_homologous_protein_(ash1)_mrna,_complete_cds_
 l23116_3296-3644,galactocerebrosidase_(galc)_mrna,_complete_cds_
 m34715mrna_1750-2206,pregnancy-specific_beta-1-
 glycoprotein_mrna_psg95,_complete_cds_
 m57423_485-
 1016,phosphoribosylpyrophosphate_synthetase_subunit_iii_mrna,_3'_end.

m80359_2409-2835,protein_p78_mrna,_complete_cds
s69370_234-
761,_pax3b=transcription_factor_{alternatively_spliced}_[human,_adult_cerebellu
m,_mrna,_8
u25750_3002-3380,chromosome_17q21_mrna_clone_1046:1-1
u35139_1111-1507,necdin_related_protein_mrna,_complete_cds_
u39447_3452-3980,placenta_copper_monamine_oxidase_mrna,_complete_cds_
u42390_8359-8863,trio_mrna,_complete_cds
u82130_1151-1451,tumor_susceptibility_protein_(tsg101)_mrna,_complete_cds_
x53793cds_873-
1227,ade2h1_mrna_showing_homologies_to_saicar_synthetase_and_air_carboxylase_of
_the_pu
x54150mrna_978-1530,mrna_for_fc_receptor_
x63422cds_305-461:in_reversesequence,_688-916,mrna_for_delta-
subunit_of_mitochondrial_f1f0_atp-synth
all_x63546_7261-7856,mrna_for_tre_oncogene_(clone_210)_
all_z25535_4922-5463,mrna_for_nuclear_pore_complex_protein_hnup153_

Metagene 370

l20971_3698-3992,phosphodiesterase_mrna,_complete_cds
u03272_9619-10081,fibrillin-2_mrna,_complete_cds_
u07802exon#2_2748-3228,tis11d_gene,_complete_cds_
all_x78565_6971-7512,mrna_for_tenascin-c,_7560bp_

Metagene 371

d86096_cds6_at_d86096_d86096,not_in_gb_record,_ep3-
iv_gene_extracted_fromdna_for_prostaglandin_e_rec
s62907_1577-2136,_gamma-
aminobutyric_acida_receptor_alphasubunit_[human,_fetal_brain,_mrna,_2189_nt]
u33920_2564-2644,clone_lambdasemaphorin_mrna,_complete_cds
u87309_4315-4843,hvps41p_(hvps41)_mrna,_complete_cds_
u96114_2964-3390,nedd-4-like_ubiquitin-protein_ligase_wwp2_mrna,_complete_cds.
all_x82018_2942-3459,mrna_for_zid_protein

Metagene 372

ac002486cds_812-1358,bac_clone_rg367o17_from_7p15-
p21,_complete_sequence/gb=ac002486_/ntype=dna_/ann
af002700_931-1471,tgf-
beta_related_neurotrophic_factor_receptor(trnr2)_mrna,_complete_cds
d13168exon_2254-2800,gene_for_endothelin-b_receptor_(het-br)_
j00148cds#1_103-613:in_reversesequence,_1796-
1841,growth_hormone_(somatotropin,_gh1)_gene,_complete_
j04093_1842-2342,phenol_udp-glucuronosyltransferase_(udpgt)_mrna,_complete_cds
m22995_1008-1542,ras-related_protein_(krev-1)_mrna,_complete_cds_
u90336_2606-3074,peg3_mrna,_partial_cds
all_x69886_1163-1504,mrna_for_glycerol_kinase
x92814cds_194-458:in_reversesequence,_907-937,mrna_for_rat_hrev107-
like_protein_

z20656mrna_5438-5751,of_cardiac_alpha-myosin_heavy_chain_gene

Metagene 373

d26350_10043-10481,mrna_for_typeinositol_1,4,5-
triphosphate_receptor,_complete_cds_
hg4747-ht5195_at_hg4747-ht5195_nadh-ubiquinone_oxidoreductase,_51_kda_subunit
m22612_188-759,pancreatic_trypsin(try1)_mrna,_complete_cds
all_x74008_1842-2245,mrna_for_protein_phosphatasegamma

Metagene 374

ab000896_49-391,mrna_for_cadherin_fib2,_partial_cds/gb=ab000896/_ntype=rna
ac002115mrna#1_932-
1448,_cox6b_gene_(coxg)_extracted_fromdna_from_overlapping_chromosomecosmids_r3
13
d29641_2800-3292,mrna_for_kiaa0052_gene,_partial_cds_
d83699_623-
1001,brain_3'_utr_of_mrna_for_neuronal_death_protein,_partial_sequence
d86960_5652-6168,mrna_for_kiaa0205_gene,_complete_cds
hg2152-ht2222_at_hg2152-ht2222_zinc_finger_protein_92
hg3707-ht3922_f_at_hg3707-ht3922_guanine_nucleotide-
binding_protein,_alpha_inhibiting_activity_polyp
l13994_2830-3196,prec_gene,_complete_cds;orf_x,_complete_cds_
l22343_1136-1517,nuclear_phosphoprotein_mrna,_complete_cds_
l41607mrna_1772-2330,beta-1,6-n-acetylglucosaminyltransferase_(ignt)_gene
all_m11437_1562-2440:in_m11437cds#1_1198-
1226,_kng_gene_(kininogen)_extracted_fromkininogen_gene,_kn
m27533_883-1451,ig_rearranged_b7_protein_mrna_vc1-region,_complete_cds.
m61764mrna_1015-1495,gamma-tubulin_mrna,_complete_cds
m65085_1792-2302,follicle_stimulating_hormone_receptor_mrna,_complete_cds
m81778_2123-2689,serotonin_5-ht1c_receptor_mrna,_complete_cds
s66541cds_375-687:in_reversesequence,_99-314,_b-
50=neural_phosphoprotein_[human,_genomic,_1845_ntseg
u03911_2485-3013,mutator_gene_(hmsh2)_mrna,_complete_cds_
u22816_3784-4288,lar-interacting_protein_1b_mrna,_complete_cds_
u51095_1230-1656,homeobox_protein_cdx1_mrna,_complete_cds
u59748_28-187,desert_hedgehog_(hdhh)_mrna,_partial_cds/gb=u59748/_ntype=rna
u61538_199-751,calcium-binding_protein_chp_mrna,_complete_cds
u74324_1797-2349,guanine_nucleotide_exchange_factor_mss4_mrna,_complete_cds
u81787_1686-2238,wnt10b_mrna,_complete_cds.
u90437_43-259,rp1_homolog_mrna,_3'_utr_region/gb=u90437/_ntype=rna_
all_x04391_1779-2320,mrna_for_lymphocyte_glycoprotein_tl/leu-1_
x15673mrna_623-1121,ptr2_mrna_for_repetitive_sequence/gb=x15673/_ntype=rna_
all_x15949_1543-2144,mrna_for_interferon_regulatory_factor-2_(irf-2)_
x56667mrna_915-1341,mrna_for_calretinin
x78924cds_55-466:in_reversesequence,_622-631,hzfl_mrna_for_zinc_finger_protein
x97630_2420-2897,mrna_for_serine/threonine_protein_kinase_emk
all_x99657_783-1318,mrna_for_protein_containing_sh3_domain,_sh3gl2_

Metagene 375

m37981_1751-1829,alpha-
 3_neuronal_nicotinic_acetylcholine_receptor_subunit_mrna,_complete_cds
 m74290_1261-1741,substance_p_receptor_protein_mrna_
 m76729_6573-7077,pro-alpha-1(v)_collagen_mrna,_complete_cds_
 s46622_1569-
 2055,_calcineurin_a_catalytic_subunit_[human,_testis,_mrna,_2134_nt]
 u10473_333-895,clone_p4betagt/3_beta-1,4-
 galactosyltransferase_mrna,_partial_cds/gb=u10473_/ntype=rn
 u16720mrna_959-1508,interleukin(il10)_gene,_complete_cds
 u28015_1201-1351,cysteine_protease_(icer1-iii)_mrna,_complete_cds_
 u80184mrna_3661-4093,flil1_gene,_complete_cds_
 u89336exon#46-49_2-
 143:in_fullsequence,_26932:,_unknown_gene_extracted_fromhla_iii_region_containi
 ng
 x52221mrna_1674-2244,ercc2_gene,_exons&(partial)_
 x69090_4322-4880,mrna_for_skeletal_muscle_190kd_protein
 x76302exon#3_386-923,ry-1_mrna_for_putative_nucleic_acid_binding_protein_
 x91141mrna_2412-2904,mrna_for_rabaptin-5_protein_
 all_x91249_2428-2855,mrna_for_white_gene_protein_

Metagene 376

all_ac000061_18132-
 57268:in_ac000061cds#2_1270,_wugsc:h_133k23.1c_gene_extracted_frombac_clone_133
 k2
 ad000092_21426-21637:in_ad000092cds#1_3369-3688:in_all_ad000092_21396-
 21427,_hypotheticalserine-thre
 af002224_24-373,angelman_syndrome_gene,_e6-
 ap_ubiquitin_protein_ligase_3a_(ube3a)_mrna_from_promoter
 d21851_3680-4148,mrna_for_kiaa0028_gene,_partial_cds_
 hg3934-ht4204_at_hg3934-ht4204_g1_phase-specific_gene
 hg4272-ht4542_at_hg4272-ht4542_hepatocyte_growth_factor_receptor_
 hg4490-ht4876_f_at_hg4490-ht4876_proline-rich_protein_prb4,_allele_
 hg846-ht846_at_hg846-ht846_cyclophilin-related_protein_
 j03069mrna_2331-2907,mycl2_gene,_complete_cds_
 j03634_1563-1815,erythroid_differentiation_protein_mrna_(edf),_complete_cds
 j04101_861-1425,erythroblastosis_virus_oncogene_homolog(ets-
 1)_mrna,_complete_cds.
 102840mrna_3224-3602:in_reversesequence,_3674-
 3710,potassium_channel_kv2.1_mrna,_complete_cds
 107540_721-1159,replication_factor_36-kda_subunit_mrna,_complete_cds
 m21539_521-557,small_proline_rich_protein_(spril)_mrna,_clone_1292_
 m24248exon_201-220:not_in_gb_record,mlc-1v/sb_isoform_gene_
 m25296_82-649,natriuretic_peptide_precursor_mrna,_complete_cds_
 m37245cds_272-434:in_reversesequence,_113-353,ig_superfamily_cytotoxic_t-
 lymphocyte-associated_prote
 m60165mrna_571-1069,_hla-dqb1_gene_extracted_fromguanine_nucleotide-
 binding_regulatory_protein_(go-a
 all_m62628_1743-2182,alpha-1_ig_germline_c-region_membrane-
 coding_region,_3'_end_
 m87499cds_586-880:in_reversesequence,_2927-3041,uracil-
 dna_glycosylase_(ung)_gene,_complete_cds_
 m95740exon#12_279-381,alpha-1-iduronidase_gene_
 m99063_1942-2452,cytokeratinmrna,_complete_cds_

s70348_55-
 367, integrin_beta{alternatively_spliced, clone_beta_3c}_[human, erythroleukemia_cell_hel,
 u00951_1325-1691, clone_a9a2br11_(cac)n/(gtg)n_repeat-containing_mrna_
 u08377_2654-3134, homolog_of_drosophila_splicing_regulator_suppressor-of-white-apricot_mrna, complete
 u09550_1597-2149, oviductal_glycoprotein_mrna, complete_cds_
 u11870mrna_1901-2411, interleukin-
 8_receptor_type_a_(il8rba)_gene, promoter_and_complete_cds_
 u16261_1147-1657, mda-7_(mda-7)_mrna, complete_cds
 u18271exon#3_51-512, thymopoietin_(tmpo)_gene, thymopoietin_(tmpo)_gene
 u19495_1634-2204, intercrine-alpha_(hirh)_mrna, complete_cds
 u26914_3113-3533, ras-responsive_element_binding_protein_(rreb-1)_mrna, complete_cds
 u28150cds_281-
 839, adrenoleukodystrophy_related_protein_(haldr)_gene, partial_cds/gb=u28150_/n
 type=dn
 u36759_486-1016, pre-t_cell_receptor_alpha-type_chain_precursor, mrna, complete_cds_
 u39905_2148-2670, vesicular_monoamine_transporter_vmat1_mrna, complete_cds
 u54804_2444-2912, has2_mrna, complete_cds_
 u56976_1664-
 2240, calmodulin_dependent_phosphodiesterase_pde1b1_mrna, complete_cds
 u61166_2652-3150, sh3_domain-containing_protein_sh3p17_mrna, complete_cds_
 u64197_250-658, chemokine_exodus_mrna, complete_cds_
 u66559_4812-5244, anaplastic_lymphoma_kinase_receptor_mrna, complete_cds
 all_u66726_2378-
 2421, testis_specific_rna_binding_protein_(spgyla)_mrna, complete_cds, testis_specific
 u67733_3650-4178, cgmp-stimulated_3', 5'-
 cyclic_nucleotide_phosphodiesterase_pde2a3_(pde2a)_mrna, co
 x16260cds_2053-2485:in_reversesequence, 2508-2631, mrna_for_inter-alpha-trypsin_inhibitor_subunit_3
 all_x51801_1415-1824, op-1_mrna_for_osteogenic_protein
 x53683mrna_377-638, lag-1_mrna
 all_x56677_1103-1584, myod_mrna_
 x74614exon#2_17-377:in_reversesequence, 1279-
 1387:not_in_gb_record, odf2_(allele_2)_gene_for_outer_de
 x80590cds_653-1109, phkg1_mrna
 x82634_1048-1378, partial_mrna_for_hair_keratin_acidic_3-ii_
 y10256_2797-3247, mrna_for_serine/threonine_protein_kinase, _nik_
 y11710mrna_2222-
 2642, mrna_for_extracellular_matrix_protein_collagen_type_xiv, c-terminus
 z48519exon#3_11-223, xg_gene_(clone_race5)/gb=z48519_/ntype=rna_
 all_z50053_2518-3047, mrna_for_alpha2i-subunit_of_soluble_guanylyl_cyclase
 z50194cds_664-856:in_reversesequence, 1345-1372, mrna_for_pq-rich_protein
 all_z68193_17672-
 20477, dna_sequence_from_cosmid_qc8b6, on_chromosome_xq28, containing_red_opsin_gene
 z83745exon_49-367, dna_sequence_from_pac_453a3_contains_est_and_sts.

Metagene 377

d49488_640-1138, mrna_for_alpha-tocopherol_transfer_protein, complete_cds_

l34363cds_3540-3847:in_reversesequence, 4791-4896, x-linked_nuclear_protein_(xnp)_gene, _complete_cds_
 l39064mrna_3922-4348, interleukinreceptor_(il9r)_gene, _complete_cds_
 m20218exon_15-249: not_in_gb_record, coagulation_factor_xi_gene_
 m26665_267-484, histatin(his2)_mrna, _complete_cds, histatin(his2)_mrna, _complete_cds_
 m59499mrna#1_3549-3891, lipoprotein-associated_coagulation_inhibitor_(laci)_gene_
 m61176_1093-1549, brain-derived_neurotrophic_factor_(bdnf)_mrna, _complete_cds_
 u02632_2711-3047, calcium-activated_potassium_channel_mrna, _partial_cds_
 u27193_1872-2346, protein-tyrosine_phosphatase_mrna, _complete_cds_

Metagene 378

d87011cds_1308-1590:in_fullsequence, 24060-24222, (lamuda)_dna_for_immunoglobulin_light_chain_
 j04156mrna_1030-1510, interleukin(il-7)_mrna, _complete_cds_
 s95936_1806-2268, transferrin_[human, liver, _mrna, 2347_nt]_
 u24153_1796-1994, p21-activated_protein_kinase_(pak2)_gene, _complete_cds_

Metagene 379

d85425_758-1328, mrna_for_transactivator_hsm-1, _complete_cds_
 d86977_3721-4141, mrna_for_kiaa0224_gene, _complete_cds_
 all_d88422_230-483:in_d88422cds_13-188, dna_for_cystatin_a_
 hg2743-ht2845_at_hg2743-ht2845_caldesmon_1, _altsplice_3, _non-muscle_
 hg2743-ht2846_s_at_hg2743-ht2846_caldesmon_1, _altsplice_4, _non-muscle_
 hg4068-ht4338_at_hg4068-ht4338_phosphoprotein_tal2_
 l22524cds_462-734:in_reversesequence, 46-197, matrilysin_gene_
 all_m13792_34370-35897:in_m13792cds_995: not_in_gb_record, adenosine_deaminase_(ada)_gene, _complete_cds_
 m16038_1817-2255, lyn_mrna_encoding_a_tyrosine_kinase_
 m36284mrna_315-852, glycophorin_c_mrna, _complete_cds_
 all_m37485_1008-1230, igh@_gene_(ig_dxp_heavy-chain_gene)_extracted_from_ig_germline_h-chain_d-region_
 m77349_2102-2642, transforming_growth_factor-beta_induced_gene_product_(bigh3)_mrna, _complete_cds_
 all_m83216_3388-3584, aorta_caldesmon_mrna, _complete_cds_
 u03688_4501-5047, dioxin-inducible_cytochrome_p450_(cyp1b1)_mrna, _complete_cds_
 u04313_1983-2523, maspin_mrna, _complete_cds_
 u17077_1716-2190, bene_mrna, _partial_cds_
 u20240_448-898, c/ebp_gamma_mrna, _complete_cds_
 u27185_263-791, rar-responsive_(tig1)_mrna, _complete_cds_
 u31201mrna_4592-5106, laminin_gamma2_chain_gene_(lamc2), laminin_gamma2_chain_gene_(lamc2)_
 u75968_3641-4139, clone_c3_chl1_protein_(chlrl1)_mrna, _alternatively_spliced, _complete_cds_
 u90905_452-992, clone_23574_mrna_sequence_
 u90908_1268-1784, clones_23549_and_23762_mrna, _complete_cds_
 all_x04011_3678-4255, mrna_of_x-cgd_gene_involved_in_chronic_granulomatous_disease_located_on_chromos_
 x04470cds_24-374:in_reversesequence, 408-495, mrna_for_antileukoprotease_(alp)_from_cervix_uterus

all_x16662_1399-1916,mrna_for_vascular_anticoagulant-beta_(vac-beta)_
all_x56692_1122-1585,mrna_for_c-reactive_protein_
x95325mrna_783-1250,mrna_for_dna_binding_protein_a_variant_

Metagene 380

m27281_642-1116,vascular_permeability_factor_mrna,_complete_cds
m75110_814-1312,h,k-atpase_beta_subunit_mrna,_complete_cds_
m99487_2039-2555,prostate-specific_membrane_antigen_(psm)_mrna,_complete_cds_
u73704_1248-1764,48_kda_fkbp-associated_protein_fap48_mrna,_complete_cds

Metagene 381

af005361_1159-1663,importin_alphamrna,_complete_cds/gb=af005361/_ntype=rna_
hg3731-ht4001_r_at_hg3731-ht4001_immunoglobulin_heavy_chain,_vdjrc_regions_
l38616mrna_1184-1634,brain_and_reproductive_organ-
expressed_protein_(bre)_gene,_complete_cds
u46746_1183-1708,dystrobrevin-epsilon_mrna,_complete_cds_
all_u61500_6060-6577,gt334_protein_(gt334)_gene_mrna,_complete_cds_

Metagene 382

hg4458-ht4727_at_hg4458-ht4727_immunoglobulin_heavy_chain,_vdjc_regions
all_100058_470-855,(gh)_germline_c-myc_proto-oncogene,_5'_flank
u16258_1212-1776,i_kappa_br_mrna,_complete_cds_
all_x82629_1744-2297,mrna_for_mox-2
x97324cds_749-1277,mrna_for_adipophilin/gb=x97324/_ntype=rna_

Metagene 383

l11005_4386-4878,aldehyde_oxidase_(haox)_mrna,_complete_cds
u81262_2433-2877,lerk-5_(lerk-5)_mrna,_complete_cds
all_x89426_1465-1958,mrna_for_esm-1_protein

Metagene 384

x92689cds_1457-1853,mrna_for_udp-galnac:polypeptide_n-
acetylgalactosaminyl_transferase/gb=x92689/_nt

Metagene 385

m32402mrna_1851-2253,placental_protein_(pp11)_mrna,_complete_cds_
m93107_978-1278,heart_(r)-3-hydroxybutyrate_dehydrogenase_mrna,_3'_end

Metagene 386

ab000584_618-1032,mrna_for_tgf-beta_superfamily_protein,_complete_cds
 ab002366_5112-5616,mrna_for_kiaa0368_gene,_partial_cds/gb=ab002366_/ntype=rna
 ab004884_2491-2995,mrna_for_pku-alpha,_partial_cds/gb=ab004884_/ntype=rna
 d10995cds_828-1128:in_reversesequence,_1245-
 1401,gene_for_serotonin_1b_receptor,_complete_cds_
 d28588_2747-3263,mrna_for_kiaa0048_gene,_complete_cds
 d63813_1154-1676,mrna_for_rod_photoreceptor_protein,_complete_cds
 hg2730-ht2828_s_at_hg2730-
 ht2828_fibrinogen,_a_alpha_polypeptide,_altsplce_3,_e_
 j05428_1624-1800,3,4-catechol_estrogen_udp-
 glucuronosyltransferase_mrna,_complete_cds
 l27080cds_538-946:in_reversesequence,_1159-
 1207,melanocortinreceptor_(mc5r)_gene,_complete_cds_
 m34192mrna_1406-1826,isovaleryl-coa_dehydrogenase_(ivd)_mrna,_complete_cds_
 m37075_at_m37075_m37075,not_in_gb_record,embryonic/atrial_myosin_light_chain_(m
 lc-1-emb/a_isoform)_g
 m58285_3356-3788,membrane-associated_protein_(hem-1)_mrna,_complete_cds
 m93143_461-499,plasminogen-like_protein_(plgl)_mrna,_complete_cds
 m93415_1865-2303,activin_type_ii_receptor_mrna,_complete_cds_
 m97496_25-409,guanylin_mrna,_complete_cds_
 u03858_806-1040,flt3_ligand_mrna,_complete_cds_
 u09579_1537-2041,melanoma_differentiation_associated_(mda-6)_mrna,_complete_cds
 u10690exon#3_934-1499,mage-5b_antigen_(mage5b)_gene,_complete_cds
 u11863_1914-1974,clone_hp-
 dao2_diamine_oxidase,_copper/topa_quinone_containing_mrna,_complete_cds
 u15197_74-363,histo-blood_group_abo_protein_mrna,_partial_3'_utr_sequence
 u17838_7401-7899,zinc_finger_protein_riz_mrna,_complete_cds
 u55853_1917-2433,130_kd_golgi-
 localized_phosphoprotein_(gpp130)_mrna,_complete_cds
 all_x83127_1494-1624,mrna_for_voltage_gated_potassium_channels,_beta_subunit_
 x95654cds_2682-2862:in_reversesequence,_3022-3202,mrna_for_scpl_protein_
 all_x98253_1221-1334,znf183_gene/gb=x98253_/ntype=rna

Metagene 387

ab002409_293-791,mrna_for_slc,_complete_cds/gb=ab002409_/ntype=rna
 af009368_901-1345,luman_mrna,_complete_cds/gb=af009368_/ntype=rna_
 d11327_2099-2638,mrna_for_protein-tyrosine_phosphatase,_complete_cds_
 d16827cds_767-1064:in_reversesequence,_1124-
 1132,gene_for_fifth_somatostatin_receptor_subtype_
 d17461exon#1-3_13-102:not_in_gb_record,gulo_gene_for_l-gulono-gamma-
 lactone_oxidase,_exon_9,10_and/g
 d21089_2957-3515,mrna_for_xp-
 c_repair_complementing_protein_(p125),_complete_cds_
 d31891_3786-4275,mrna_for_kiaa0067_gene,_complete_cds
 d32002_2454-3001,mrna_for_nuclear_cap_binding_protein,_complete_cds
 d42053_3755-4277,mrna_for_kiaa0091_gene,_complete_cds
 d50312_1206-1668,mrna_for_ukatp-1,_complete_cds
 d63485_2710-3196,mrna_for_kiaa0151_gene,_complete_cds
 d85939_746-1037,mrna_for_p97_homologous_protein,_complete_cds
 d87012cds_1986-2226:in_fullsequence,_34522-
 34687,(lambda)_dna_for_immunoglobulin_light_chain

d87432_5731-6253,mrna_for_kiaa0245_gene,_complete_cds
 d90279_5154-5590,mrna_for_collagen_alpha_1(v)_chain,_complete_cds
 hg2442-ht2538_at_hg2442-
 ht2538_tropomyosin,_alpha,_muscle,_altsplice_2,_skeletal_muscle_(fibroblast)
 hg2686-ht2782_at_hg2686-ht2782_ryanodine_receptor_
 hg2992-ht5186_at_hg2992-ht5186_beta-
 hexosaminidase,_alpha_polypeptide,_abnormal_splice_mutation
 hg3175-ht3352_at_hg3175-ht3352_carcinoembryonic_antigen
 hg3254-ht3431_at_hg3254-ht3431_phosphatidylinositol_3-kinase_p110,_beta_isoform
 j00220_cds4_at_j00220_j00220,not_in_gb_record,ig_germline_h-chain_g-e-
 a_region_a:_gamma-3_5'_flank,i
 j02854_531-1089,20-kda_myosin_light_chain_(mlc-2)_mrna,_complete_cds_
 j03810_2627-3113,liver_glucose_transporter-like_protein_(glut2),_complete_cds
 all_k03430_414-853,complement_c1q_b-chain_gene_
 104751_1994-2510,cytochrome_p-450_4a_(cyp4a)_mrna,_complete_cds
 110378_1130-1640,(clone_ctg-b43a)_mrna_sequence
 110955cds#1_184-560:in_reversesequence,_394-
 467,_carbonic_anhydrase_iv_gene_extracted_fromcarbonic_a
 111369_756-
 1296,protocadherin_42_mrna,_3'_end_of_cds_for_alternative_splicing_pc42-8_
 all_111672_3552-
 3579,kruppel_related_zinc_finger_protein_(htf10)_mrna,_complete_cds,kruppel_rel
 ated_
 113329exon_434-938,iduronate-2-sulfatase_(ids)_gene_
 114565exon#9_5-359,peripherin_(prph)_gene_exons_1-9,_complete_cds
 115409_1227-1719,(clone_g7)_von_hippel-
 lindau_disease_tumor_suppressor_mrna_sequence
 120815_2031-2445,s_protein_mrna,_complete_cds
 129376_616-1126,(clone_3.8-1)_mhc_i_mrna_fragment_
 133930_1504-2054,cd24_signal_transducer_mrna,_complete_cds_and_3'_region
 142324cds_530-944,(clone_gpcr_w)_g_protein-
 linked_receptor_gene_(gpcr)_gene,_5'_end_of_cds/gb=142324
 142450mrna_1022-
 1448,pyruvate_dehydrogenase_kinase_isoenzyme_(pdk1)_mrna,_complete_cds
 147125mrna_1504-2055,(chromosome_x)_glypican_(gpc3)_mrna,_complete_cds
 148211cds_31-151:in_reversesequence,_1691-
 1775,angiotensin_ii_receptor_gene,_complete_cds
 149173cds_13-116,ocp2_gene,_partial_cds/gb=149173/_ntype=dna/_annot=cds
 m14539_3238-3730,factor_xiii_subunit_a_mrna,_3'_end
 m19507mrna#4_2620-3184,myeloperoxidase_mrna,_complete_cds
 m20778_401-974,_homo_sapien,_alpha-3_(vi)_collagen
 m20786exon_630-1146,alpha-2-plasmin_inhibitor_gene_
 all_m21494_152-645:in_m21494cds_888-
 967,muscle_creatine_kinase_gene_(ckmm),_5'_flank
 all_m22919_3226-3665,_mlc_gene_(non-
 muscle_myosin_light_chain)_extracted_fromnonmuscle/smooth_muscle
 m37755exon_15-256:in_reversesequence,_280-453:not_in_gb_record,pregnancy-
 specific_beta-1-glycoprotei
 m58583_989-1487,precerebellin_and_cerebellin_mrna,_complete_cds
 m64347_3336-3720,novel_growth_factor_receptor_mrna,_3'_cds_
 m74297_1161-1551,homeobox_1.4_protein_mrna,_complete_cds_
 m75106_1138-1618,prepro-plasma_carboxypeptidase_b_mrna,_complete_cds_
 m77810_2324-2585,transcription_factor_gata-2_(gata-2)_mrna,_complete_cds_
 m82827mrna_2078-2228,fusion_protein_mrna,_complete_cds.
 m91467_1375-1861,serotonin_receptor_(5ht1e)_mrna,_complete_cds_
 m95929_1015-1399,homeobox_protein_(phox1)_mrna,_3'_end_

s76638_2553-3003, _p50-nf-
 kappa_b_homolog_[human, _peripheral_blood_t_cells, _mrna, _3113_nt]
 s82240_274-
 802, _rho=26_kda_gtpase_homolog_[human, _hela_cell_line, _mrna, _833_nt]
 u03090_457-955, ca2+-dependent_phospholipase_a2_mrna, _complete_cds
 all_u04325_3581-3780, _psg11_gene_(pregnancy-specific_beta-1-glycoprotein_c-
 a_domain)_extracted_frompr
 u07969_2956-3259, intestinal_peptide-associated_transporter_hpt-
 1_mrna, _complete_cds
 u08438_exon#15_1106-1571, beta-adrenergic_receptor_kinase_(adrbk1)_gene
 u17034_4182-4584, soluble_pla2_receptor_mrna, _complete_cds
 u18550_exon_1402-1954, gpr3_g_protein-coupled_receptor_gene, _complete_cds
 u22961_2627-3194, mrna_clone_with_similarity_to_1-glycerol-3-
 phosphate:nad_oxidoreductase_and_albumin
 u24685_cds_123-336:in_reversesequence, _420-447, anti-
 b_cell_autoantibody_igm_heavy_chain_variable_v-d-
 u40152_2541-3103, origin_recognition_complex(hsorc1)_mrna, _complete_cds
 u55766_535-1081, rev_interacting_protein_rip-1_mrna, _complete_cds
 u64805_1668-2218, brca1-delta11b_(brca1)_mrna, _complete_cds/gb=u64805/_ntype=rna
 u65011_1625-
 2039, preferentially_expressed_antigen_of_melanoma_(prame)_mrna, _complete_cds.
 u69961_1565-1997, solurshin_(rgs)_mrna, _complete_cds
 u70136_4546-4957, megakaryocyte_stimulating_factor_mrna, _complete_cds
 u71598_444-792, zinc_finger_protein_zfp2_(zf2)_mrna, _partial_cds
 u88726_55-433, symplekin_mrna, _partial_cds/gb=u88726/_ntype=rna
 u90919_1637-2129, clones_23667_and_23775_zinc_finger_protein_mrna, _complete_cds
 all_x05276_1466-2031, mrna_for_fibroblast_tropomyosin_tm30_(pl)
 all_x05309_4846-5240, mrna_for_c3b/c4b_receptor_(cr1)_f_allotype
 x14046_cds_479-809:in_reversesequence, _944-1082, mrna_for_leukocyte_antigen_cd37
 all_x14362_1961-2370, cr1_mrna_for_c3b/c4b_receptor_secreted_form
 x14675_cds_31-163, bcr-abl_mrna_5'_fragment_(clone_3c)/gb=x14675/_ntype=rna
 x55448_exon#22_131-683, _g6pd_gene_(glucose-6-
 phosphate_dehydrogenase)_extracted_fromg6pd_gene_for_glu
 x61373_mrna#1_3441-3693:not_in_gb_record, microtubule-
 associated_protein_tau_(tau)_gene, _alternatively
 all_x62078_1997-2400, mrna_for_gm2_activator_protein
 x68264_mrna_3300-
 3552, _muc18_gene_(melanoma_associated_glycoprotein)_extracted_frommgf_gene_exon
 s_1&2
 x77567_cds_853-1215:in_reversesequence, _1354-1518, mrna_for_insp3_5-phosphatase_
 all_x77753_2390-2787, trop-2_gene_
 all_x83492_418-500, mrna_for_fas/apo-1_(clone_pcrtm11-
 fasdelta(4,7))/gb=x83492/_ntype=rna, mrna_for_fa
 x85740_mrna_1112-1604, mrna_for_c-c_chemokine_receptor-4_
 x87211_cds_486-1041, mrna_for_anion_exchange_protein/gb=x87211/_ntype=rna
 all_x90846_2935-
 3407, mrna_for_mixed_lineage_kinase_2, mrna_for_mixed_lineage_kinase_2
 x97303_mrna_11-93, mrna_for_ptg-12_protein/gb=x97303/_ntype=rna
 x98260_cds_1280-1706, mrna_for_m-phase_phosphoprotein, _mpp11_
 y08134_cds_1026-1362:in_reversesequence, _1531-1573, mrna_for_asm-
 like_phosphodiesterase_3b
 all_y08223_2471-2952, mfh-1_gene
 z11518_mrna_1546-2066, mrna_for_histidyl-trna_synthetase_
 z26256_exon_64-364, isoformgene_for_l-
 type_calcium_channel, _exon/gb=z26256/_ntype=dna/_annot=exon

Metagene 388

d38128exon_604-1126,ip_gene_for_prostacyclin_receptor
 d43638_2961-3393,mrna_for_mtg8a_protein,_complete_cds
 hg2167-ht2237_at_hg2167-ht2237_protein_kinase_ht31,_camp-dependent_
 hg2715-ht2811_at_hg2715-ht2811_tyrosine_kinase_
 hg3492-ht3686_at_hg3492-ht3686_uncoupling_protein_ucp
 l11373_4183-4609,protocadherin_43_mrna,_complete_cds_for_abbreviated_pc43
 l34409_624-990,(clone_b3b3e13)_chromosome_4p16.3_dna_fragment_
 l36645mrna_2716-3034,receptor_protein-
 tyrosine_kinase_(hek8)_mrna,_complete_cds_
 m16801mrna_5250-5724,mineralocorticoid_receptor_mrna_(hmr),_complete_cds_
 m60556mrna#1_503-839,_tgfb3_gene_(transforming_growth_factor-
 beta_3)_extracted_fromtransforming_grow
 m74096_1694-2096,long_chain_acyl-coa_dehydrogenase_(acadl)_mrna,_complete_cds
 m97676_1406-1646,(region_7)_homeobox_protein_(hox7)_mrna,_complete_cds
 s73840_408-
 784,_type_iix_myosin_heavy_chain_{3'_region}_[human,_skeletal_muscle,_mrna_part
 ial,_827_n
 s81661_588-1164,_keratinocyte_growth_factor_[human,_mrna,_1200_nt]
 u02683_2758-3318,alpha_palindromic_binding_protein_mrna,_complete_cds
 u08096exon_31-481,peripheral_myelin_protein-22_(pmp22)_gene,_non-
 coding_exon_1b/gb=u08096_/ntype=dna
 u37122_1877-2387,adducin_gamma_subunit_mrna,_complete_cds
 u44754_809-1253,pse-binding_factor_ptf_gamma_subunit_mrna,_complete_cds
 u69546_1903-2299,rna_binding_protein_etr-3_mrna,_complete_cds
 u79251_1285-1747,clone_23878_mrna_sequence_
 all_x04325_1113-1558,liver_mrna_for_gap_junction_protein_
 all_x59350_2679-3220,mrna_for_b_cell_membrane_protein_cd22_
 x67697cds_1-145:in_reversesequence,_63-603,he2_mrna_

Metagene 389

j05125_1038-1422,triglyceride_lipase_mrna,_complete_cds
 m68840_1558-1924,monoamine_oxidase_a_(maoa)_mrna,_complete_cds_
 u85707_1922-2426,leukemogenic_homolog_protein_(meis1)_mrna,_complete_cds_
 u90916_1309-1825,clone_23815_mrna_sequence_

Metagene 390

d88795_13-379,mrna_for_cadherin,_partial_cds/gb=d88795_/ntype=rna_
 d88797_49-379,mrna_for_cadherin,_partial_cds/gb=d88797_/ntype=rna_
 hg273-ht273_s_at_hg273-ht273_lymphocyte_antigen_hla-g3_
 hg3454-ht3647_at_hg3454-ht3647_zinc_finger_protein_
 hg644-ht644_at_hg644-ht644_histone_h1.1
 l35251mrna_801-1281,extracellular_matrix_protein_(mfap3)_gene,_complete_cds
 all_m11437_1562-
 2440,_kng_gene_(kininogen)_extracted_fromkininogen_gene,_kng_gene_(kininogen)_e
 xtrac
 u28727_7835-8357,pregnancy-associated_plasma_protein-
 a_preproform_(pappa)_mrna,_complete_cds_
 u43279_3409-3955,nucleoporin_nup_36_mrna,_complete_cds/gb=u43279_/ntype=rna

x05615cds_7824-8238:in_reversesequence,_8327-8423,mrna_for_thyroglobulin
 x51823cds_5-34,mrna_for_b-
 subunit_of_coagulation_factor_xiii_(fxiiib)_(partial)/gb=x51823_/ntype=rna
 x82279exon_54-169,fas,_apo-
 l_gene_(promoter_and_exon_i)/gb=x82279_/ntype=dna_/annot=exon_

Metagene 391

l76627mrna_5831-
 6329,metabotropic_glutamate_receptoralpha_(mglur1alpha)_mrna,_complete_cds_
 m55422_2463-2733,krueppel-related_zinc_finger_protein_(h-
 plk)_mrna,_complete_cds_
 all_m61855_1535-1714,cytochrome_p4502c9_(cyp2c9)_mrna,_clone_25
 all_x14968_1221-1636,testis_mrna_for_the_rii-
 alpha_subunit_of_camp_dependent_protein_kinase
 x61079mrna_10-211,mrna_for_t_cell_receptor,_clone_igra24.
 z16411cds_2917-3110:in_reversesequence,_3137-3441,mrna_encoding_phospholipase_c

Metagene 392

d49728_2002-2330,nak1_mrna_for_dna_binding_protein,_complete_cds_
 l10717_6303-6332,t_cell-specific_tyrosine_kinase_mrna,_complete_cds_
 l25119_1561-2119,mu_opiate_receptor_(mor1)_mrna,_complete_cds_
 m32304_423-983,metalloproteinase_inhibitor_mrna,_complete_cds_
 m84526_470-890,adipsin/complement_factor_d_mrna,_complete_cds_
 u44103_339-559,small_gtp_binding_protein_rab9_mrna,_complete_cds.
 u60319_2133-2643,hereditary_haemochromatosis_protein_hla-h_mrna,_complete_cds_
 u63825_269-
 737,hepatitis_delta_antigen_interacting_protein_a_(dipa)_mrna,_complete_cds_
 u77735_1516-2026,pim-2_protooncogene_homolog_pim-2h_mrna,_complete_cds_
 u90544_1665-2145,sodium_phosphate_transporter_(npt3)_mrna,_complete_cds_
 all_x76092_1925-2460,hrrfx3_mrna
 z22780cds_1528-1774:in_reversesequence,_1780-1870,cylicin_mrna_

Metagene 393

j03474cds_3-255,serum_amyloid_a_gene,_complete_cds_
 all_m63262_161-540:in_m63262cds_231-340,5-
 lipxygenase_activating_protein_(flap)_gene_
 all_x51441_55-90,mrna_for_serum_amyloid_a_(saa)_protein_partial,_clone_pas3-
 alpha,mrna_for_serum_amy
 x75042cds_1607-1817:in_reversesequence,_2024-2252,rel_proto-oncogene_mrna_

Metagene 394

d38537_1174-1689,mrna_for_protoporphyrinogen_oxidase,_complete_cds.
 d50692_31-469,mrna_for_c-myc_binding_protein,_complete_cds_
 d86062_286-862,mrna_for_knp-ib,_complete_cds_
 l07548_886-1390,aminoacylase-1_(acyl1)_mrna,_complete_cds_

148546exon#1-4_54-264: not_in_gb_record, tuberlin (tsc2)_gene_
 176517_2497-2977, (clone_cc44)_senilin(ps1;_s182)_mrna, complete_cds
 u79252_1026-1530, clone_23679_mrna, complete_cds
 u80040_2167-
 2647, nuclear_aconitase_mrna, encoding_mitochondrial_protein, complete_cds
 x12492cds_1087-1474: in_reversesequence, _1544-1718, mrna_for_caat-
 box_binding_transcription_factor_ctf
 x57398mrna_3503-4007, mrna_for_pm5_protein
 all_x59766_583-1166, mrna_for_zn-alpha2-glycoprotein
 all_x77794_1678-2171, mrna_for_cyclin_g1
 all_z31695_2159-2592, mrna_for_43_kda_inositol_polyphosphate_5-phosphatase

Metagene 395

hg881-ht881_at_hg881-ht881_mucin_6, _gastric
 100190mrna_912-1384, antithrombin_iii_(ataiii)_gene, _exonand_complete_cds
 m16973mrna_1406-1910, complement_protein_c8_beta_subunit_mrna, complete_cds_
 all_m21642_180-
 301, (dysfunctional)_antithrombin_iii_(atiii)_utah_gene, (dysfunctional)_antithro
 mbin_i
 m26682_721-1171, t-cell_translocation_gene(ttg-1)_mrna, complete_cds_
 m54992_924-1494, b_cell_differentiation_antigen_mrna, complete_cds
 m81883mrna_3226-3538, glutamate_decarboxylase_(gad67)_mrna, complete_cds
 m83712_1078-1646, nicotinic_receptor_alphasubunit_mrna, complete_cds.
 s75174_1316-1511, _e2f-
 4=transcription_factor_[human, nalm6_and_hela_cells, mrna, _1539_ntl]
 u16129_2108-2684, glutamate_receptor_(glur4)_mrna, complete_cds.
 u50360_81-385, calcium, _calmodulin-
 dependent_protein_kinase_ii_gamma_mrna, _partial_cds/gb=u50360/_nty
 u79248_1157-1553, clone_23826_mrna_sequence_
 x51698cds_39-343: in_reversesequence, _387-465, spasmolytic_polypeptide_(sp)_mrna
 all_x72925_3671-4008, mrna_for_desmocollin_type_1_
 x90828exon#2_233-752, mrna_for_transcription_factor, _lbx1_
 y11180mrna_31-247, mrna_for_twist_protein, _partial/gb=y11180/_ntype=rna_

Metagene 396

d14043_1834-2362, mrna_for_mgc-24, _complete_cds_
 d26067_2680-3166, mrna_for_kiaa0033_gene, _partial_cds_
 d29805_3485-3995, mrna_for_beta-1,4-galactosyltransferase, _complete_cds_
 d29963mrna_885-1443, sfa-
 1_(a_member_of_transmembranesuperfamily)_mrna, complete_cds_
 d30655_1263-1809, mrna_for_eukaryotic_initiation_factor_4a11
 d43636_3576-4080, mrna_for_kiaa0096_gene, _partial_cds_
 d50919_3864-4404, mrna_for_kiaa0129_gene, _complete_cds
 d50926_3626-4124, mrna_for_kiaa0136_gene, _partial_cds_
 d87446_5583-6135, mrna_for_kiaa0257_gene, _partial_cds_
 d87685_5584-5920, mrna_for_kiaa0244_gene, _partial_cds_
 j04058_767-1217, electron_transfer_flavoprotein_alpha-subunit_mrna, _complete_cds
 l14837_7335-7839, tight_junction_(zonula_occludens)_protein_zo-
 1_mrna, complete_cds_
 l19872_4756-5059, ah-receptor_mrna, complete_cds
 l40027mrna_1586-2132, glycogen_synthase_kinase_mrna, complete_cds

140392mrna_1818-2280,(clone_s164)_mrna,_3'_end_of_cds_
 148513mrna_941-1445,paraoxonase(pon2)_mrna,_complete_cds_
 m20867_2463-2986,glutamate_dehydrogenase_(gdh)_mrna,_complete_cds_
 m29204mrna#1_2236-2782,dna-binding_factor_mrna,_complete_cds_
 m31013mrna_4587-5091,nonmuscle_myosin_heavy_chain_(nmhc)_mrna,_3'_end
 m62831mrna_1210-1750,transcription_factor_etr101_mrna,_complete_cds_
 m65217_1840-2278,heat_shock_factor(hsf2)_mrna,_complete_cds_
 m77142_1629-2193,polyadenylate_binding_protein_(tia-1)_mrna,_complete_cds_
 m96954_806-1313,nucleolysin_tiar_mrna,_complete_cds_
 s72008_1731-2229,_hcdc10=cdc10_homolog_[human,_fetal_lung,_mrna,_2314_nt]_
 s80562_1042-1582,_acidic_calponin_[human,_kidney,_mrna,_1607_nt]
 u11313mrna_2104-2587,sterol_carrier_protein-x/sterol_carrier_protein-2_(scp-
 x/scp-2)_gene,_promoter_
 u14588_3012-3570,paxillin_mrna,_complete_cds_
 u23942_2811-3129,lanosterol_14-
 demethylase_cytochrome_p450_(cyp51)_mrna,_complete_cds_
 u31383_755-1151,g_protein_gamma-10_subunit_mrna,_complete_cds_
 u35113_2039-2555,metastasis-associated_mta1_mrna,_complete_cds_
 u43077_964-1510,cdc37_homolog_mrna,_complete_cds_
 u53209_968-1436,transformer-2_alpha_(htra-2_alpha)_mrna,_complete_cds_
 u61167_3488-4028,sh3_domain-containing_protein_sh3p18_mrna,_complete_cds_
 u79267_987-1437,clone_23840_mrna,_partial_cds_
 u90909_944-1412,clone_23722_mrna_sequence
 x04654cds_1467-1819:in_reversesequence,_2524-2634,mrna_for_u1_rna-
 associated_70k_protein_
 all_x72727_2460-2794,tunp_mrna_for_transformation_upregulated_nuclear_protein
 all_x76061_4282-4793,p130_mrna_for_130k_protein
 x80230mrna_1187-1697,mrna_(clone_c-2k)_mrna_for_serine/threonine_protein_kinase
 all_x87838_2803-3320,mrna_for_beta-catenin_
 all_x98172_2240-2754,mrna_for_mach-alpha-1_protein_
 all_z15115_2781-3346,top2_mrna_for_dna_topoisomerase_ii_(partial)
 all_z24725_2759-3210,mitogen_inducible_gene_mig-2,_complete_cds

Metagene 397

u91618_167-671,proneurotensin/proneuromedin_n_mrna,_complete_cds.
 x78121mrna_1730-1940:in_reversesequence,_1970-2036,mrna_for_choroideremia_
 y07828cds_345-675:in_reversesequence,_844-994,mrna_for_ring_protein_

Metagene 398

hg2507-ht2603_at_hg2507-ht2603_potassium_channel,_voltage-gated_kcnc1
 j03258mrna_4003-4561,vitamin_d_receptor_mrna,_complete_cds_
 k02268mrna_3155-3677,enkephalin_b_(enkb)_gene,_5'_flank_and
 105606_1219-1741,myosin_binding_protein_h_mrna,_complete_cds_
 l12392_9795-10257,huntington_disease_(hd)_mrna,_complete_cds_
 l15533mrna_236-764,pancreatitis-associated_protein_(pap)_gene,_complete_cds_
 l76380mrna_2459-2969,(clone_hsnme29)_cgrp_typerceptor_mrna,_complete_cds_
 all_m16424_135-664,beta-hexosaminidase_alpha_chain_(hexa)_gene_
 s78296_2596-3076,_neurofilament-66_[human,_fetal_brain,_mrna,_3197_nt]
 u57092_317-779,small_gtp-binding_protein_rab30_
 u76369_13-325,cationic_amino_acid_transporter-
 2b_(atrc2)_mrna,_partial_cds/gb=u76369_/ntype=rna

x52425mrna_3032-3536,il-4-r_mrna_for_the_interleukinreceptor

Metagene 399

d87328_5900-6404,mrna_for_hcs,_complete_cds
 j05096mrna_5006-5456,na,k-atpase_subunit_alpha(atp1a2)_gene,_complete_cds
 reverse_176568_31050-
 31356,_s26_fromexcision_and_cross_link_repair_protein_(ercc4)_gene,_complete_ge
 all_u67092_1093-1868:not_in_gb_record,ataxia-
 telangiectasia_locus_protein_(atm)_gene,_exons_1a,_1b,_
 all_x13227_1080-1567,mrna_for_d-amino_acid_oxidase_(ec_1.4.3.3)
 x59710cds_75-585:in_reversesequence,_714,mrna_for_caat-
 box_dna_binding_protein_subunit_b_(nf-yb)
 x64559cds_202-580:in_reversesequence,_679-823,mrna_for_tetranectin

Metagene 400

hg3085-ht3254_s_at_hg3085-ht3254_phosphodiesterase_
 all_m60748_1209-1615,histone_h1_(h1f4)_gene,_complete_cds
 m63623_2390-2900,oligodendrocyte-myelin_glycoprotein_(omgp)_mrna,_complete_cds_
 all_x74837_2811-3196,humm9_mrna
 all_x78578_3781-4268,ppplr3_mrna_for_protein_phosphatase_1,_glycogen-
 binding_regulatory_subunit

Metagene 401

d42055_5178-5718,mrna_for_kiaa0093_gene,_partial_cds_
 hg3740-ht4010_at_hg3740-ht4010_basic_transcription_factor_2,_34_kda_subunit
 l15702_1778-2279,complement_factor_b_mrna,_complete_cds
 l34673mrna_2853-3381,atpase,_dna-binding_protein_(hip116)_mrna,_3'_end_
 m11717mrna_2135-2393,heat_shock_protein_(hsp_70)_gene,_complete_cds_
 m93056_859-1273,monocyte/neutrophil_elastase_inhibitor_mrna_sequence
 u00957_1638-2136,clone_kdb1.2_(cac)n/(gtg)n_repeat-containing_mrna_
 u09759_1308-1830,protein_kinase_(jnk2)_mrna,_complete_cds
 u48736_1195-1693,serine/threonine-
 protein_kinase_prp4h_(prp4h)_mrna,_complete_cds
 v00533mrna_391-915,_ifna_gene_(interferon_alpha-
 h2)_extracted_fromgene_for_leukocyte_(alpha)_interfe
 x99920cds_6-198:in_reversesequence,_31-403,mrna_for_s100_calcium-
 binding_protein_al3

Metagene 402

d12686_4468-4909,mrna_for_eukaryotic_initiation_factorgamma_(eif-4_gamma)_
 d13636_3011-3539,mrna_for_kiaa0011_gene,_complete_cds
 d29958_446-962,mrna_for_kiaa0116_gene,_partial_cds_
 d42054_2354-2828,mrna_for_kiaa0092_gene,_complete_cds
 d82345_86-578,mrna_for_nb_thymosin_beta,_complete_cds
 d83783_6249-6579,mrna_for_kiaa0192_gene,_partial_cds_

hg1078-ht1078_at_hg1078-ht1078_lamin-like_protein
 hg1614-ht1614_at_hg1614-ht1614_protein_phosphatase_1_alpha_catalytic_subunit
 hg1733-ht1748_at_hg1733-ht1748_moloney_murine_sarcoma_viral_oncogene_homolog
 hg3432-ht3621_at_hg3432-ht3621_fibroblast_growth_factor_receptor_k-
 sam_altsplice_4_k-sam_iv
 hg4073-ht4343_at_hg4073-ht4343_cytosolic_acetoacetyl-coenzyme_a_thiolase_
 hg4155-ht4425_s_at_hg4155-ht4425_zinc_finger_protein_hzf8
 hg4542-ht4947_at_hg4542-ht4947_ribosomal_protein_l10_
 j05272_2311-2809,imp_dehydrogenase_typemrna_complete_cds
 k02574mrna_817-1363,purine_nucleoside_phosphorylase_(pnp)_mrna,_complete_cds_
 l07592_2760-3228,peroxisome_proliferator_activated_receptor_mrna,_complete_cds_
 l11285_957-1509,homosapiens_erk_activator_kinase_(mek2)_mrna_
 l26339_4094-4580,autoantigen_mrna,_complete_cds
 l35854mrna_3-75,dystrophin_(dp140)_mrna,_5'_end/gb=l35854_/ntype=rna_
 l38487mrna_1623-2115,estrogen_receptor-
 related_protein_(herral)_mrna,_3'_end,_partial_cds
 m13955mrna_904-1450,mesothelial_keratin_k7_(type_ii)_mrna,_3'_end
 m30938mrna#2_2781-3261,ku_(p70/p80)_subunit_mrna,_complete_cds_
 m33518exon_5570-5900:in_reversesequence,_6168-6198,hla-b-
 associated_transcript(bat2)_gene,_5'_flank
 m33764cds_1158-1350:in_reversesequence,_7989-
 8235,ornithine_decarboxylase_gene,_complete_cds
 m35198_2073-2589,integrin_b-6_mrna,_complete_cds_
 m80244_3401-3869,e16_mrna,_complete_cds
 m83651_1947-2451,beta-1,4_n-acetylgalactosaminyltransferase_mrna,_complete_cds_
 u09578_2012-2456,mapkap_kinase_(3pk)_mrna,_complete_cds
 u23143cds_1258-1426:in_reversesequence,_3604-
 3844,mitochondrial_serine_hydroxymethyltransferase_gene
 u33818_1889-2351,inducible_poly(a)-binding_protein_mrna,_complete_cds
 u50939_1224-1662,amyloid_precursor_protein-binding_proteinmrna,_complete_cds
 u68105mrna_2540-2765,poly(a)-binding_protein_(pabp)_gene,_promoter_region_and
 u78525_2480-
 2942,eukaryotic_translation_initiation_factor_(eif3)_mrna,_complete_cds
 u79254_693-1113,clone_23693_mrna_sequence
 u82613_163-685,dna-binding_protein_abp/zf_mrna,_complete_cds_
 all_x15414_844-1349,mrna_for_aldose_reductase_(ec_1.1.1.2)_
 x52882cds_1171-1639:in_reversesequence,_1672-1732,t-complex_polypeptidegene
 x60489mrna_381-915,mrna_for_elongation_factor-1-beta_
 all_x67698_228-709,tissue_specific_mrna
 all_x74570_1140-1711,mrna_for_gal-beta(1-3/1-4)glcnac_alpha-2.3-
 sialyltransferase
 z25749mrna_98-608,gene_for_ribosomal_protein_s7_
 z34918cds_1559-2051,mrna_for_translation_initiation_factor_eif-4gamma_(partial)

Metagene 403

d90276_757-1156,cgm7_gene_for_nonspecific_cross-reacting_antigen_(nca)_
 m92642_5127-5311,alpha-1_type_xvi_collagen_(col16a1)_mrna,_complete_cds_
 u68233_1565-2063,farnesol_receptor_hrr-1_(hrr-1)_mrna,_complete_cds
 u90911_1165-1549,clone_23652_mrna_sequence_
 x61070mrna_61-379,mrna_for_t_cell_receptor,_clone_igra15.
 all_x72012_2495-3060,end_mrna_for_endoglin_
 y12394_1326-1770,mrna_for_srp1-like_protein

Metagene 404

d87009cds#5_1325-1565:in_fullsequence,_35519-
 35735,_5'_oyl1.1_gene_extracted_from(lambda)_dna_for_im
 m68895mrna_858-1278,alcohol_dehydrogenasegene,_complete_cds
 x54489mrna_660-1034,gene_for_melanoma_growth_stimulatory_activity_(mgsa)
 all_x68242_408-889,mrna_for_hin-1

Metagene 405

ab000381exon#2-4_45-395:not_in_gb_record,dna_for_gpi-anchored_molecule-
 like_protein,_complete_cds_
 all_d16154_2725-2751:not_in_gb_record,gene_for_cytochrome_p-450c11,_exon_3-
 9/gb=d16154_/ntype=dna_/a
 j02982_23-439,glycophorin_b_mrna,_complete_cds_
 l10373_1311-1713,(clone_ccg-b7)_mrna_sequence
 l21893_1039-1537,na/taurocholate_cotransporting_polypeptide_mrna,_complete_cds_
 m13928mrna_542-1020,delta-aminolevulinate_dehydratase_mrna,_complete_cds.
 all_m29037_3259-3548,_humanbeta-
 hydroxysteroid_dehydrogenase_(17bhsdi)_gene,_exons_1-5,_complete_cds
 s78825_523-667,_id1_(id1-b)=transcription_regulator_helix-loop-
 helix_protein_{alternatively_spliced}
 u12424_2016-2564,mitochondrial_glycerol-3-
 phosphate_dehydrogenase_mrna,_complete_cds_
 u61276_4243-4777,transmembrane_protein_jagged(hj1)_mrna,_complete_cds_
 all_u83598_780-
 815,death_domain_receptorsoluble_form_(ddr3)_mrna,_partial_cds,death_domain_rec
 eptors
 v01510mrna_506-
 1022,_pomc_gene_(proopiomelanocortin)_extracted_fromgene_coding_for_acth_and_be
 ta-lph
 x92493mrna_2160-2672,mrna_for_stm-7_protein
 y10511mrna_16-343,mrna_for_cd176_protein/gb=y10511_/ntype=rna

Metagene 406

u06454_1832-2288,amp-activated_protein_kinase_(hampk)_mrna,_complete_cds_
 all_y00705_5-
 356,psti_mrna_for_pancreatic_secretory_inhibitor_(expressed_in_neoplastic_tissu
 e)

Metagene 407

d28539_4017-
 4549,mrna_for_metabotropic_glutamate_receptor_subtype_5b,_complete_cds_
 d83195cds_448-802:in_reversesequence,_3957-
 3963,dnase1_gene_for_deoxyribonuclease_i,_complete_cds_
 m21665mrna_1535-1621,beta-myosin_heavy_chain_mrna,_3'_end
 m32315_3202-3604,tumor_necrosis_factor_receptor_mrna,_complete_cds_
 z70295exon#2-3_7-252:not_in_gb_record,gcap-ii_gene

Metagene 408

d42039_3568-4074,mrna_for_kiaa0081_gene,_partial_cds_
 d55643_443-1019,spleen_pabl_(pseudoautosomal_boundary-
 like_sequence)_mrna,_clone_sp2/gb=d55643_/ntyp
 hg3993-ht4263_at_hg3993-ht4263_cpg-enriched_dna,_clone_s12_
 l02785_2412-2790,colon_mucosa-associated_(dra)_mrna,_complete_cds_
 m28826_976-1252,thymocyte_antigen_cd1b_mrna,_complete_cds

Metagene 409

d50683_5296-5680,mrna_for_tgf-beta1r_alpha,_complete_cds
 d59253_306-618,mrna_for_ncbp_interacting_protein_1,_complete_cds_
 d79990_5065-5383,mrna_for_kiaa0168_gene,_complete_cds
 d86961_3678-4188,mrna_for_kiaa0206_gene,_partial_cds_
 d87465_4793-5243,mrna_for_kiaa0275_gene,_complete_cds
 j04162mrna_1406-1940,leukocyte_igg_receptor_(fc-gamma-r)_mrna,_complete_cds
 m14636_2317-2665,liver_glycogen_phosphorylase_mrna,_complete_cds_
 m31153exon_34-232:in_reversesequence,_280-484:not_in_gb_record,steroid_17-
 alpha-hydroxylase_gene_
 m59465_3867-
 4341,tumor_necrosis_factor_alpha_inducible_protein_a20_mrna,_complete_cds
 m59964_816-1380,stem_cell_factor_mrna,_complete_cds
 m59979_2109-2511,prostaglandin_endoperoxide_synthase_mrna,_complete_cds
 m77016_2106-2622,tropomodulin_mrna,_complete_cds_
 s50223_197-773,_hkr-t1=kruppel-like_zinc_finger_protein_[human,_moltt-
 cells,_mrna,_798_nt]_
 s72869_2415-
 2955,_h4(d10s170)=putative_cytoskeletal_protein_[human,_thyroid,_mrna,_3011_nt]
 _
 u09284_693-1173,pinch_protein_mrna,_complete_cds_
 u11732_997-1531,ets-like_gene_(tel)_mrna,_complete_cds_
 u17760mrna_3684-4158,laminin_s_b3_chain_(lamb3)_gene
 u28014_1086-1233,cysteine_protease_(icerel-ii)_mrna,_complete_cds
 u32849_867-1383,hou_mrna,_complete_cds_
 u37359_1964-2414,mrel1_homolog_hmrel1_mrna,_complete_cds_
 u60800_3638-4010,semaphorin_(cd100)_mrna,_complete_cds_
 u63824_1129-1645,transcription_factor_rtef-1_(rtef1)_mrna,_complete_cds
 u68135_7-204,scs-
 slc_mrna_expressed_in_metastatic_and_relatively_radioresistant_squamous_cell_ca
 rcin
 u76638_1947-2505,brca1-
 associated_ring_domain_protein_(bard1)_mrna,_complete_cds_
 all_x07109_2732-3303,mrna_for_protein_kinase_c_(pkc)_type_beta_ii
 x54870mrna_1162-1702,mrna_for_nkg2-d_gene
 x65965exon#1-2_32-94,sod-
 2_gene_for_manganese_superoxide_dismutase/gb=x65965_/ntype=dna_/annot=exon
 all_x66079_925-1400,spi-b_mrna_
 all_x66533_1884-2365,soluble_guanylate_cyclase_small_subunit_mrna
 x69819cds_1122-1620:in_reversesequence,_1640-1700,icam-3_mrna_
 x99050mrna_3041-3461,_orf_gene_extracted_frommrna_for_63_kda_protein

z25521cds_526-884:in_reversesequence,_1068-
1179,integrin_associated_protein_mrna,_complete_cds,.

Metagene 410

d17547_2106-2262,mrna_for_dopachrome_tautomerase_(tyrosinase-related_protein-
2),_complete_cds
k02054mrna_238-676,gastrin-releasing_peptide_mrna,_complete_cds
l33404_464-890,stratum_corneum_chymotryptic_enzyme_mrna,_complete_cds
m64108_2031-2571,udulinmrna,_3'_end_
s83198_412-916,_bplp=basic_proline-
rich_protein_[human,_lacrimal_gland,_mrna,_947_nt]_
u60206_1537-2003,stress_responsive_serine/threonine_protein_kinase_krs-
1_mrna,_complete_cds
u73960_566-1022,adp-ribosylation_factor-like_proteinmrna,_complete_cds

Metagene 411

d17570_565-1083,mrna_for_zona-pellucida-binding_protein_(sp38),_complete_cds.
d49394_1619-2123,mrna_for_serotonin_5-ht3_receptor,_complete_cds_
hg2358-ht4858_s_at_hg2358-ht4858_proto-oncogene_ets-1,_altsplice_2_
l39833_2587-3097,(clone_hkvbeta3)_k+_channel_beta_subunit_mrna,_complete_cds
m13577mrna_1550-2096,myelin_basic_protein_(mbp)_mrna,_complete_cds_
m14113mrna_8440-8986,coagulation_factor_viii:c_mrna,_complete_cds
all_m33987_2226-2701,carbonic_anhydrase_i_(cai)_mrna,_complete_cds_
m35296_3284-3758,tyrosine_kinase_arg_gene_mrna_
m64934_1917-2397,kell_blood_group_protein_mrna_
all_s71129_3-426,_acetylcholinesterase_{i4-
e5_doman}_[human,_tumor_cell_lines,_genomic,_847_nt]_
s78234_2755-3259,_nuc2_homolog_[human,_fibroblasts,_mrna,_3320_nt]
u00238_3024-3552,glutamine_prpp_amidotransferase_(gpat)_mrna_complete_cds
u00943_1017-1203,clone_a9a2brb2_(cac)n/(gtg)n_repeat-containing_mrna_
u03397_787-1358,receptor_protein_4-lbb_mrna,_complete_cds
u15460_322-844,bzip_protein_b-atf_mrna,_complete_cds_
u27326_1666-
2123,alpha_(1,3/1,4)_fucosyltransferase_(fut3)_mrna,_major_transcript_i,_comple
te_cds
u31875_979-1399,hep27_protein_mrna,_complete_cds.
u40846_1964-2399,alpha-n-acetylglucosaminidase_(nag)_mrna,_complete_cds
u51477_2883-3444,diacylglycerol_kinase_zeta_mrna,_complete_cds_
u62317mrna#6_1634-
2156,_hypothetical_protein_384d8gene_extracted_from_chromosome_22q13_bac_clone_
cit
u71364_1097-1553,serine_proteinase_inhibitor_(p19)_mrna,_complete_cds
all_u73167_4971-
35099,_h_luca14.2a_gene_extracted_fromcosmid_luca14,_h_luca14.2a_gene_extracted
_from
u79274_883-1381,clone_23733_mrna,_complete_cds.
v00574cds_225-538:in_reversesequence,_3330-
3468,germ_line_gene_homologous_to_bladder_carcinoma_oncog
all_x17622_3693-4210,hbk2_mrna_for_potassium_channel_protein_
x51688mrna_1054-1438,mrna_for_cyclin_a_
all_x62515_13260-13708,mrna_for_basement_membrane_heparan_sulfate_proteoglycan_

x70040cds_3944-4130:in_reversesequence, 4236-4470, ron_mrna_for_tyrosine_kinase_
x85781exon_2-551, nos2_gene, _exon_27_/gb=x85781_/ntype=dna_/annot=exon
y10055cds_2802-3096:in_reversesequence, 3310-3532, mrna_for_phosphoinositide_3-
kinase_

Metagene 412

d87462_3013-3403, mrna_for_kiaa0272_gene, _partial_cds_
d89858_671-1157, mrna_for_d-aspartate_oxidase, _complete_cds_
m10050mrna_25-424, liver_fatty_acid_binding_protein_(fabp)_mrna, _complete_cds_
u63717_402-852, osteoclast_stimulating_factor_mrna, _complete_cds

Metagene 413

all_u03877_2037-2512, extracellular_protein_(s1-5)_mrna, _complete_cds_

Metagene 414

d86640_2374-2902, mrna_for_stac, _complete_cds_
hg2157-ht2227_at_hg2157-ht2227_mucin_4, _tracheobronchial_
j03507_3421-3865, complement_protein_component_c7_mrna, _complete_cds_
all_l15296_3031-3082, clone_hrcnc2b_retinal_rod_cyclic_nucleotide-
gated_cation_channel_gene, _complete
l41390exon#1_244-395, corebeta-1, 6-n-
acetylglucosaminyltransferase_(coregnt)_gene, _exon/gb=l41390_/nt
m59820mrna_2435-2975, granulocyte_colony-
stimulating_factor_receptor_(csf3r)_mrna, _complete_cds_
m77481mrna_1021-1566, antigen_(mage-1)_gene, _complete_cds_
m82962mrna_2313-2835, n-benzoyl-l-tyrosyl-p-amino-
benzoic_acid_hydrolase_alpha_subunit_(pph_alpha)_mr
m87284_2479-2923, 69_kda_2'5'_oligoadenylate_synthetase_(p69_2-
5a_synthetase)_mrna, _complete_cds_
u05291_1363-1849, fibromodulin_mrna, _partial_cds
u29589exon_2948-
3488, m3_muscarinic_acetylcholine_receptor_(chrm3)_gene, _complete_cds_
u43672_2939-3443, putative_transmembrane_receptor_il-1rrp_mrna, _complete_cds_
u71601_960-1422, zinc_finger_protein_zfp47_(zf47)_mrna, _partial_cds_
x06482cds_60-405:in_reversesequence, 884-887, theta_1-globin_gene
all_x14975_7566-8337, cd1_r2_gene_for_mhc-related_antigen_
x55989mrna_169-354, ecrp_gene_for_eosinophil_cationic_related_protein
y10512mrna_14-452, mrna_for_cd282_protein/gb=y10512_/ntype=rna

Metagene 415

d83657exon#1-3_13-
167:in_reversesequence, 2025:not_in_gb_record, dna_for_caaf1_(calcium-
binding_prote
hg4740-ht5187_at_hg4740-ht5187_transcription_factor_eb_

m64925_1400-
 1940, palmitoylated_erythrocyte_membrane_protein_(mpp1)_mrna,_complete_cds
 u18088_1188-1742, 3', 5' -
 cyclic_amp_phosphodiesterase_inactive_splice_variant_hspde4a8a_mrna,_comple
 u22377_5634-6168, zn-15_related_zinc_finger_protein_(rlf)_mrna,_complete_cds
 u41766_3235-3653, metalloprotease/disintegrin/cysteine-
 rich_protein_precursor_(mdc9)_mrna,_complete_c
 u43185_3667-
 4243, signal_transducer_and_activator_of_transcription_stat5a_mrna,_complete_cds
 u53476_841-1351, proto-oncogene_wnt7a_mrna,_complete_cds
 v00536_mrna_811-1135, ifng_gene_extracted_fromimmune_interferon_(ifn-
 gamma)_gene_
 y00282_cds_1657-1849:in_reversesequence, 2341-2383, mrna_for_ribophorin_ii

Metagene 416

all_m16404_1576-2153, m2_muscarinic_acetylcholine_receptor_gene_
 m73746_2409-
 2894, lutropin/choriogonadotropin_receptor_(lhcg_r)_mrna,_complete_cds

Metagene 417

hg3299-ht3476_at_hg3299-ht3476_acetyl-coenzyme_a_carboxylase_
 u79265_1269-1623, clone_23614_mrna_sequence_
 x12901_cds_2080-2431:in_reversesequence, 2551-2629, mrna_for_villin_

Metagene 418

hg458-ht458_f_at_hg458-ht458_beta-1-glycoprotein_1,_pregnancy-specific_
 m22324_2954-
 3416, aminopeptidase_n/cd13_mrna_encoding_aminopeptidase_n,_complete_cds
 u04343_815-1361, cd86_antigen_mrna,_complete_cds
 u20760_4534-4966, extracellular_calcium-sensing_receptor_mrna,_complete_cds_
 u67849_25-187, beta-galactoside_alpha2,6-
 sialyltransferase_(sialt1)_mrna,_exon_w/gb=u67849/_ntype=rna
 x59372_mrna_610-1090, hox4c_mrna_for_a_homeobox_protein
 x65614_cds_10-262:in_reversesequence, 19-391, mrna_for_calcium-
 binding_protein_s100p_
 x81892_cds_2760-2994:in_reversesequence, 3126-3204, mrna_for_he6_tm7_receptor_
 all_x95525_2560-3071, mrna_for_tafii100_protein_

Metagene 419

d13264_1681-
 2167, mrna_for_macrophage_scavenger_receptor_type_i,_3'_untranslated_region_
 d38122_1307-1829, mrna_for_fas_ligand,_complete_cds_
 hg1686-ht4572_s_at_hg1686-
 ht4572_transcription_factor_e4tfl1_respiratory_gamma_subunit,_altsplice_4_
 u25029_1010-1556, glucocorticoid_receptor_alpha_mrna,_variant_3'_utr

u34844exon_40-259,mercurial-insensitive_water-
channel_gene,_5'_region_and_partial_exon/gb=u34844_/nt
u52191_4854-5396,smcy_(h-y)_mrna,_complete_cds_

Metagene 420

d14838_915-1317,mrna_for_fgf-9,_complete_cds_
d38548_4682-5210,mrna_for_kiaa0076_gene,_complete_cds
d63851_3157-3643,mrna_for_unc-18_homologue,_complete_cds_
d87073_5307-5847,mrna_for_kiaa0236_gene,_complete_cds
hg1728-ht1734_s_at_hg1728-ht1734_non-
specific_cross_reacting_antigen,_altsplice_form_2_
m28827_620-1112,thymocyte_antigen_cd1c_mrna,_complete_cds
m92449_668-1190,ltr_mrna,_3'_end_of_coding_region_and_3'_flank_
u02388_2097-2337,cytochrome_p450_4f2_(cyp4f2)_mrna,_complete_cds_
u59632_2578-
3138,h5_mrna,_partial_cds,_and_platelet_glycoprotein_ib_beta_chain_mrna,_comple
te_cds
u72517_413-
953,alternatively_spliced_variant_c7f_(c3f)_mrna,_partial_3'_utr/gb=u72517_/nty
pe=rna_

Metagene 421

hg3255-ht3432_at_hg3255-ht3432_gamma-
aminobutyric_acid_(gaba)_a_receptor_betasubunit
hg4108-ht4378_at_hg4108-ht4378_olfactory_receptor_or17-24
m22490_1282-1630,bone_morphogenetic_protein-2b_(bmp-2b)_mrna_
m95925_1366-1852,leucine_zipper_on_the_d14s46e_locus_mrna,_complete_cds
u27333_2523-
2728,alpha_(1,3)_fucosyltransferase_(fut6)_mrna,_major_transcript_i,_complete_c
ds,alpha_
u35735_2115-2442,rach1_(rach1)_mrna,_complete_cds
u44799_299-860,u1-snrnp_binding_protein_homolog_mrna,_complete_cds_

Metagene 422

d14678_1244-1748,mrna_for_kinesin-related_protein,_partial_cds_
d31833_1212-1768,mrna_for_vasopressin_v1b_receptor,_complete_cds_
d86043_1741-1829,mrna_for_shps-1,_complete_cds_
l03427_4325-4844,zinc_finger_protein_basonuclin_mrna,_complete_cds_
l15344_1360-1768,high_molecular_weight_b_cell_growth_factor_mrna_sequence
m85165_1311-1809,srf_accessory_protein_1a_(sap-1)_mrna,_complete_cds
m95936_1148-1466,protein-serine/threonine_(akt2)_mrna,_complete_cds
s78271_4580-5111,_sb1.8/dxs423e=mitosis-
specific_chromosome_segregation_protein_smc1_homolog_[human,
u03905_1438-1858,monocyte_chemoattractant_proteinreceptor_(mcp-
1rb)_alternatively_spliced_mrna,_comp
u09002_5527-6082,n-methyl-d-
aspartate_receptor_modulatory_subunit_2a_(hnr2a)_mrna,_complete_cds
u13395_994-1450,oxidoreductase_(hhcma56)_mrna,_complete_cds

u28281_1162-1618,secretin_receptor_mrna,_complete_cds_
u50531_4295-4847,brca2_region,_mrna_sequence_cg030_
u66618_1518-2016,swi/snf_complex_60_kda_subunit_(baf60b)_mrna,_complete_cds_
u85767_13-505,myeloid_progenitor_inhibitory_factor-1_mpif-1_mrna,_complete_cds_
x14767mrna_1685-1832,mrna_for_gaba-a_receptor,_betasubunit

Metagene 423

d38549_3838-4336,mrna_for_kiaa0068_gene,_partial_cds_
d63877_2386-2908,mrna_for_kiaa0241_gene,_partial_cds_
d86967_5483-5873,mrna_for_kiaa0212_gene,_complete_cds_
hg4063-ht4333_s_at_hg4063-ht4333_transcription_factor_hbf-2
j03171_2250-2700,interferon-alpha_receptor_(huifn-alpha-rec)_mrna,_complete_cds_
j04760mrna_233-791,slow-twitch_skeletal_troponin_i_(tnn1)_mrna,_complete_cds_
l07956_2402-2930,1,4-alpha-glucan_branching_enzyme_(hgbe)_mrna,_complete_cds_
l35546mrna_1027-1543,gamma-
glutamylcysteine_synthetase_light_subunit_mrna,_complete_cds_
m35128cds_1044-1320:in_reversesequence,_1936-
2038,muscarinic_acetylcholine_receptor_gene,_complete_c
m63582mrna_1062-1518,preprothyrotropin-releasing_hormone_gene
u05321mrna_3734-4220,x-linked_pest-
containing_transporter_(xpct)_gene,_promoter_and
x13794mrna_713-
1229,lactate_dehydrogenase_b_gene_exonand(ec_1.1.1.27)_(and_joined_cds)
x82224cds_733-1165:in_reversesequence,_1273-
1303,mrna_for_glutamine_transaminase_k

Metagene 424

hg311-ht311_at_hg311-ht311_ribosomal_protein_l30_
m26167mrna_385-730,platelet_factorvariation(pf4var1)_gene,_complete_cds_
m28219_7-
253,low_density_lipoprotein_receptor_(fhmutant_causing_familial_hypercholesterolemia)_mrna,
m57892mrna_775-1267,carbonic_anhydrase_isozyme_vi_(ca6)_mrna,_complete_cds_
u09303_2354-2870,t_cell_leukemia_lerk-2_(eplg2)_mrna,_complete_cds_
v00594mrna_15-316,mrna_for_metallothionein_from_cadmium-treated_cells,mrna_for_metallothionein_from_
x59871mrna_2672-2836,tcf-1_mrna_for_t_cell_factor(splice_form_c)
z47556mrna#2_1596-
1866,_semenogelin_ii_gene_extracted_fromgenes_for_semenogelin_i_and_semenogelin_ii

Metagene 425

ab000410mrna_947-1442,hogg1_mrna,_complete_cds_
d13118_61-
523:in_reversesequence,_529,mrna_for_atp_synthase_subunit_c_encoded_by_p1_gene
d16611_1726-2299,mrna_for_coproporphyrinogen_oxidase,_complete_cds_
d85418_875-1403,mrna_for_phosphatidylinositol-glycan-class_c_(pig-c),_complete_cds_

d86519_1368-1932,mrna_for_neuropeptide_y/peptide_yy_y6_receptor,_complete_cds
 d87845_1946-2216,mrna_for_platelet-
 activating_factor_acetylhydrolase_2,_complete_cds_
 hg3491-ht3685_at_hg3491-ht3685_zinc_finger_protein_zfp-36
 j03925_4110-4656,mac-
 1_gene_encoding_complement_receptor_type_3,_cd11b,_complete_cds_
 j04970_1397-1715,carboxypeptidase_m,_3'_end
 l14595_1801-
 2077,alanine/serine/cysteine/threonine_transporter_(asct1)_mrna,_complete_cds
 l34657mrna_2757-3219,platelet/endothelial_cell_adhesion_molecule-1_(pecam-
 1)_gene_
 m28212_175-691,gtp-binding_protein_(rab6)_mrna,_complete_cds
 m55543mrna_1356-1872,guanylate_binding_protein_isoform_ii_(gbp-
 2)_mrna,_complete_cds_
 m55683_2732-3242,cartilage_matrix_protein_(cmp)_mrna,_exons_8-mar
 m62424_2868-3117,thrombin_receptor_mrna,_complete_cds
 m63154_977-1541,intrinsic_factor_mrna,_complete_cds
 m95809_1310-1850,basic_transcription_factor_62kd_subunit_(btf2),_complete_cds
 s83249_19-349,_ng-
 tra=transporter_protein/putative_hormone_extrusion_pump_[human,_liver_and_vario
 us_
 u03270_626-1136,centrin_mrna,_complete_cds_
 u20938_3946-4348,lymphocyte_dihydropyrimidine_dehydrogenase_mrna,_complete_cds.
 u40992_839-1175,heat_shock_protein_hsp40_homolog_mrna,_complete_cds
 u68133_4-133,scs-
 s4_mrna_expressed_in_primary_and_relatively_radiosensitive_squamous_cell_carcin
 oma,
 u88667_6771-7251,atp_binding_cassette_transporter_(abcr)_mrna,_complete_cds
 all_x00088_334-787,histone_h2b_gene
 all_x67081_578-810,histone_h4_gene_
 x69089_4333-4849,mrna_for_skeletal_muscle_165kd_protein
 x89101exon#3_8-96:in_reversesequence,_183-188,mrna_for_fas_(apo-
 1,_cd95)/gb=x89101/_ntype=rna_
 x90530cds_632-1100:in_reversesequence,_1548-1554,mrna_for_ragb_protein
 z68747cds_656-1106:in_reversesequence,_1177,mrna_for_imogen_38
 z69915mrna_31-244,mrna_(clone_icrfp50711876) .

Metagene 426

d30037_609-1179,mrna_for_phosphatidylinositol_transfer_protein_(pi-
 tpbeta),_complete_cds_
 all_j03027_3437-3996,mhc_i_hla-6.09_gene,_complete_cds_
 all_m14306_171-361,beta-a3/a1-crystallin_gene_(hu-beta-a3/a1)
 all_m30703_55-142:not_in_gb_record,amphiregulin_(ar)_gene_
 u14407_601-1147,interleukin(il15)_mrna,_complete_cds_
 u33054_1584-2010,g_protein-
 coupled_receptor_kinase_grk4_mrna,_alpha_splice_variant,_complete_cds_
 x94629_618-1128,mrna_for_metaphase_chromosomal_protein
 y10518mrna_138-648,mrna_for_cd202_protein/gb=y10518/_ntype=rna_
 z83804_29-261,mrna_for_axonemal_dynein_heavy_chain_(partial,_id_hdhc7) .

Metagene 427

m60459_1277-1745,erythropoietin_receptor_mrna,_complete_cds
 u45880_1969-2515,x-linked_inhibitor_of_apoptosis_protein_xiap_mrna,_complete_cds
 u89326_1533-1965,bone_morphogenetic_protein_receptor_type_i_alk-
 6_mrna,_complete_cds_
 all_x66610_1372-1697,mrna_for_enolase
 all_x78678_1384-1871,khk_mrna_for_ketohexokinase,_clone_phkhk3a

Metagene 428

hg3344-ht3521_at_hg3344-ht3521_ubiquitin-conjugating_enzyme_ubch5
 all_m35999_3904-4463,platelet_glycoprotein_iiia_(gp11a)_mrna,_complete_cds
 all_u19906_5284-5711,arginine_vasopressin_receptor(avpr1)_gene,_complete_cds
 u54617_1233-1737,pyruvate_dehydrogenase_kinase_isoformmrna,_complete_cds
 x94703cds_244-628:in_reversesequence,_640-748,rab28_mrna

Metagene 429

d13628_2506-2998,mrna_for_kiaa0003_gene,_complete_cds
 hg2171-ht2241_r_at_hg2171-ht2241_12-lipoxygenase_
 147726_2090-2552,phenylalanine_hydroxylase_(pah)_mutant_q20stop_mrna
 all_m11591_5495-6174:in_m11591cds_567-598,mhc_ii_hla-sx-alpha_gene
 u55764_784-1072,estrogen_sulfotransferase_mrna,_partial_cds
 all_x51362_2101-2583,mrna_for_dopamine_d2_receptor_
 x60708mrna_2812-3364,pchdp7_mrna_for_liver_dipeptidyl_peptidase_iv_

Metagene 430

d87458_3244-3784,mrna_for_kiaa0282_gene,_partial_cds_
 m99564_2505-2991,(clone_dn10mel)_p_protein_mrna,_complete_cds_

Metagene 431

y08374mrna#1_1414-1882,_gp-
 39_cartilage_protein_gene_extracted_fromgene_encoding_cartilage_gp-39_pro

Metagene 432

ac002115_66940-67151:in_ac002115cds#2_675-
 1000,_cox6b_gene_(coxg)_extracted_fromdna_from_overlapping
 hg371-ht26388_s_at_hg371-ht26388_mucin_1,_epithelial,_altsplice_9
 j05252_1611-2178,kex2-like_endoprotease_mrna,_complete_cds.
 j05556mrna_1640-2198,collagenase_mrna,_complete_cds_
 all_m18255_18-408:in_m18255cds_47,_prkacb_gene_(protein_kinase_c-beta-
 2)_extracted_fromprotein_kinas
 m60614_1996-2060,wilms_tumor_(wit-1)_associated_protein_mrna,_complete_cds_
 s75213_1727-2087,_type-
 iva_cyclic_amp_specific_phosphodiesterase_hpde4a_[human,_t-cells,_mrna_partia

u00954_738-1224,clone_ce29_7.2_(cac)n/(gtg)n_repeat-containing_mrna
 u38904_1210-1744,zinc_finger_protein_c2h2-25_mrna,_complete_cds
 u45976_1748-
 2210,clathrin_assembly_protein_lymphoid_myeloid_leukemia_(calm)_mrna,_complete_cds
 u52682_4755-
 5241,lymphocyte_specific_interferon_regulatory_factor/interferon_regulatory_factor(lsirf
 u58096_798-1056,testis-specific_protein_(tspy)_mrna,_complete_cds
 u65406mrna#1_1860-2370,_kcnj1_gene_(potassium_channel_roman-
 k3)_extracted_fromalternatively_spliced_po
 u71203_339-753,rit_mrna,_complete_cds
 u89336exon#13_173-
 695,_unknown_gene_extracted_fromhla_iii_region_containing_notch4_gene,_partial_seq
 all_x16660_1795-2049,_open_reading_frame_p25_(aa_1-
 223)_gene_extracted_fromhtlv-i_related_endogenous
 x71877cds_587-767:in_reversesequence,_783-1089,mrna_for_chymotrypsin-like_protease_ctrl-1
 all_x89894_2017-2486,mrna_for_nuclear_receptor_
 x93498mrna_589-1117,mrna_for_21-glutamic_acid-rich_protein_(21-garp)_
 x93512cds_61-157:in_reversesequence,_175-
 211,mrna_for_telomeric_dna_binding_protein_(orf2)
 y00067mrna_2655-3207,gene_for_neurofilament_subunit_m_(nf-m)
 y10262cds_1163-1693,eya3_gene/gb=y10262_/ntype=dna_/annot=cds

Metagene 433

af000573mrna_1162-1666,homogentisate_1,2-dioxygenase_gene,_complete_cds
 d45399mrna_155-
 629,adult_neural_retina_mrna_forcone_cgmp_phosphodiesterase_gamma_subunit,_complete_c
 hg4557-ht4962_r_at_hg4557-ht4962_small_nuclear_ribonucleoprotein_u1,_lsnrp_
 k03189cds_2-404,chorionic_gonadotropin_beta_subunit_gene_
 all_143579_398-
 428,(clone_110298)_mrna/gb=143579_/ntype=rna,(clone_110298)_mrna/gb=143579_/ntype=rna
 all_m17236_1896-2224,mhc_ii_hla-dq-alpha_gene_(dr4,w6),mhc_ii_hla-dq-alpha_gene_(dr4,w6)
 all_m17236_1896-2224,mhc_ii_hla-dq-alpha_gene_(dr4,w6),mhc_ii_hla-dq-alpha_gene_(dr4,w6)
 m60828_3252-3720,keratinocyte_growth_factor_mrna,_complete_cds_
 s76853_1683-2244,_cerebrin-
 50=cerebrospinal_fluid_protein_[human,_cerebral_brain,_mrna,_2295_nt]
 u43189_2384-2942,ets_transcription_factors_nerf-1a_and_nerf-1b_(nerf-1a,b)_mrna,_complete_cds
 v00571mrna_714-
 1218,gene_encoding_prepro_form_of_corticotropin_releasing_factor_
 all_x04571_4306-4835,mrna_for_kidney_epidermal_growth_factor_(egf)_precursor_
 x61755mrna_1020-1562,hox3d_gene_for_homeoprotein_hox3d
 all_x66403_1856-2301,mrna_for_acetylcholine_receptor_(epsilon_subunit)_
 x80695cds_938-1250:in_reversesequence,_1298-1496,oxalhs_mrna_
 all_z22535_2433-2932,alk-3_mrna
 z50781cds_100-205:in_reversesequence,_346-394,mrna_for_leucine_zipper_protein_

Metagene 434

all_m26665_267-
 307,histatin(his2)_mrna,_complete_cds,histatin(his2)_mrna,_complete_cds
 m28130mrna_654-1002,interleukin(il8)_gene,_complete_cds
 m33684cds_288-788,(clone_lambda-10-2)_non-
 receptor_tyrosine_phosphatase(ptpn1)_gene_
 u10492_1894-2266,mox1_protein_(mox1)_mrna,_complete_cds
 u18985_2460-2922,triadin_mrna,_complete_cds
 u48213mrna_1031-1601,d-site_binding_protein_gene,_promoter_region_and

Metagene 435

d14874_908-1406,mrna_for_adrenomedullin,_complete_cds
 d50857_5954-6440,dock180_protein_mrna,_complete_cds
 hg1428-ht1428_s_at_hg1428-ht1428_globin,_beta
 hg2815-ht2931_s_at_hg2815-
 ht2931_myosin,_light_chain,_alkali,_smooth_muscle,_non-muscle,_altsplice_2
 hg3523-ht4899_s_at_hg3523-ht4899_proto-oncogene_c-myc,_altsplice_3,_orf_114
 l09235_1323-1845,vacuolar_atpase_(isoform_va68)_mrna,_complete_cds_
 l10838_79-499,sr_protein_family,_pre-
 mrna_splicing_factor_(srp20)_mrna,_complete_cds
 l42601cds_1334-1665:in_reversesequence,_247-
 470,keratinisoform_k6c_(krt6c)_gene_
 m81637_1078-1603,grancalcin_mrna,_complete_cds_
 s82297_3-391,_beta_2-microglobulin_{11bp_deleted_between_nucleotides_98-
 99}_[human,_colon_cancer_cel
 u07158_641-1169,syntaxin_mrna,_complete_cds
 u37518_1162-1390,tnf-related_apoptosis_inducing_ligand_trail_mrna,_complete_cds
 u43083_1408-1582,g_alpha-q_(gaq)_mrna,_complete_cds
 u84569_647-1217,yf5_mrna,_complete_cds_
 u91327mrna_156-654,chromosome_12p15_bac_clone_cit987sk-
 99d8_complete_sequence/gb=u91327_/ntype=dna/
 x03689cds_17-255,mrna_fragment_for_elongation_factor_tu_(n-
 terminus)/gb=x03689_/ntype=rna
 x89399_s_at_x89399_x89399,not_in_gb_record,mrna_for_ins(1,3,4,5)p4-
 binding_protein
 x95073_657-1119,mrna_for_translin_associated_protein_x_

Metagene 436

d31884_2579-3023,mrna_for_kiaa0063_gene,_complete_cds
 d63998_3542-4046,mrna_for_golgi_alpha-mannosidaseii,_complete_cds
 l13740_2002-2047,tr3_orphan_receptor_mrna,_complete_cds
 l13852_2790-3270,ubiquitin-
 activating_enzyme_e1_related_protein_mrna,_complete_cds
 l13972_1930-2224,beta-galactoside_alpha-2,3-
 sialyltransferase_(siat4a)_mrna,_complete_cds_
 l35475cds_642-888:in_reversesequence,_1441-1675,olfactory_receptor-
 like_gene,_complete_cds

l40366mrna_31-
 223,thyroid_receptor_interactor_(trip2)_mrna,_partial_cds/gb=l40366_/ntype=rna
 m18391_2780-3147,tyrosine_kinase_receptor_(eph)_mrna,_complete_cds_
 m27826mrna_464-1025,endogenous_retroviral_protease_mrna,_complete_cds
 m31165mrna_843-1353,tumor_necrosis_factor-inducible_(tsg-
 6)_mrna_fragment,_adhesion_receptor_cd44_pu
 m59371mrna_3386-3878,protein_tyrosine_kinase_mrna,_complete_cds
 m83308_31-343,mitochondrial_cytochrome-
 c_oxidase_subunit_via_(cox6a)_mrna,_complete_cds
 s80335_2197-2719,_integrin_betasubunit_[human,_mrna,_2798_nt]
 s82024_20-548,_scg10=neuron-specific_growth-
 associated_protein/stathmin_homolog_[human,_embryo,_mrna
 all_s83366_910-
 2840,_region_centromeric_to_t(12;17)_brakepoint:_orf1/unknown_43_amino_acid_tra
 nscrip
 u15172_619-967,nip1_(nip1)_mrna,_complete_cds
 u56998_1628-
 2048,putative_serine/threonine_protein_kinase_prk_(prk)_mrna,_complete_cds_
 u89336exon#30-33_48-
 208:in_reversesequence,_22261:not_in_gb_record,_unknown_gene_extracted_fromhla_
 i
 all_x51602_7115-7680,flt_mrna_for_receptor-related_tyrosine_kinase_
 all_x52005_476-969,skeletal_embryonic_myosin_light_chain(mlc1)_mrna_
 x62535mrna_1975-2515,mrna_for_diacylglycerol_kinase
 all_x89985_1010-1389,mrna_for_bcl7b_protein
 x90761mrna_1365-1683,hha2_gene_
 all_x92762_1360-1883,mrna_for_tafazzins_protein

Metagene 437

all_m73548_9853-10274,polyposis_locus_(dp2.5_gene)_mrna,_complete_cds
 u30245exon_3-
 56,myelomonocytic_specific_protein_(mnda)_gene,_5'_flanking_sequence_and_comple
 te_exon/
 u36448_1252-1792,ca2+-
 dependent_activator_protein_for_secretion_mrna,_complete_cds_
 u41737_103-
 523,pancreatic_beta_cell_growth_factor_(ingap)_mrna,_complete_cds/gb=u41737_/nt
 ype=rna
 u48697_1787-2276,mariner-like_element-containing_mrna,_clone_pchmt2
 x89986cds_271-387:in_reversesequence,_794-
 1043,mrna_for_nbk_apoptotic_inducer_protein_

Metagene 438

ab000115_1469-1973,_complete_cds
 d14664_3255-3639,mrna_for_kiaa0022_gene,_complete_cds
 d26361_5991-6543,mrna_for_kiaa0042_gene,_complete_cds
 l38951mrna_3611-4151,importin_beta_subunit_mrna,_complete_cds_
 l40399mrna_993-1467,(clone_s240iii117/zap112)_mrna,_complete_cds_
 m15353mrna_1277-1769,cap-binding_protein_mrna,_complete_cds_
 m69043_985-1459,mad-3_mrna_encoding_ikb-like_activity,_complete_cds_
 u05040_1814-2282,fuse_binding_protein_mrna,_complete_cds_

u08998_962-1280,tar_rna_binding_protein(trbp2)_mrna,_complete_cds_
u22431_3070-3644,hypoxia-inducible_factoralpha_(hif-
1_alpha)_mrna,_complete_cds_
u41515_61-397,deleted_in_split_hand/split_foot(dss1)_mrna,_complete_cds_
u43522_3580-4072,cell_adhesion_kinase_beta_(cakbeta)_mrna,_complete_cds_
u44111mrna_1108-1642,histamine_n-methyltransferase_(hnmt)_gene_
u51166_2941-3361,g/t_mismatch-
specific_thymine_dna_glycosylase_mrna,_complete_cds_
u70063_1750-2266,acid_ceramidase_mrna,_complete_cds_
all_x83228_3359-3561,mrna_for_li-cadherin
z79581exon_19-226,laz3/bcl6_gene,_first_non_coding_exon

Metagene 439

d13645_1517-2027,mrna_for_kiaa0020_gene,_complete_cds_
v00542mrna_375-902,_messenger_rna_forleukocyte_(alpha)_interferon
all_x62822_2104-2645,gene_encoding_beta-galactoside_alpha-2,6-sialyltransferase

Metagene 440

d10925_1613-2123,mrna_for_hm145
u29680_251-659,a1_protein_mrna,_complete_cds_
u45878_2591-2689,inhibitor_of_apoptosis_proteinmrna,_complete_cds_

Metagene 441

d16350_1280-1826,sa_mrna_for_sa_gene_product,_complete_cds_
d38073_2590-3022,mrna_for_hrlf_beta_subunit_(p102_protein),_complete_cds_
d63481_4350-4890,mrna_for_kiaa0147_gene,_partial_cds_
l42373mrna_2651-3071,protein_phosphatase_2a_b56-alpha_mrna,_complete_cds_
m29277_2335-
2901,isolate_juso_muc18_glycoprotein_mrna_(3'_variant),_complete_cds,isolate_ju
so_muc18_
m34458mrna_1900-2463,lamin_b_mrna,_complete_cds_
u33286_2642-3092,chromosome_segregation_gene_homolog_cas_mrna,_complete_cds_
u37426_4269-4815,kinesin-like_spindle_protein_hksp_(hksp)_mrna,_complete_cds_
u53204_14286-14721,plectin_(plec1)_mrna,_complete_cds_
u56816_1376-1838,kinase_myt1_(myt1)_mrna,_complete_cds.
u73843_1356-1860,epithelial-specific_transcription_factor_ese-1b_(ese-
1)_mrna,_complete_cds_
all_x74331_1801-2288,mrna_for_dna_primase_(subunit_p58)
all_x99459_1516-1799,mrna_for_sigma_3b_protein_
y00486mrna_252-
786,_adenine_phosphoribosyltransferase_(aprt)_gene_extracted_fromaprt_gene_for_
adenin
all_z22555_2041-2516,encoding_cla-1_mrna_
z37986cds_409-631:in_reversesequence,_826-
1000,mrna_for_phenylalkylamine_binding_protein

Metagene 442

hg2075-ht2137_s_at_hg2075-ht2137_camp-responsive_element_modulator,_altsplice_1
 m30135cds_139-361:in_reversesequence,_4255-4303,p40_t-
 cell_and_mast_cell_growth_factor_(hp40)_gene,_
 u13680_767-1160,lactate_dehydrogenase-c_(ldh-c)_mrna,_complete_cds_
 u66033_1937-2495,glypican-5_(gpc5)_mrna,_complete_cds_
 all_x51420_2264-2781,mrna_for_tyrosinase-related_protein_
 x58298cds_824-1371:in_reversesequence,_1441,mrna_for_interleukin-6-receptor_

Metagene 443

ab000468_2302-2860,mrna_for_zinc_finger_protein,_clone_res4-26,_complete_cds_
 ab002533_1726-2128,mrna_for_qip1,_complete_cds_
 reverse_ac002077_3475-3730,cosmid_clone_luca17_from_3p21.3_
 ad000092cds#2_714-1008:in_fullsequence,_87557-87797,_hypotheticalserine-
 threonine_protein_kinase_r31
 d16480_2089-2641,mrna_for_mitochondrial_enoyl-coa_hydratase/3-hydroxyacyl-
 coa_dehydrogenase_alpha-su
 d38552_1532-2012,mrna_for_kiaa0073_gene,_partial_cds_
 d63475_1309-1819,mrna_for_kiaa0109_gene,_complete_cds_
 d63477_4745-5243,mrna_for_kiaa0143_gene,_partial_cds_
 d79206exon#5_1513-2053,gene_for_ryudocan_core_protein,_exon1-5,_complete_cds_
 d85245_1248-1806,mrna_for_tr3beta,_complete_cds_
 all_d87017_16956-
 20256,_c7_segment_gene_extracted_from(lambda)_dna_for_immunoglobulin_light_chain_
 d87116_1514-2048,mrna_for_map_kinase_kinase_3b,_complete_cds_
 hg2290-ht2386_at_hg2290-ht2386_calcitonin
 hg2755-ht2862_at_hg2755-ht2862_t-plastin
 hg2887-ht3031_at_hg2887-ht3031_sry-related_hmg-boxprotein
 hg331-ht331_at_hg331-ht331_tenascin
 hg3897-ht4167_at_hg3897-ht4167_sodium_channel,_type_iii,_alpha_subunit,_brain
 hg3925-ht4195_s_at_hg3925-ht4195_surfactant_protein_sp-a2_delta_
 j02906mrna_1254-1782,cytochrome_p450iif1_protein_(cyp2f)_mrna,_complete_cds_
 l25444_2124-2694,(tafii70-alpha)_mrna,_complete_cds_
 m22960mrna_1352-1760,protective_protein_mrna,_complete_cds_
 m24439exon_492-912,liver/bone/kidney-type_alkaline_phosphatase_(alpl)_gene_
 m60284cds_835-1144:in_reversesequence,_251-479,neurokinin_a_receptor_(nk-
 2r)_gene_
 m68941mrna_3078-3618,protein-tyrosine_phosphatase_mrna,_complete_cds_
 m91669_4061-4636,bullous_pemphigoid_autoantigen_bp180_gene,_3'_end_
 m92303_3057-3633,voltage-dependent_calcium_channel_beta-
 1_subunit_mrna,_complete_cds_
 m95623exon#14-15_2-
 383:not_in_gb_record,_pbgd_gene_(hydroxymethylbilane_synthase)_extracted_fromhy
 dr
 s38742_1370-1835,_hox11=hox11_homeodomain_{homeobox}_[human,_mrna,_1988_nt]_
 s65583mrna_588-1068,_sp-10=intra-
 acrosomal_protein_{alternatively_spliced}_[human,_liver,_genomic,_2
 s87759_1823-
 2321,_protein_phosphatase_2c_alpha_[human,_teratocarcinoma,_mrna,_2346_nt]
 u01337exon#16_412-553,ser/thr_protein_kinase_(a-raf-1)_gene,_complete_cds_
 u04898_1421-1877,orphan_hormone_nuclear_receptor_roralpha2_mrna,_complete_cds_
 u11292_2353-2863,ki_nuclear_autoantigen_mrna,_complete_cds_
 u15655_2102-2576,ets_domain_protein_erf_mrna,_complete_cds_

u25034_588-1127,neuronatin_beta_mrna,_complete_cds_
 u25956mrna_1470-2046,p-selectin_glycoprotein_ligand_(selplg)_gene
 u30894_2068-2626,n-sulphoglucosamine_sulphohydrolase_mrna,_complete_cds
 u32439_1324-1822,regulator_of_g-
 protein_signaling_similarity_(rgs7)_mrna,_partial_cds
 u32674cds_593-1060:in_reversesequence,_1181-
 1191,orphan_receptor_gpr9_(gpr9)_gene,_partial_cds
 u39573_2173-2689,salivary_peroxidase_mrna,_complete_cds
 u40391mrna_464-980,serotonin_n-acetyltransferase_gene,_complete_cds_
 u40434_1561-2071,mesothelin_or_cak1_antigen_precursor_mrna,_complete_cds_
 u42031_1655-2201,54_kda_progesterone_receptor-
 associated_immunophilin_fkbp54_mrna,_partial_cds_
 u43374_775-1069,normal_keratinocyte_mrna_
 u45973_1634-2192,phosphatidylinositol_(4,5)bisphosphate_5-
 phosphatase_homolog_mrna,_partial_cds
 u46751_1562-
 2012,phosphotyrosine_independent_ligand_p62_for_the_lck_sh2_domain_mrna,_comple
 te_cds
 u49857_314-749,transcriptional_activator_mrna,_complete_cds
 u50330_3071-3515,procollagen_c-proteinase_(pcp-2)_mrna,_complete_cds_
 u68111mrna_858-1374,protein_phosphatase_inhibitor(ppplr2)_gene
 u70671_695-1115,ataxin-2_related_protein_mrna,_partial_cds_
 u72206_3122-
 3590,guanine_nucleotide_regulatory_factor_(lfp40)_mrna,_complete_cds_
 u92457_2832-3375,metabotropic_glutamate_receptormrna,_complete_cds
 x05855cds_12-
 65:not_in_gb_record,histone_h3.3_gene_exon_2,histone_h3.3_gene_exon_2_
 all_x07290_1212-1723,hf.12_gene_mrna_
 all_x07767_1948-2516,mrna_for_camp-
 dependent_protein_kinase_catalytic_subunit_type_alpha_(ec_2.7.1.3
 all_x07948_3-428,mrna_for_transition_protein(tp1)_
 x59932mrna_1557-2063,mrna_for_c-src-kinase_
 all_x66945_3582-3931,n-sam_mrna_for_fibroblast_growth_factor_receptor
 x78687exon#6_172-670,g9_gene_encoding_sialidase
 x79865cds_267-411:in_reversesequence,_922,mrp17_mrna
 x81372cds_701-791:in_reversesequence,_1027-1195,mrna_for_biphenyl_hydrolase-
 related_protein
 all_x89066_3817-4019,mrna_for_trpc1_protein
 all_x91504_970-1523,mrna_for_arp1_protein
 all_x94232_2035-2528,mrna_for_novel_t-cell_activation_protein
 all_x98482_45-
 72,tnnt2_gene_exon/gb=x98482_/ntype=dna_/annot=mrna,tnnt2_gene_exon/gb=x98482_
 ntype=d
 all_z12962_31-398,mrna_for_homologue_to_yeast_ribosomal_protein_l41
 z22548cds_310-547:in_reversesequence,_684-894,thiol-
 specific_antioxidant_protein_mrna_
 z73497cds_28-
 229,dna_sequence_from_cosmid_u240c2,_between_markers_dxs366_and_dxs87_on_chromo
 some_xco

Metagene 444

af014958_1175-
 1619,chemokine_receptor_x_(ckrx)_mrna,_complete_cds/gb=af014958_/ntype=rna
 d16688_876-1448,ltg9/mlt3_mrna,_c-terminal

d29956_3758-4328,mrna_for_kiaa0055_gene,_complete_cds
 d31888_4700-5186,mrna_for_kiaa0071_gene,_partial_cds_
 d38037_292-826,mrna_for_fk506-binding_protein_12kda_(hfkbp-
 12)_homologue,_complete_cds_
 d63135mrna_31-499,mrna_for_ets-like_30_kda_protein/gb=d63135_/ntype=rna
 d79987_6109-6523,mrna_for_kiaa0165_gene,_complete_cds
 d86957_3869-4265,mrna_for_kiaa0202_gene,_partial_cds_
 d88213_2085-2481,mrna_for_retina-specific_amine_oxidase,_complete_cds
 hg2383-ht4824_s_at_hg2383-ht4824_cystathionine_beta_synthase,_altsplce_3
 hg25930-ht26386_at_hg25930-ht26386_estradiol_17-beta_dehydrogenase
 hg2841-ht2968_s_at_hg2841-ht2968_albumin,_altsplce_1
 hg2987-ht3136_s_at_hg2987-ht3136_vasoactive_intestinal_peptide_
 hg3264-ht3441_at_hg3264-ht3441_af-6
 hg4027-ht4297_f_at_hg4027-ht4297_beta-1-
 glycoprotein,_domains_n_and_iiia,_pregnancy-specific
 hg4390-ht4660_at_hg4390-ht4660_ribosomal_protein_l18a_homolog
 l06133_7979-8435,putative_cu++-transporting_p-type_atpase_mrna,_complete_cds_
 all_l08904_1372-1667,h2k_binding_factor(kbf2)_mrna,_complete_cds_
 l12468_3246-3780,aminopeptidase_a_mrna,_complete_cds
 l14812_3349-3936,retinoblastoma_related_protein_(p107)_mrna,_complete_cds
 l20826_3074-3572,i-plastin_mrna,_complete_cds
 l22569_1685-2243,cathepsin_b_mrna,_3'_utr_with_a_stem-
 loop_structure_providing_mrna_stability_
 l39060mrna_1037-1547,transcription_factor_sl1_mrna,_complete_cds
 m11025mrna_783-1263,asialoglycoprotein_receptor_h2_mrna,_complete_cds
 m17252mrna_934-1198,cytochrome_p450c21_mrna,_3'_end
 all_m24364_1059-
 1435,mhc_ii_lymphocyte_antigen_dqb_mrna,_complete_cds,_haplotype_dr7,_dqw9_
 m29581_1469-1853,zinc-finger_protein(zfp8)_mrna,_3'_end_
 m57464_3899-4439,ret_proto-oncogene_mrna,_complete_cds_
 m63962mrna_2985-3507,gastric_h,k-atpase_catalytic_subunit_gene,_complete_cds
 m74525_2002-2536,hhr6b_(yeast_radhomologue)_mrna,_complete_cds
 m87860cds_25-331:in_reversesequence,_176-212,s-lac_lectin_l-14-
 ii_(lgals2)_gene_
 m89955cds_635-1085:in_reversesequence,_1391-1439,5-ht1d-
 type_serotonin_receptor_gene,_complete_cds
 s48983cds_36-282:in_reversesequence,_204-
 408,_saa4=serum_amyloid_a_[human,_genomic,_858_ntsegments]
 s59184_2487-
 2979,_ryk=related_to_receptor_tyrosine_kinase_[human,_hepatoma,_mrna,_3068_nt]
 s61953_516-798,_c-
 erbb3=receptor_tyrosine_kinase_{alternatively_spliced}_[human,_gastric_cancer_c
 ell
 u16811_1491-2034,bak_mrna,_complete_cds
 all_u18914_2694-3199,19.8_kda_protein_mrna,_complete_cds_
 u28758_45-626,nmda_receptor_subtype_2b_subunit_(grin2b)_mrna,_partial_cds
 u40215_1479-2049,synapsin_iib_mrna,_complete_cds_
 u40763_2251-2803,clk-associated_rs_cyclophilin_cars-cyp_mrna,_complete_cds_
 u43286_1633-2155,selenophosphate_synthetase(sps2)_mrna,_complete_cds
 u44848_7-
 187,nuclear_respiratory_factor(nrfl1)_mrna,_3'_utr/gb=u44848_/ntype=rna_
 u48807_1652-2156,map_kinase_phosphatase_(mkp-2)_mrna,_complete_cds_
 u49974cds_444-
 1017,mariner2_transposable_element,_complete_consensus_sequence/gb=u49974_/ntyp
 e=dna/
 u52518_399-825,grb2-related_adaptor_protein_(grap)_mrna,_complete_cds

u71092cds_954-1158:in_reversesequence,_1611-1767,somatostatin_receptor-
 like_protein_(slc1)_gene,_com
 u79257_952-1432,clone_23932_mrna_sequence
 u88666_3113-3653,serine_kinase_srp_k2_mrna,_complete_cds
 all_u90552_3170-
 3242,butyrophilin_(btf5)_mrna,_complete_cds,butyrophilin_(btf5)_mrna,_complete_
 cds
 u90912_1074-1584,clone_23865_mrna_sequence_
 u94332_761-1331,osteoprotegerin_(opg)_mrna,_complete_cds.
 all_x06268_1159-1337,mrna_for_pro-alpha(ii)_collagen_3'_end_c-
 termtriple_helical_and_c-terminal_non-
 all_x13956_694-
 1163,12s_rna_induced_by_poly(ri),_poly(rc)_and_newcastle_disease_virus
 x15954mrna_729-1240,mbp1_gene,_exon(and_joined_cds)
 x16707cds_379-733:in_reversesequence,_869-923,fra-1_mrna
 x17360mrna_4536-5034,hox_5.1_gene_for_hox_5.1_protein_
 all_x63575_3903-4466,mrna_for_plasma_membrane_calcium_atpase_
 all_x64838_5256-5833,mrna_for_restin_
 x66171cds_341-623:in_reversesequence,_892-1108,cmrf35_mrna,_complete_cds
 all_x77383_1094-1599,mrna_for_cathepsin-o
 x78031_1113-1629,alpha-1,_3-fucosyltransferase_mrna
 all_x95289_48-625,mrna_for_hcgix_protein_
 y11651cds_750-960:in_reversesequence,_1250-1466,mrna_for_phosphate_cyclase

Metagene 445

ab002314_6334-6898,mrna_for_kiaa0316_gene,_complete_cds/gb=ab002314_/ntype=rna_
 hg2600-ht2696_at_hg2600-ht2696_guanine_nucleotide-binding_protein_rap2b,_ras-
 oncogene_related
 hg2602-ht2698_at_hg2602-ht2698_succinate_dehydrogenase,_flavoprotein_subunit_
 127586_1755-2205,tr4_orphan_receptor_mrna,_complete_cds
 all_m24748_1170-1531,_thra1_gene_(thyroid_receptor_alpha-
 1)_extracted_fromthyroid_hormone_receptor_a
 u45983cds_789-1005:in_reversesequence,_1304-1496,g_protein-
 coupled_receptor_gpr-cy6_gene,_complete_c
 u49187_1780-2206,placenta_(diff48)_mrna,_complete_cds
 u66464_2131-2701,hematopoietic_progenitor_kinase_(hpk1)_mrna,_complete_cds_
 u70321_1127-1643,herpesvirus_entry_mediator_mrna,_complete_cds_
 x66360cds_1134-1518:in_reversesequence,_1629-1689,mrna_pctaire-
 2_for_serine/threonine_protein_kinase
 all_x90840_6383-6942,mrna_for_axonal_transporter_of_synaptic_vesicles
 all_z80777_449-807,h2a/k_gene

Metagene 446

d17391_2957-3497,mrna_for_alpha_4(iv)_collagen,_c-terminal_
 hg4582-ht4987_at_hg4582-ht4987_glucocorticoid_receptor,_beta_
 104569_8323-8890,(clone_hht-1)_l-type_voltage-
 dependent_calcium_channel_a1_subunit_(hht)_mrna,_compl
 m37815mrna#1_1079-1589,_cd28_gene_(glycoprotein_cd28)_extracted_fromt-
 cell_membrane_glycoprotein_cd2
 z49995mrna_2014-2590,mrna_(non-coding;_clone_h2a)

Metagene 447

af006084_935-1277, arp2/3_protein_complex_subunit_p41-
 arc(arc41)_mrna,_complete_cds/gb=af006084_/nty
 d00017_851-1319, lipocortin_ii_mrna_
 d26129_1145-1577, mrna_for_ribonuclease_a_(rnase_a),_complete_cds_
 d42043_2329-2863, mrna_for_kiaa0084_gene,_partial_cds_
 d87292_572-1052, mrna_for_rhodanese,_complete_cds_
 d88152_2081-2639, mrna_for_acetyl-coenzyme_a_transporter,_complete_cds_
 j04456_31-469, humankd_lectin_mrna,_complete_cds_
 l13720_1860-2436, growth-arrest-specific_protein_(gas)_mrna,_complete_cds_
 l25080_1212-1692, gtp-binding_protein_(rhoa)_mrna,_complete_cds_
 l33075_6978-7530, ras_gtpase-activating-
 like_protein_(iggap1)_mrna,_complete_cds_
 l40379mrna_181-541, thyroid_receptor_interactor_(trip10)_mrna,_3'_end_of_cds_
 l41147mrna_1383-1959, 5-ht6_serotonin_receptor_mrna,_complete_cds_
 m13450_636-1020, esterase_d_mrna,_3'_end_
 all_m14338_2740-3281, mrna_for_protein_s_and_intron_
 all_m14949_1905-2423, r-ras_gene_
 m23294mrna#1_1219-1651; beta-hexosaminidase_beta-subunit_(hexb)_gene_
 m26576exon_43-289: not_in_gb_record, col4a1_gene_(alpha-
 1_type_iv_collagen)_extracted_from_alpha-1_col
 m27492_4336-4864, interleukin_receptor_mrna,_complete_cds_
 m28713exon_536-1052, nadh-cytochrome_b5_reductase_(b5r)_gene_
 m33680_879-1431, 26-kda_cell_surface_protein_tapa-1_mrna,_complete_cds_
 m36341_912-1458, adp-ribosylation_factor(arf4)_mrna,_complete_cds_
 m63256_1975-2497, major_yo_paraneoplastic_antigen_(cdr2)_mrna,_3'_end_
 m64571mrna_4553-4931, microtubule-associated_protein_mrna,_complete_cds_
 m76378mrna_1294-1768, cysteine-rich_protein_(crp)_gene_
 m82809_1465-1915, annexin_iv_(anx4)_mrna,_complete_cds_
 m83751_539-1013, arginine-rich_protein_(arp)_gene,_complete_cds_
 u01691mrna_1257-1743, annexin_v_(anx5)_gene,_5'_-untranslated_region_
 u02570_2792-3290, cdc42_gtpase-activating_protein_mrna,_partial_cds_
 u44378_2091-
 2655, homozygous_deletion_target_in_pancreatic_carcinoma_(dpc4)_mrna,_complete_c
 ds_
 u46006_140-620, smooth_muscle_lim_protein_(h-
 smlim)_mrna,_complete_cds/gb=u46006_/ntype=rna_
 u46499_at_u46499_u46499, not_in_gb_record, microsomal_glutathione_transferase_(gs
 t12)_gene,_5'_sequenc
 u93205_588-1020, nuclear_chloride_ion_channel_protein_(ncc27)_mrna,_complete_cds_
 x04412cds_2047-2305: in_reversesequence, 2421-2529, mrna_for_plasma_gelsolin_
 all_x05610_1701-2098, mrna_for_type_iv_collagen_alpha_-2_chain_
 all_x07979_3223-3596, mrna_for_fibronectin_receptor_beta_subunit_
 all_x54304_391-878, mrna_for_myosin_regulatory_light_chain_
 y00433cds_233-581: in_reversesequence, 905-
 1109, mrna_for_glutathione_peroxidase_(ec_1.11.1.9.)_

Metagene 448

ab000449_1091-1607, mrna_for_vrk1,_complete_cds_
 dl4689_6077-6557, mrna_for_kiaa0023_gene,_complete_cds_
 x55668mrna_550-940, mrna_for_proteinase_3_

all_x75917_1064-1602,mrna_for_fetal_beta-mhc_binding_factor

Metagene 449

d79988_6383-6899,mrna_for_kiaa0166_gene,_complete_cds
 d80001_4465-4939,mrna_for_kiaa0179_gene,_partial_cds_
 d87450_5572-6034,mrna_for_kiaa0261_gene,_partial_cds_
 hg2573-ht2669_at_hg2573-ht2669_zinc_finger_protein_kup_
 m22638exon#4_154-682,lyl-1_protein_gene,_complete_cds
 m62402_453-927,insulin-
 like_growth_factor_binding_protein(igfbp6)_mrna,_complete_cds
 m85164_1354-1852,srf_accessory_protein_1b_(sap-1)_mrna,_complete_cds
 s79873_3394-3969,_h-lamp-2=lysosome-associated_membrane_protein-
 2_{alternatively_spliced}_[human,_li
 u15174_224-746,nip3_(nip3)_mrna,_complete_cds
 u24186cds_465-747:in_reversesequence,_1223-
 1391,replication_protein_a_complex_subunit_homolog_rpa4_g
 u34976_1059-1575,gamma-sarcoglycan_mrna,_complete_cds
 u47677mrna_2495-2636,transcription_factor_e2f1_(e2f1)_gene,_promoter_and_
 u59914_802-1240,chromosomemad_homolog_smad6_mrna,_complete_cds_
 u80628_2216-
 2588,thymidine_kinaseisoform_b_(tk2)_mrna,_alternatively_spliced,_partial_cds_
 all_x16323_5339-5814,mrna_for_hepatocyte_growth_factor_(hgf)_
 x52009cds_813-1315:in_reversesequence,_1629,alpha-
 1_strychnine_binding_subunit_of_inhibitory_glycine

Metagene 450

hg3548-ht3749_at_hg3548-
 ht3749_ccaat_displacement_protein,_cut_homolog,_altsplice_1
 l27559utr#1_111-166,insulin-like_growth_factor_binding_protein(igfbp5)_gene_
 m62782_392-958,insulin-like_growth_factor_binding_protein(igfbp-
 5)_mrna,_complete_cds
 u51336_2520-3024,inositol_1,3,4-trisphosphate_5/6-kinase_mrna,_complete_cds
 x16665cds_871-1039:in_reversesequence,_1135-
 1369,hox2h_mrna_from_the_hox2_locus_
 all_z48605_61-326,partial_mrna_for_pyrophosphatase/gb=z48605_/ntype=rna

Metagene 451

d10923_1452-1962,mrna_for_hm74_
 d42038_3730-4216,mrna_for_kiaa0087_gene,_complete_cds
 d50917_4943-5489,mrna_for_kiaa0127_gene,_complete_cds
 d50918_4053-4563,mrna_for_kiaa0128_gene,_partial_cds_
 hg2530-ht2626_at_hg2530-ht2626_adenylyl_cyclase-associated_protein
 hg2796-ht2904_at_hg2796-ht2904_neural_cell_adhesion_molecule_
 hg3248-ht3425_at_hg3248-ht3425_fibroblast_growth_factor,_antisense_mrna
 all_k01884_587-888,blym-1_transforming_gene,_complete_coding_region
 l05568_1937-2459,na+/cl- dependent_serotonin_transporter_mrna,_complete_cds
 l10374_1461-1977,(clone_ctg-a4)_mrna_sequence
 l11695_1767-2247,activin_receptor-like_kinase_(alk-5)_mrna,_complete_cds_

113436mrna_3522-4020,guanylate_cyclase_mrna,_complete_mature_peptide
 120321_3112-3655,protein_serine/threonine_kinase_stk2_mrna,_complete_cds_
 122206exon#3_63-639,vasopressin_receptor_v2_gene,_complete_cds_
 138500cds_1574-2102,na+/myo-
 inositol_cotransporter_(slc5a3)_gene,_complete_cds/gb=138500/_ntype=dna_
 177563mrna_129-591,dgs-f_partial_mrna/gb=177563/_ntype=rna
 reverse_178833_2267-
 2337,_brca1_gene_extracted_frombrca1,_rho7_and_vati_genes,_complete_cds,_and_ip
 f
 m17863mrna_242-822,preproinsulin-like_growth_factor_ii_(igf-
 ii)_variant_mrna,_complete_cds_
 all_m19720_2034-2557,_l-myc_gene_(l-myc_protein)_extracted_froml-
 myc_protein_gene,_complete_cds,_l-m
 m25164cds_5-383:in_reversesequence,_265-1170,thyrotropin_beta_subunit_gene
 m55268mrna_1094-1556,casein_kinase_ii_alpha'_subunit_mrna,_complete_cds
 m62302_1939-2485,growth/differentiation_factor(gdf-1)_mrna,_complete_cds
 m64788_2759-3209,gtpase_activating_protein_(rap1gap)_mrna,_complete_cds
 m65290_1957-
 2215,natural_killer_cell_stimulatory_factor_(nksf)_mrna,_complete_cds,_clone_p4
 0_
 m95549_1774-2194,sodium/glucose_cotransporter-like_protein_mrna,_complete_cds_
 m98776mrna_1864-2266,keratogene,_complete_cds_
 s78432mrna#1_3-87,_un-named-transcript-
 1_from_sas=transmembraneprotein_{5'_region}_[human,_sarcomas,
 u10686exon#2_730-1267,mage-11_antigen_(mage11)_gene,_complete_cds
 u12897_1564-1870:in_reversesequence,_1900-1996,non-translated_mrna_sequence_
 u15173_1781-2303,nip2_(nip2)_mrna,_complete_cds
 u23736_779-1348,gata-3_binding_protein_g3b_mrna,_partial_cds.
 u28831_532-964,protein_immuno-reactive_with_anti-
 pth_polyclonal_antibodies_mrna,_partial_cds_
 u37352_3505-
 3961,protein_phosphatase_2a_b'alpha1_regulatory_subunit_mrna,_complete_cds_
 u37431mrna#1_2114-
 2540,hoxa1_mrna,_long_transcript_and_alternatively_spliced_forms,_complete_cds_
 u43527_180-728:not_in_gb_record,malignant_melanoma_metastasis-suppressor_(kiss-
 1)_gene,_mrna,_comple
 u43944_1705-1978,breast_cancer_cytosolic_nadp(+)-
 dependent_malic_enzyme_mrna,_partial_cds
 u47931mrna_63-537,g-protein_beta-
 3_subunit_alternatively_spliced_form_mrna_sequence/gb=u47931/_ntype
 u52830_19-271,cri-du-chat_region_mrna,_clone_csc8.
 u55209_3812-3977,myosin_vii_a_transcriptmrna,_complete_cds_
 u63329cds_1128-
 1554:in_reversesequence,_1814,muty_homolog_(hmyh)_gene,_complete_cds_
 u84011_6566-
 7127,glycogen_debranching_enzyme_isoform(agl)_mrna,_alternatively_spliced_isofo
 rm,_compl
 x04145cds_286-454:in_reversesequence,_593-689,mrna_for_t-
 cell_receptor_t3_gamma_polypeptide_
 x14690cds_1150-1604:in_reversesequence,_1636-1676,mrna_for_plasma_inter-alpha-
 trypsin_inhibitor_heav
 all_x16983_3252-3787,mrna_for_integrin_alpha-4_subunit_
 all_x65962_1115-1174,mrna_for_cytochrome_p-450_
 all_x79984_16-269,aa1_mrna/gb=x79984/_ntype=rna
 x89398exon#7_695-1121,_ung_gene_(uracil-dna-
 glycosylase,_ung2)_extracted_fromung_gene_for_uracil_dna
 all_z48541_4517-5100,mrna_for_protein_tyrosine_phosphatase_

z48579cds_1852-2050:in_reversesequence,_2062-2392,mrna_for_disintegrin-metalloprotease_(partial)_
reverse_z84722_11257-
11453,dna_sequence_from_cosmid_gg4_from_a_contig_from_the_tip_of_the_short_arm_

Metagene 452

m38180mrna_1319-1623,3-beta-hydroxysteroid_dehydrogenase/delta-5-delta-4-isomerase_(3-beta-hsd)_gene

Metagene 453

d16481_1438-1942,mrna_for_mitochondrial_3-ketoacyl-coa_thiolase_beta-subunit_of_trifunctional_protei
d50914_1543-2077,mrna_for_kiaa0124_gene,_partial_cds_
d82060_1801-
2215,kidney_mrna_for_putative_membrane_protein_with_histidine_rich_charge_clusters,_comp
d83778_4662-5154,mrna_for_kiaa0194_gene,_partial_cds_
d87443_5442-5988,mrna_for_kiaa0254_gene,_complete_cds
hg1400-ht1400_s_at_hg1400-
ht1400_carboxyl_methyltransferase,_aspartate,_altspllice_1
hg2463-ht2559_at_hg2463-ht2559_guanine_nucleotide-binding_protein_g25k_106845_1728-2268,cysteiny1-trna_synthetase_mrna,_partial_cds_
l13278_1231-1753,zeta-crystallin/quinone_reductase_mrna,_complete_cds_
l13773_8844-9252,af-4_mrna,_complete_cds_
l21954exon_36-384:not_in_gb_record,peripheral_benzodiazepine_receptor_gene
l25085_103-361,sec61-complex_beta-subunit_mrna,_complete_cds_
l38961_1919-
2429,putative_transmembrane_protein_precursor_(b5)_mrna,_complete_cds
l42572mrna_2192-2648,p87/89_gene,_complete_cds
m14200mrna_139-469,diazepam_binding_inhibitor_(dbi)_mrna,_complete_cds
m24400mrna_282-840,chymotrypsinogen_mrna,_complete_cds_
m31899_2318-2708,dna_repair_helicase_(ercc3)_mrna,_complete_cds
m64992_741-1185,prosomeal_protein_p30-33k_(pros-30)_mrna,_complete_cds
m65131mrna_2187-2709,methylmalonyl-coa_mutase_(mcm)_mrna,_complete_cds
m73547_2649-3153,polyposis_locus_(dpl_gene)_mrna,_complete_cds_
m83233_3488-3974,transcription_factor_(htf4a)_mrna,_complete_cds
s74728_1245-
1773,_antiquitin=26g_turgor_protein_homolog_[human,kidney,_mrna,_1809_nt]
s78569_5723-6161,_laminin_alphachain_[human,_fetal_lung,_mrna,_6204_nt]
u10117mrna_474-954,endothelial-monocyte_activating_polypeptide_ii_mrna,_complete_cds_
u10439_5983-6529,double-stranded_rna_adenosine_deaminase_mrna,_complete_cds
u12535_3273-
3783,epidermal_growth_factor_receptor_kinase_substrate_(eps8)_mrna,_complete_cd
s_
u14193_135-687,tfiia_gamma_subunit_mrna,_complete_cds
u15009_25-541,snrnp_core_protein_sm_d3_mrna,_complete_cds
u26312_166-686,heterochromatin_protein_hplhs-gamma_mrna,_complete_cds
u28686_973-1486,putative_rna_binding_protein_rnpl_mrna,_complete_cds_
u41654_1159-1525,adenovirus_protein_e3-14.7k_interacting_protein(fip-1)_mrna,_complete_cds

u41740_7119-7635,trans-golgi_p230_mrna,_complete_cds_
 u43899_2320-2740,signal_transducing_adaptor_molecule_stam_mrna,_complete_cds_
 u50523_858-1344,brca2_region,_mrna_sequence_cg037
 u50950_1546-2074,infant_brain_unknown_product_mrna,_complete_cds_
 u57099_666-1158,apeg-1_mrna,_complete_cds
 u67319_2133-2529,lice2_beta_cysteine_protease_mrna,_complete_cds.
 u69645_551-1037,zinc_finger_protein_mrna,_complete_cds_
 u70987_1308-1830,gap_binding_protein_p62dok_(dok)_mrna,_complete_cds_
 u93237mrna#1_2162-
 2738,_men1_gene_(menin)_extracted_frommenin_(men1)_gene,_complete_cds.
 all_x12791_311-870,mrna_for_19kd_protein_of_signal_recognition_particle_(srp)
 x52151cds_1148-1394:in_reversesequence,_1884-
 1980,arylsulphatase_a_mrna,_complete_cds
 x52730mrna#1_455-911,_phenylethanolamine_n-
 methyltransferase_gene_extracted_fromgene_for_phenylethan
 x54326cds_4149-4299:in_reversesequence,_4363-4507,mrna_for_glutaminyll-
 trna_synthetase_
 all_x63469_962-1467,mrna_for_transcription_factor_tfiie_beta_
 all_x65644_8589-9100,mrna_mbp-2_for_mhc_binding_protein_2
 x75535exon#8_2216-2768,mrna_for_pxf_protein
 all_x75962_913-1340,mrna_for_ox40_homologue
 all_x77548_2835-3418,_hsapiens_cdna_for_rfg_
 all_x84195_230-723,mrna_for_acylphosphatase,_muscle_type_(mt)_isoenzyme
 x99296exon#1_28-
 223,_rd_fromrd_gene_(5'_partial)_and_g11a_gene_(5'_partial)/gb=x99296/_ntype=dn
 a/_an
 all_y00264_2984-3321,mrna_for_amyloid_a4_precursor_of_alzheimer_disease
 all_z22551_4012-4595,kinectin_gene_
 z46973cds_2460-2634:in_reversesequence,_2711-
 2891,mrna_for_phosphatidylinositol_3-kinase
 z97074_852-1176,mrna_for_rab9_effector_p40,_complete_cds

Metagene 454

all_102326_2-320,(clone_hu_lambda-17)_lambda-like_gene,_complete_cds
 all_m34516_426-
 469,omega_light_chain_protein_14.1_(ig_lambda_chain_related)_gene,omega_light_c
 hain_p
 all_m34516_426-
 469,omega_light_chain_protein_14.1_(ig_lambda_chain_related)_gene,omega_light_c
 hain_p
 m63438_794-1195,ig_rearranged_gamma_chain_mrna,_v-j-c_region_and_complete_cds
 m87789_1021-1512,(hybridoma_h210)_anti-
 hepatitis_a_igg_variable_region,_constant_region,_complementa
 v00563mrna_19-127,gene_for_immunoglobulin_mu,_part_of_exon_8.
 x53961cds_1772-2060:in_reversesequence,_2450-2564,mrna_for_lactoferrin
 x57809mrna_309-
 449,rearranged_immunoglobulin_lambda_light_chain_mrna,rearranged_immunoglobulin
 _lambd

Metagene 455

l12060mrna_1032-1411,retinoic_acid_receptor_(gamma-7)_mrna

132832_11295-11853,zinc_finger_homeodomain_protein_(atbf1-
a)_mrna,_complete_cds.
133842mrna_1213-1639,(clone_ffe-
7)_type_ii_inosine_monophosphate_dehydrogenase_(impdh2)_gene,_exons_
136644mrna_3085-3137,receptor_protein-tyrosine_kinase_(hek7)_mrna,_3'_end_
149219exon_2-42:in_reversesequence,_70-
79,retinoblastoma_susceptibility_protein_(rb1)_1486wbp_deleti
u21943_2246-
2678,organic_anion_transporting_polypeptide_(oatp)_mrna,_complete_cds
u41767_2113-2688,metargidin_precursor_mrna,_complete_cds_
u46461_1591-2152,dishevelled_homolog_(dvl)_mrna,_complete_cds
u50062_1713-2181,rip_protein_kinase_gene,_complete_cds_
x52213cds_810-1371,ltk_mrna
x57025mrna_6635-7151,igf-i_mrna_for_insulin-like_growth_factor_i_
x66142cds_2216-2539:in_reversesequence,_2600-
2643,mrna_for_rod_cgmp_phosphodiesterase_
x99897cds_6561-6760:in_reversesequence,_7057-7274,mrna_for_p/q-
type_calcium_channel_alpha1_subunit_

Metagene 456

u30246_3599-4019,bumetanide-sensitive_na-k-
cl_cotransporter_(nkcc1)_mrna,_complete_cds_

Metagene 457

d10202_1209-1557,mrna_for_platelet-activating_factor_receptor,_complete_cds
d13643_3585-4131,mrna_for_kiaa0018_gene,_complete_cds
d49387_401-917,mrna_for_nadp_dependent_leukotriene_b4_12-
hydroxydehydrogenase,_partial_cds/gb=d49387
hg4606-ht5011_at_hg4606-ht5011_centractin,_alpha_
j03890mrna#1_482-1022:not_in_gb_record,_sp-
cl_gene_(pulmonary_surfactant_protein_sp-c)_extracted_fro
k03195_2303-2813,(hepg2)_glucose_transporter_gene_mrna,_complete_cds_
l13210_1668-2214,mac-2_binding_protein_mrna,_complete_cds
l20348exon_15-219:not_in_gb_record,oncomodulin_gene
l42563mrna_3011-3443,(clone_lsw34)_non-gastric_h,k-atpase_(atp1a1)_gene
m27504_2078-
2626,topoisomerase_type_ii_(topo_ii)_mrna,_partial_cds/gb=m27504/_ntype=rna_
m28215_130-676,gtp-binding_protein_(rab5)_mrna,_complete_cds
u20648_316-766,zinc_finger_protein_(znf154)_mrna,_partial_cds
y00318cds#1_1317-1653:in_reversesequence,_1814-
1916,mrna_for_complement_control_protein_factor_i
all_z15108_1535-2130,mrna_for_protein_kinase_c_zeta

Metagene 458

hg2339-ht2435_at_hg2339-ht2435_nuclear_factor_1,_variant_hepatic_
l11702_2837-3335,phospholipase_d_mrna,_complete_cds
l38820exon_170-620,hmc_i_antigen-like_glycoprotein_(cd1d)_gene
m93119_2345-2777,zinc-finger_dna-binding_motifs_(ia-1)_mrna,_complete_cds

all_u34301_1497-
 1528,nonmuscle_myosin_heavy_chain_iib_gene,_promoter_region_and_exon/gb=u34301_/
 ntyp
 u66497_3549-4047,leptin_receptor_splice_variant_form_13.2_mrna,_complete_cds.
 u73191_1078-1582,inward_rectifier_potassium_channel_(kir1.3),_complete_cds_
 all_x75756_3248-3699,mrna_for_protein_kinase_c_mu

Metagene 459

d21853_1111-1543,mrna_for_kiaa0111_gene,_complete_cds
 d79986_4973-5513,mrna_for_kiaa0164_gene,_complete_cds
 d87077_5465-5975,mrna_for_kiaa0240_gene,_partial_cds_
 hg3076-ht3238_s_at_hg3076-
 ht3238_heterogeneous_nuclear_ribonucleoprotein_k,_altsplice_1
 hg3514-ht3708_at_hg3514-ht3708_tropomyosin_tm30nm,_cytoskeletal
 hg4322-ht4592_at_hg4322-ht4592_tubulin,_beta_
 j02621mrna_653-1214,non-histone_chromosomal_protein_hmg-14_mrna,_complete_cds
 j04029_1450-
 2007,keratintype_i_intermediate_filament_(krt10)_mrna,_complete_cds_
 j04152mrna_1181-1648,_mls1_gene_extracted_fromgastrointestinal_tumor-
 associated_antigen_ga733-1_prot
 l37368_1849-2359,(clone_e5.1)_rna-binding_protein_mrna,_complete_cds_
 l40397mrna_979-1267,(clone_s31i125)_mrna,_3'_end_of_cds_
 l42379mrna_2645-3155,bone-derived_growth_factor_(bpgf-1)_mrna,_complete_cds_
 m16342mrna#2_1287-
 1581,nuclear_ribonucleoprotein_particle_(hnrrp)_c_protein_mrna,_complete_cds_
 m19311mrna_520-
 1052,calmodulin_mrna,_complete_cds,calmodulin_mrna,_complete_cds_
 m23379_3723-4179,gtpase-activating_protein_ras_p21_(rasa)_mrna,_complete_cds_
 u00947_1301-1347,clone_c4e_3.2_(cac)n/(gtg)n_repeat-containing_mrna
 u06631_3269-3779,(h326)_mrna,_complete_cds_
 u20998_973-1417,signal_recognition_particle_subunit(srp9)_mrna,_complete_cds_
 u35048_1159-1675,tsc-22_protein_mrna,_complete_cds_
 u35451_1643-2027,heterochromatin_protein_p25_mrna,_complete_cds
 u57877_766-1144,integral_membrane_protein_cii-
 3_mrna,_nuclear_gene_encoding_mitochondrial_protein,_c
 u77948_2714-3236,bruton_tyrosine_kinase-associated_protein-
 135_mrna,_complete_cds
 u79282_1087-1651,clone_23801_mrna_sequence_
 u90549_1452-1932,non-histone_chromosomal_protein_(nhc)_mrna,_complete_cds
 u90551_1071-1623,histone_2a-like_protein_(h2a/l)_mrna,_complete_cds
 u95740mrna#1_5316-
 5856,_362g6.1_gene_(unknown_protein_cit987sk_362g6_1)_extracted_fromchromosome_
 16p
 x01703exon#4_929-1151,gene_for_alpha-tubulin_(b_alpha_1)_
 x15729cds_1538-1820:in_reversesequence,_2069-2215,mrna_for_nuclear_p68_protein
 x59405exon#12_1560-2040,_h.sapiens,_gene_for_membrane_cofactor_protein
 all_x63753_5116-5621,son-a_mrna
 all_x68194_1513-2090,h-sp1_mrna
 all_x72841_1378-1937,ief_7442_mrna_
 all_x74104_650-1059,mrna_for_trap_beta_subunit_
 all_x75304_9705-10252,giantin_mrna_
 x81003mrna_1032-1560,hcg_v_mrna
 all_x81198_3084-3673,mrna_(clone_p5)_for_archain_
 all_x81625_3058-3617,mrna_for_cll1_protein

all_x84908_3722-3975,mrna_for_phosphorylase-kinase,_beta_subunit_
 all_x86098_2367-2704,mrna_for_bs69_protein_
 all_x95648_1063-1658,mrna_for_eif-2b_alpha_subunit_
 all_z72499_3157-3740,mrna_for_herpesvirus_associated_ubiquitin-
 specific_protease_(hausp) .

Metagene 460

m62994_1478-1964,thyroid_autoantigen_(truncated_actin-
 binding_protein)_mrna,_complete_cds_
 u00968_3595-4069,srebp-1_mrna,_complete_cds
 u53468_862-
 1390,nadh:ubiquinone_oxidoreductase_subunit_b13_(b13)_mrna,_complete_cds
 u79751_2171-2615,basic-leucine_zipper_nuclear_factor_(jem-
 1)_mrna,_complete_cds/gb=u79751_/ntype=rna
 x14885mrna_2506-2558,gene_for_transforming_growth_factor-beta(tgf-
 beta_3)_exon(and_joined_cds)

Metagene 461

hg4340-ht4610_at_hg4340-ht4610_soxa
 u63332_3-361,super_cysteine_rich_protein_mrna,_partial_cds.
 u77413_2543-2975,o-
 linked_glcnae_transferase_mrna,_complete_cds/gb=u77413_/ntype=rna_
 x97675mrna_3636-
 4212,_plakophilin_2a_gene_extracted_frommrna_for_plakophilin_2a_and_b_
 all_z80781_583-748,h2b/j_gene

Metagene 462

d88155cds_1025-1357:in_reversesequence,_439-576,dna_for_ad4bp_(sf-1)_gene_
 hg3925-ht4195_at_hg3925-ht4195_surfacant_protein_sp-a2_delta_
 j02960cds#1_394-729:in_reversesequence,_1015-
 1252,_unknown_protein_gene_extracted_frombeta-2-adrener
 178833exon#24_1038-
 1476,_brca1_gene_extracted_frombrca1,_rho7_and_vati_genes,_complete_cds,_and_ip
 f3
 m16937_806-1310,homeo_box_c1_protein,_mrna,_complete_cds_
 all_m21064_1360-1426,migration_inhibitory_factor-
 related_protein(mrp14)_gene,_complete_cds_
 m76558_7124-7592,neuronal_dhp-sensitive,_voltage-
 dependent,_calcium_channel_alpha-1d_subunit_mrna,_c
 u18548exon_620-1046,gpr12_g_protein_coupled-receptor_gene,_complete_cds
 u29195exon_927-1443,neuronal_pentraxin_ii_(nptx2)_gene_
 u32324_1353-1671,interleukin-11_receptor_alpha_chain_mrna,_complete_cds
 u92027_524-1028,clone_61501_defective_mariner_transposon_hsmar2_mrna_sequence
 all_x15218_3012-3511,ski_oncogene_mrna_
 x51954exon_10-
 148,ucp_gene_for_uncoupling_protein_exon/gb=x51954_/ntype=dna_/annot=exon_
 x52282cds_1092-
 1597,mrna_for_atrial_natriuretic_peptide_clearance_receptor_(anp-c_receptor)

all_x96698_662-1245,mrna_for_d1075-like_gene_
y09615cds_891-1131:in_reversesequence,_1268-
1472,mrna_for_mitochondrial_transcription_termination_fa
y13618_7553-7895,mrna_for_dffry_protein,_abundant_transcript
z73677mrna_91-137,gene_encoding_plakophilin_1b.

Metagene 463

hg2709-ht2805_at_hg2709-ht2805_serine/threonine_kinase_
hg3137-ht3313_at_hg3137-ht3313_zinc_finger_protein_znf81_
hg4052-ht4322_at_hg4052-ht4322_glutamate_ionotropic_receptor
m13666_800-992,c-myb_mrna,_3'_end
m15656cds_712-1066:in_reversesequence,_3992-4082,aldolase_b_(aldob)_gene
m54995_108-603,connective_tissue_activation_peptide_iii_mrna,_complete_cds_
s69790_962-1412,_brush-
1=tumor_suppressor_{3'_region}_[human,_breast_epithelium,_mrna_partial,_1485_
all_x53065_85-462,spr2-1_gene_for_small_proline_rich_protein_(exon_2)
y10571cds_696-978:in_reversesequence,_1002-1194,mrna_for_ding_gene
all_y11897_19-320,brx_gene_3'_utr/gb=y11897/_ntype=rna_
z75330cds_3384-3714:in_reversesequence,_4156-4312,mrna_for_nuclear_protein_sa-
1.

Metagene 464

d16593_290-812,bdr-2_mrna_for_hippocalcin,_complete_cds
d88460_1233-1695,mrna_for_n-wasp,_complete_cds_
d89016_1618-2116,mrna_for_neuroblastoma,_complete_cds
hg2280-ht2376_at_hg2280-ht2376_d-amino-acid_oxidase
hg908-ht908_at_hg908-ht908_mg61_protein
100635_1029-1437,farnesyl-protein_transferase_beta-subunit_mrna,_complete_cds
134355_827-961,(clone_p4)_50_kd_dystrophin-
associated_glycoprotein_mrna,_complete_cds_
136818_4098-4608,(clone_51c-3)_51c_protein_mrna,_complete_cds
144140exon#61-62_44-
221:not_in_gb_record,_dn111_gene_extracted_fromchromosome_x_region_from_filamin
-
m38258_2000-2486,retinoic_acid_receptor_gammamrna,_complete_cds_
m77348mrna_1757-1786,pmelmrna,_complete_cds_
m92432_3098-3566,retinal_guanylyl_cyclase_(retgc)_mrna,_complete_cds
m96759mrna_783-1299,rod_outer_segment_membrane_protein(rom1)_gene_exons_1-
3,_complete_cds
all_s58733_264-
357,_pp52=b_lymphocyte_signal_transduction_gene_{group_3,_inverted_repeat}_[hum
an,_tu
u07418_2004-2454,dna_mismatch_repair_(hmlh1)_mrna,_complete_cds
u37529_556-1030,substance_p_beta-ppt-a_mrna,_complete_cds
u43177exon#1_62-464,urocortin_gene,_complete_cds_
u49928_2513-3035,tak1_binding_protein(tab1)_mrna,_complete_cds
u62966_2137-2635,na+/nucleoside_cotransporter_(hcnt1a)_mrna,_complete_cds
u68536_1918-2410,zinc_finger_protein_mrna,_complete_cds
u71087_1092-1126,map_kinase_kinase_mek5b_mrna,_complete_cds
u92314_840-
1415,hydroxysteroid_sulfotransferase_sult2b1a_(hsst2)_mrna,_complete_cds.

all_x06256_3681-4180,mrna_for_fibronectin_receptor_alpha_subunit_
 all_x13589_2395-2936,mrna_for_aromatase_(estrogen_synthetase)
 all_x54871_1059-1612,mrna_for_ras-related_protein_rab5b
 all_x86681_1848-2257,mrna_for_nucleolar_protein_hnp36_
 all_x94453_2396-2907,mrna_for_pyrroline_5-carboxylate_synthetase_

Metagene 465

af015913_1437-1947,skblhs_mrna,_complete_cds/gb=af015913_/ntype=rna_
 d11428_1253-1757,mrna_for_pmp-22(pas-ii/sr13/gas-
 3)_of_peripheral_myelin,_complete_cds_
 d16294_1019-1523,mrna_for_mitochondrial_3-oxoacyl-coa_thiolase,_complete_cds_
 d21063_2853-3303,mrna_for_kiaa0030_gene,_partial_cds_
 d38524_2673-3213,mrna_for_5'-nucleotidase_
 d63476_4587-4953,mrna_for_kiaa0142_gene,_complete_cds_
 hg1827-ht1856_s_at_hg1827-
 ht1856_cytochrome_p450,_subfamily_iic,_altssplice_form_2
 hg2981-ht3127_s_at_hg2981-ht3127_epican,_altssplice_11
 hg3521-ht3715_at_hg3521-ht3715_ras-related_protein_rap1b_
 j05682_1023-1575,subunit_c_of_v-atpase_(vat_c)_mrna,_3'_end
 l28997_443-953,arll1_mrna,_complete_cds_
 l31801_2229-2535,monocarboxylate_transporter(slc16a1)_mrna,_complete_cds_
 m25753mrna_1103-1427,cyclin_b_mrna,_3'_end_
 all_m27161_6940-7265,mhc_i_cd8_alpha-chain_(leu-2/t8)_gene,_complete_cds_
 m67468_3244-3720,fragile_x_mental_retardationfmr-
 1_gene,_3'_end,_clones_bc72_and_bc22_
 m74524_1190-1658,hhr6a_(yeast_radhomologue)_mrna,_complete_cds_
 m90656_2044-2590,gamma-glutamylcysteine_synthetase_(gcs)_mrna,_complete_cds_
 u00001_2019-2547,homologue_of_spombe_nuc2+_and_anidulans_bima
 u01833_690-1164,nucleotide-binding_protein_mrna,_complete_cds_
 u09564_3725-4205,serine_kinase_mrna,_complete_cds_
 u15128cds_1011-1299:in_reversesequence,_2065-2233,beta-1,2-n-
 acetylglucosaminyltransferase_ii_(mgat2
 u17714_2774-
 3068:not_in_gb_record,putative_tumor_suppressor_(snc6)_mrna,_complete_cds_
 u27460_1582-1798,uridine_diphosphoglucose_pyrophosphorylase_mrna,_complete_cds_
 u39318_159-
 675,e2_ubiquitin_conjugating_enzyme_ubch5c_(ubch5c)_mrna,_complete_cds_
 u61145_2035-2509,enhancer_of_zeste_homolog(ezh2)_mrna,_complete_cds_
 u61232_1407-1869,tubulin-folding_cofactor_e_mrna,_complete_cds_
 u69141_1311-1719,glutaryl-coa_dehydrogenase_mrna,_complete_cds_
 u72263_2410-
 2931,multiple_exostoses_type_ii_protein_ext2.i_mrna,_complete_cds/gb=u72263_/nt
 ype=rna_
 u88047_1567-1969,dna_binding_protein_homolog_(drx)_mrna,_partial_cds_
 all_x02160_4717-4976,mrna_for_insulin_receptor_precursor_
 all_x54993_1096-1685,tfiid_mrna_
 all_x56807_2617-3194,dsc2_mrna_for_desmocollins_type_2a_and_2b_
 x59244mrna_2391-2967,znf43_mrna_
 x61100mrna_1983-
 2445,_75_kda_subunit_nadh_dehydrogenase_precursor_gene_extracted_frommrna_for_m
 itoch
 all_x63468_2398-2915,mrna_for_transcription_factor_tfiie_alpha_
 all_x64229_888-1393,dek_mrna_

x65867cds#1_1157-1409:in_reversesequence,_1447-
 1639,mrna_for_adenylosuccinate_lyase_
 all_x79201_2342-2775,mrna_for_syt
 x85753_1268-1646,mrna_for_cdk8_protein_kinase
 y00971mrna_1891-
 2419,mrna_for_phosphoribosyl_pyrophosphate_synthetase_subunit_ii_(ec_2.7.6.1)-
 y09943cds_117-452:in_reversesequence,_561-602,mrna_for_ngf-inducible_pc3_anti-
 proliferative_protein_

Metagene 466

hg3920-ht4521_s_at_hg3920-ht4521_homeotic_protein_a1,_i,_altsplice_1_
 hg4517-ht4920_s_at_hg4517-
 ht4920_immunoglobulin_recombination_signal_sequence_binding_protein,_altsp
 l34155_4838-5306,laminin-related_protein_(lama3)_mrna,_complete_cds_
 m21305cds_39-
 119,alpha_satellite_and_satellitejunction_dna_sequence/gb=m21305_/ntype=dna_/an
 not=cds_
 u60808_1423-2000,cdp-diacylglycerol_synthase_(cds)_mrna,_complete_cds
 x60673mrna_1091-1649,ak3_mrna_for_adenylate_kinase_3

Metagene 467

d38502_850-
 1120,pms4_mrna_(yeast_mismatch_repair_gene_pms1_homologue),_partial_cds_(c-
 terminal_regio
 d84145_458-980,ws-3_mrna,_complete_cds_
 hg1828-ht1857_at_hg1828-ht1857_nexin,_glia-derived_
 hg3513-ht3707_at_hg3513-ht3707_myosin,_heavy_polypeptide,_light_meromyosin_
 hg3954-ht4224_s_at_hg3954-ht4224_landsteiner-
 wiener_blood_group_glycoprotein_(lw)
 hg4114-ht4384_at_hg4114-ht4384_olfactory_receptor_or17-209_
 reverse_j04742_384-607:in_j04742cds_49-
 110,autonomous_replicating_sequence_h1_(arsh1)_
 l03785_72-582,regulatory_myosin_light_chain_(myl5)_mrna,_complete_cds
 all_126336_2691-3220,heat_shock_protein_hspa2_gene,_complete_cds_
 l35253_972-1047,p38_mitogen_activated_protein_(map)_kinase_mrna,_complete_cds
 l40388mrna_195-
 675,thyroid_receptor_interactor_(trip15)_mrna,_5'_end_of_cds/gb=l40388_/ntype=r
 na
 all_m21388_2-95,unproductively_rearranged_ig_mu-chain_mrna_v-
 region_(vd),_5'_end,_clone_mu-3a1a.,unp
 m21984_441-951,(clone_pwhtnt16)_skeletal_muscle_troponin_t_mrna,_complete_cds
 m31523_4155-4353,transcription_factor_(e2a)_mrna,_complete_cds_
 m33653_467-965,(clones_ht-[125,133])_alpha-
 2_type_iv_collagen_(col4a2)_mrna,_complete_cds
 m62840mrna_1755-2175,acyloxyacyl_hydrolase_mrna,_complete_cds
 m65134mrna_3588-4102,complement_component_c5_mrna,_3'_end
 m90391_1736-2866,putative_il-16_protein_precursor,_mrna,_complete_cds
 s66427_4218-4764,_rbp1=retinoblastoma_binding_protein[human,_nalm-6_pre-
 b_cell_leukemia,_mrna,_4834_
 s70609_1781-
 2339,_glycine_transporter_type_1b_[human,_substantia_nigra,_mrna,_2364_nt]

s81264_50-243, _hs-tbx2=t-box_gene_{t-
 box_region}_[human, fetal_kidney, _mrna_partial, _283_nt]/gb=s812
 u03486cds_625-1045:in_reversesequence, _1121-1211, connexin40_gene, _complete_cds
 u06632_2039-2579, p80-coilin_mrna, _complete_cds_
 u16997_1218-1764, orphan_receptor_ror_gamma_mrna, _complete_cds
 u19487_1843-2329, prostaglandin_e2_receptor_mrna, _complete_cds
 u21936_2630-3038, peptide_transporter_(hpept1)_mrna, _complete_cds_
 u27459_2534-
 2984, origin_recognition_complex_protein_homolog_horc21_mrna, _complete_cds
 u43318_1805-
 2291, putative_transmembrane_receptor_(frizzled_5)_mrna, _complete_cds_
 u51010_exon_17-222, nicotinamide_n-
 methyltransferase_gene, _exon_and_5'_flanking_region/gb=u51010_/ntype
 u59289_3350-3824, h-cadherin_mrna, _complete_cds_
 u61374_1265-
 1715, novel_protein_with_short_consensus_repeats_of_six_cysteines_mrna, _complete
 _cds
 u61836_mrna_540-
 972, putative_cyclin_g1_interacting_protein_mrna, _partial_sequence_
 u62317_mrna#7_2016-
 2532, _hypothetical_protein_384d8_gene_extracted_from_chromosome_22q13_bac_clone_
 cit
 u66617_2252-
 2786, swi/snf_complex_60_kda_subunit_(baf60a)_mrna, _alternatively_spliced, _compl
 ete_cds_
 u78027_mrna#4_1964-2372, _l44l_gene_(l44-
 like_ribosomal_protein)_extracted_from_bruton_tyrosine_kinase_
 u82256_1325-1823, arginase_type_ii_mrna, _complete_cds_
 u82303_25-313, unknown_protein_mrna, _partial_cds/gb=u82303_/ntype=rna_
 u95020_1276-1786, voltage-dependent_calcium_channel_beta-
 4_subunit_mrna, _complete_cds.
 x04898_mrna_49-445, gene_for_apolipoprotein_a_ii_
 all_x52056_778-1304, mrna_for_spi-1_proto-oncogene
 x59770_mrna_685-1213, il-1r2_mrna_for_type_ii_interleukin-
 1_receptor,_(cell_line_cb23)_
 x61177_mrna_1495-1933, hsil5r2_gene_for_interleukin-5_receptor_type_2
 x79780cds_94-622:in_reversesequence, _646, ypt3_mrna
 all_z35085_1960-2506, mrna_for_unknown_antigen
 z47055cds_437-
 968, partial_cdna_sequence, _farnesyl_pyrophosphate_synthetase_like-
 4/gb=z47055_/ntype=d

Metagene 468

107594_3847-4159, transforming_growth_factor-beta_type_iii_receptor_(tgf-
 beta)_mrna, _complete_cds_
 all_u18422_1719-2254, dp2_(humdp2)_mrna, _complete_cds_

Metagene 469

ab002380_5644-6142, mrna_for_kiaa0382_gene, _partial_cds/gb=ab002380_/ntype=rna
 ab003103_2965-3463, mrna_for_proteasome_subunit_p55, _complete_cds_

af007875_501-
 1029,dolichol_monophosphate_mannose_synthase_(dpm1)_mrna,_partial_cds/gb=af007875_/ntyp
 all_d00596_15645-16192,thymidylate_syntase_(ec_2.1.1.45)_gene,_complete_cds
 d10522_2000-2546,mrna_for_80k-1_protein,_complete_cds
 d11094_973-1345,mrna_for_mss1,_complete_cds
 d13627_1310-1778,mrna_for_kiaa0002_gene,_complete_cds
 d13641_2748-3216,mrna_for_kiaa0016_gene,_complete_cds
 d26069_5879-6455,mrna_for_kiaa0041_gene,_partial_cds_
 d43951_4874-5264,mrna_for_kiaa0099_gene,_complete_cds
 d49493exon#3_403-811,gene_forbone_morphogenetic_protein-3b
 d49738_456-990,cytoskeleton_associated_protein_(cg22)_mrna,_complete_cds_
 d78132_373-907,mrna_for_ras_homologue_enriched_in_brain_(rheb)_gene,_ras-related_gtp_binding_protein
 d86956_3139-3589,mrna_for_kiaa0201_gene,_complete_cds
 d87127_2088-2448,mrna_for_translocation_protein-1,_complete_cds
 d87684_3222-3696,mrna_for_kiaa0242_gene,_partial_cds_
 j03473mrna_3212-3752,poly(adp-ribose)_synthetase_mrna,_complete_cds
 l40357mrna_7-463,thyroid_receptor_interactor_(trip7)_mrna,_3'_end_of_cds
 l41887mrna#1_1773-2277,splicing_factor,_arginine/serine-rich(sfrs7)_gene,_complete_cds
 l43631_2189-2753,scaffold_attachment_factor_(saf-b)_gene,_partial_cds_
 m11353_707-1226,h3.3_histone_c_mrna,_complete_cds
 ml4764mrna_2785-3337,nerve_growth_factor_receptor_mrna,_complete_cds_
 m93425_2577-3111,protein_tyrosine_phosphatase_(ptp-pest)_mrna,_complete_cds
 u14575_1842-2328,(ard-1)_mrna,_complete_cds
 u28042_2726-3104,dead_box_rna_helicase-like_protein_mrna,_complete_cds_
 u31814_1366-1876,transcriptional_regulator_homolog_rpd3_mrna,_complete_cds_
 u34252_2177-2579,gamma-aminobutyraldehyde_dehydrogenase_mrna,_complete_cds_
 u37547_2931-3477,iap_homolog_b_(mihb)_mrna,_complete_cds_
 u41815_3037-3559,nucleoporin_98_(nup98)_mrna,_complete_cds_
 u49844_7699-8095,frap-related_protein_(frp1)_mrna,_complete_cds
 u50534_10101-10671,brca2_region,_mrna_sequence_cg003_
 u59863_1541-2039,traf-interacting_protein_i-traf_mrna,_complete_cds
 u61234_986-1490,tubulin-folding_cofactor_c_mrna,_complete_cds
 u73737mrna_4359-4785,hmsh6_gene,_5'_utr_and
 u78575_3124-3634,68_kda_type_i_phosphatidylinositol-4-phosphate_5-kinase_alpha_mrna,_clone_pip5kia1,
 u79291_756-1287,clone_23721_mrna_sequence
 all_x65488_2664-3169,u21.1_mrna
 y14140exon_13-
 185,g_protein_gene_encoding_betasubunit_exonand_promoter/gb=y14140_/ntype=dna_/annot=e
 all_z29066_1451-2035,nek2_mrna_for_protein_kinase

Metagene 470

d49677_905-1445,u2af1-rs2_mrna,_complete_cds_
 hg2797-ht2905_s_at_hg2797-ht2905_clathrin,_light_polypeptide_altsplice_1
 l22548_2914-3334,collagen_type_xviii_alpha(coll18a1)_mrna,_partial_cds_
 l27624_373-917,tissue_factor_pathway_inhibitor-2_mrna,_complete_cds_
 m57710_355-865,ige-binding_protein_(epsilon-bp)_mrna,_complete_cds_
 s54005_2-197,_thymosin_beta-
 10_[human,_metastatic_melanoma_cell_line,_mrna,_453_nt]_

s75295_2339-
 2915, _nucleoprotein_interactor_1=srp1_homolog_[human, _cervical_carcinoma_hela_c
 ells, _mrn
 s81578_13-271, _dioxin-
 responsive_gene_{putative_polyadenylation_signal_region}_[human, _hepatoma_g2_c
 u09410_1481-2003, zinc_finger_protein_znf131_mrna, _partial_cds
 u26648_936-1482, syntaxin_mrna, _complete_cds
 u46025cds_2254-2710:in_reversesequence, _2777-
 2843, translation_initiation_factor_eif-3_p110_subunit_g
 all_x57348_844-1377, mrna_(clone_9112)
 all_x66087_3046-3563, a-myb_mrna
 all_x69433_1312-1733, mrna_for_mitochondrial_isocitrate_dehydrogenase_(nadp+)_
 x70476mrna_2526-3024, subunit_of_coatomer_complex_
 x98507cds_2790-3018:in_reversesequence, _3131-3293, mrna_for_myosin-i_beta
 y08136cds_292-496:in_reversesequence, _520-820, mrna_for_asm-
 like_phosphodiesterase_3a

Metagene 471

d21852_3671-4241, mrna_for_kiaa0029_gene, _partial_cds_
 d25303_2993-3539, mrna_for_integrin_alpha_subunit, _complete_cds_
 d25538_5613-6147, mrna_for_kiaa0037_gene, _complete_cds_
 d28791exon_1763-2267, pig-a_gene, _5'_flanking_region_and
 d30758_1965-2469, mrna_for_kiaa0050_gene, _complete_cds_
 d42041_3435-3771, mrna_for_kiaa0088_gene, _partial_cds_
 d50911_3298-3718, mrna_for_kiaa0121_gene, _complete_cds_
 d63506_1940-2435, mrna_for_unc-18homologue, _complete_cds_
 d79983_5024-5498, mrna_for_kiaa0161_gene, _complete_cds_
 d80003_6029-6395, mrna_for_kiaa0181_gene, _partial_cds_
 d83032_6016-6364, mrna_for_nuclear_protein, _np220, _complete_cds_
 d83777_4475-5003, mrna_for_kiaa0193_gene, _complete_cds_
 d86962_5028-5328, mrna_for_kiaa0207_gene, _complete_cds_
 d86969_4436-4886, mrna_for_kiaa0215_gene, _complete_cds_
 j03161mrna_3636-4122, serum_response_factor_(srf)_mrna, _complete_cds_
 j03779mrna_4985-
 5459, common_acute_lymphoblastic_leukemia_antigen_(calla)_mrna, _complete_cds_
 l19067_2335-2419, nf-kappa-b_transcription_factor_p65_subunit_mrna, _complete_cds_
 l29218mrna_1408-1894, clk2_mrna, _complete_cds_
 l35035mrna_629-1079, ribose_5-phosphate_isomerase_(rpi)_mrna_
 l35240cds_1065-1323:in_reversesequence, _1431-1533, enigma_gene, _complete_cds_
 all_m16505_6015-6520, steroid_sulfatase_(sts)_mrna, _complete_cds_
 m23161_3287-3791, transposon-like_element_mrna
 m29550_2005-2317, calcineurin_a1_mrna, _complete_cds_
 m33552mrna_1042-1546, lymphocyte-specific_protein(lsp1)_mrna, _complete_cds_
 m34057_4720-5044, transforming_growth_factor-
 betabinding_protein_mrna, _complete_cds_
 m87770_3759-4125, fibroblast_growth_factor_receptor_(k-sam)_mrna, _complete_cds_
 u02031_3660-4182, sterol_regulatory_element_binding_protein-2_mrna, _complete_cds_
 u16660_685-1153, peroxisomal_enoyl-coa_hydratase-
 like_protein_(hpxel)_mrna, _complete_cds_
 u35376_2006-2254, repressor_transcriptional_factor_(znf85)_mrna, _complete_cds_
 u58048_1891-2431, metalloproteinase_prsm1_mrna, _complete_cds_
 u73524_1866-2304, putative_atp/gtp-binding_protein_(heab)_mrna, _complete_cds_

u78556_2774-
 3248,cisplatin_resistance_associated_alpha_protein_(hcra_alpha)_mrna,_complete_cds_
 all_x16396_1543-2102,mrna_for_nad-
 dependent_methylene_tetrahydrofolate_dehydrogenase_cyclohydrolase_
 all_x77744_1467-1750,f11_mrna
 x90780mrna_255-765,cardiac_troponin_i_gene,_exonsto_5
 all_z48481_2878-3347,mrna_for_membrane-type_matrix_metalloproteinase_1_

Metagene 472

h46990_40-
 355,_yol6d02.s1cdna_clone_178083_3'_similar_to_gb:j02625_cytochrome_p450_1ie1_(human);
 m86873mrna_155-367,type_a_plasminogen_related_gene_
 s42303_3537-4029,_n-
 cadherin_[human,_umbilical_vein_endothelial_cells,_mrna,_4132_nt]_
 all_z80776_596-795,h2a/g_gene

Metagene 473

j00219cds_110-467:in_reversesequence,_4721-4823,immune_interferon_(ifn-gamma)_gene,_complete_cds
 s78873_291-
 835,_mss4=zn2+_binding_protein/guanine_nucleotide_exchange_factor_[human,_brain,_mrna_par
 all_s83366_910-
 2840,_region_centromeric_to_t(12;17)_breakpoint:_orf1/unknown_43_amino_acid_tra
 nscrip
 y10515mrna_79-307,mrna_for_cd58_t7_protein/gb=y10515/_ntype=rna
 z83800_115-505,mrna_for_cytoplasmic_dynein_heavy_chain_(partial,_id_hdhc11)

Metagene 474

d83243_5401-5857,npat_mrna,_complete_cds_
 hg4297-ht4567_at_hg4297-ht4567_transcriptional_coactivator_pc4_
 122075_795-1377,guanine_nucleotide_regulatory_protein_(gl3)_mrna,_complete_cds_
 140157_4445-4907,endosome-associated_protein_(eeal)_mrna,_complete_cds_
 140400mrna_2014-2542,(clone_zap113)_mrna,_3'_end_of_cds_
 176571cds_440-734:in_reversesequence,_1070-
 1310,nuclear_hormone_receptor_(shp)_gene,_3'_end_of_cds
 s62028_496-1041,_recoverin_[human,_retina,_mrna,_1108_nt]_
 u31248_1663-2209,zinc_finger_protein_(znf174)_mrna,_complete_cds_
 u49516_4157-4691,serotonin_5-ht2c_receptor_mrna,_complete_cds
 x53595cds_525-1007:in_reversesequence,_1054-1104,mrna_for_beta-2-
 glycoprotein_i_(apolipoprotein_h)
 x90858cds#2_396-888:in_reversesequence,_1270-
 1306,mrna_for_uridine_phosphorylase

Metagene 475

d31889_2835-3279,mrna_for_kiaa0072_gene,_partial_cds_
 d82326_2784-3312,mrna_for_na+-
 independent_neutral_and_basic_amino_acid_transporter,_complete_cds_
 d82347_1949-2459,mrna_for_neurod,_complete_cds_
 all_j03756_527-783,growth_hormone-variant_(gh1)_and_growth_hormone-variant-
 2_(gh2)_mrna,_complete_cd_
 l25270_5352-5856,xel69_mrna,_complete_cds
 all_m13934_834-
 l309,_rps14_gene_(unknown_protein)_extracted_fromribosomal_protein_s14_gene,_co
 mplete
 all_m16405_1994-2553,m4_muscarinic_acetylcholine_receptor_gene_
 all_m20543_2890-3542,skeletal_alpha-actin_gene,_complete_cds_
 m90359_2039-2519,camp-dependent_protein_kinase_(akap_79)_mrna,_complete_cds_
 s81893_13-
 331,_mesi3/15=extracellular_matrix_induced_gene_[human,_endometrial_adenocarcin
 oma_cells_h
 u03851_1800-2220,capping_protein_alpha_mrna,_partial_cds_
 u30998_43-166,(nmd)_mrna,_3'_utr/gb=u30998_/ntype=rna
 u90910_1208-1724,clone_23564_mrna_sequence_
 x00129cds_332-566:in_reversesequence,_671-
 851,mrna_for_retinol_binding_protein_(rbp)
 x99101cds_1121-1409:in_reversesequence,_1439-1535,mrna_for_estrogen_receptor
 all_y09858_1990-2483,mrna_for_unknown_protein
 y12856_182-668,mrna_for_amp-activated_protein_kinase_alpha-
 1,_partial/gb=y12856_/ntype=rna_

Metagene 476

d00763_609-1035,mrna_for_proteasome_subunit_hc9
 d14661_1027-1579,mrna_for_kiaa0105_gene,_complete_cds
 d43949_2627-3143,mrna_for_kiaa0082_gene,_partial_cds_
 d63879_3065-3599,mrna_for_kiaa0156_gene,_complete_cds
 d86973_7230-7716,mrna_for_kiaa0219_gene,_partial_cds_
 hg2460-ht2556_at_hg2460-ht2556_integrin_beta
 hg4194-ht4464_at_hg4194-ht4464_sodium/hydrogen_exchanger
 hg4716-ht5158_at_hg4716-ht5158_guanosine_5'_-monophosphate_synthase
 j02963_641-1049,platelet_glycoprotein_iib_mrna,_3'_end_
 j05448_1173-1665,rna_polymerase_subunit_hrp33,_mrna
 all_k01383_2141-2388,metallothionein-i-a_gene,_complete_coding_sequence
 l05500_2226-2688,fetal_brain_adenylyl_cyclase_mrna,_3'_end_
 all_l15440_5674-
 5845,tyrosine_hydroxylase_(th)_gene,_3'_end;_insulin_(ins)_gene,_complete_cds;_
 insul
 l38941mrna_19-343,ribosomal_protein_l34_(rpl34)_mrna,_complete_cds
 m18185mrna_206-656,gastric_inhibitory_polypeptide_(gip)_mrna,_complete_cds_
 m20471_512-1066,brain-type_clathrin_light-chain_a_mrna,_complete_cds_
 m77232mrna_329-
 773,ribosomal_protein_s6_gene,_complete_cds_and_flanking_regions_
 u23803_1125-1659,heterogeneous_ribonucleoprotein_a0_mrna,_complete_cds
 u31120mrna_802-1234:in_reversesequence,_5052,interleukin-13_(il-
 13)_precursor_gene,_complete_cds_
 u37408_1514-2078,ctbp_mrna,_complete_cds_
 u41371_2249-2777,spliceosome_associated_protein_(sap_145)_mrna,_complete_cds_

u68018_1512-1890, mad_protein_homolog_(hmad-2)_mrna, _complete_cds_
u90547_2553-2811, ro/ssa_ribonucleoprotein_homolog_(roret)_mrna, _complete_cds_
u96915_165-693, sin3_associated_polypeptide_p18_(sap18)_mrna, _complete_cds.
x77584cds_5-215:in_reversesequence, _43-481, mrna_for_atl-
derived_factor/thiredoxin_
x85237cds_1957-2311:in_reversesequence, _2480-
2588, mrna_for_splicing_factor_sf3a120
all_x85373_43-404, mrna_for_sm_protein_g
y00764cds_85-235:in_reversesequence, _331-
463, mrna_for_mitochondrial_hinge_protein_
all_z26634_11848-12401, mrna_for_ankyrin_b_(440_kda)

Metagene 477

ab000897_43-373, mrna_for_cadherin_fib3, _partial_cds/gb=ab000897/_ntype=rna
hg3033-ht3194_at_hg3033-ht3194_spliceosomal_protein_sap_62_
hg3426-ht3610_s_at_hg3426-ht3610_zinc_finger_protein_hzf-16, _kruppel-
like, _altsplice_1_
l24559_1634-2078, dna_polymerase_alpha_mrna, _complete_cds
u07139_2039-2459, voltage-gated_calcium_channel_beta_subunit_mrna, _complete_cds_
u36500_2741-3209, lymphoid-specific_sp100_homolog_(lysp100-b)_mrna, _complete_cds_
u46767_288-768, monocyte_chemoattractant_protein-4_precursor_(mcp-
4)_mrna, _complete_cds_
all_u60269_13-524, endogenous_retrovirus_herv-
k(hml6)_proviral_clone_hml6.17_putative_polymerase_and_
x76223exon_2-540, mal_gene_exon_4.
x89267exon#10_225-
312, dna_for_uroporphyrinogen_decarboxylase_gene/gb=x89267/_ntype=dna/_annot=exo
n_
x90978_1187-1751, mrna_for_an_acute_myeloid_leukaemia_protein_(1793bp)

Metagene 478

k02402exon#8_1383-1875, coagulation_factor_ix_gene, _complete_cds
l41162_1879-2419, collagen_alphatype_ix_(col9a3)_mrna, _complete_cds_
all_m21388_2-95, unproductively_rearranged_ig_mu-chain_mrna_v-
region_(vd), _5'_end, _clone_mu-3a1a., unp
all_m29610_446-
476, glycophorin_e_mrna, _complete_cds, glycophorin_e_mrna, _complete_cds
u79286_934-1294, arginine_methyltransferase_mrna, _complete_cds

Metagene 479

ab002318_6384-6786, mrna_for_kiaa0320_gene, _partial_cds/gb=ab002318/_ntype=rna
ac000099_12194-12426:in_ac000099cds_519-
556:in_all_ac000099_12207, _cosmid_g0771a003_
af010193_2552-3044, mad-related_gene_smad7_(smad7)_mrna, _complete_cds
d13634_1915-2419, mrna_for_kiaa0009_gene, _complete_cds
d17516_1075-1615, mrna_for_pacap_receptor, _complete_cds_
d61391_1169-1685, mrna_for_phosphoribosypyrophosphate_synthetase-
associated_protein_39, _complete_cds

d78011_1552-2098,mrna_for_dihydropyrimidinase,_complete_cds
d83920_732-1158,uterus_mrna_forficolin-1,_complete_cds
hg1723-ht1729_at_hg1723-ht1729_macrophage_scavenger_receptor,_altsplise_2
hg315-ht315_at_hg315-ht315_beta-1-glycoprotein_11,_pregnancy-specific
hg3242-ht3419_s_at_hg3242-ht3419_calcium_channel,_voltage-
gated,_alpha_1e_subunit,_altsplise_2_
j03798_1026-1536,autoantigen_small_nuclear_ribonucleoprotein_sm-
d_mrna,_complete_cds_
101664_43-529,eosinophil_charcot-
leyden_crystal_(clc)_protein_(lysophospholipase)_mrna,_complete_cds
103411_798-1260,rd_protein_(rd)_mrna,_complete_cds_
all_105512_1285-1313:not_in_gb_record,histatin(his1)_gene
125441_1410-1890,geranylgeranyltransferase_type_i_beta-
subunit_mrna,_complete_cds
126081_1959-2487,semaphorin-iii_(hsema-i)_mrna,_complete_cds
138929mrna_5668-6190,protein_tyrosine_phosphatase_delta_mrna,_complete_cds
140586_1123-1255,iduronate-2-sulphatase_(ids)_mrna,_complete_cds
141066_2321-2831,nf-at3_mrna,_complete_cds
176670_502-1071,nkat7_mrna,_complete_cds
m58297_2215-2653,zinc_finger_protein_42_(mzf-1)_mrna,_complete_cds_
m91036mrna#1_37-529,_g-gamma_globin_gene_extracted_fromg-gamma_globin_and_a-
gamma_globin_genes,_comp
m95724_2549-2939,centromere_autoantigen_c_(cenpc)_mrna,_complete_cds_
s78203_2096-
2660,_pept_2=h+/peptide_cotransporter_[human,_kidney,_mrna_partial,_2685_nt]
s83365_109-343,_putative_rab5-interacting_protein_{clone_l1-
94}_[human,_hela_cells,_mrna_partial,_36
u07223mrna_1930-2410,beta2-chimaerin_mrna,_complete_cds
u18932_4216-4756,heparan_sulfate-n-deacetylase/n-
sulfotransferase_mrna,_clone_hsst3'__,_3'_utr
u26032_2176-2596,translation_initiation_factor_eif-2alpha_mrna,_3'_utr_
u32581_2488-2884,lambdaiota-protein_kinase_c-
interacting_protein_mrna,_complete_cds_
u52700_70-328,tenascin-
x_(xb)_mrna,_race_clone_n1,_partial_cds/gb=u52700_/ntype=rna
u62438_1545-
1875,nicotinic_acetylcholine_receptor_beta3_subunit_precursor,_mrna,_complete_c
ds
u67932mrna_1128-
1700,camp_phosphodiesterase_(pde7a2)_mrna,_complete_cds/gb=u67932_/ntype=rna_
u68488_1013-1397,5-hydroxytryptamine7_receptor_isoform_d_mrna,_complete_cds
u85267_7-
145,down_syndrome_critical_region(dscr1)_gene,_alternative_exon_1,_partial_cds/
gb=u85267_/n
all_x16667_1634-1917,hox2g_mrna_from_the_hox2_locus
all_x74987_2208-2684,mrna_for_2'-5'oligoadenylate_binding_protein
all_x76040_2954-3309,mrna_for_lon_protease-like_protein
x76498exon#3_63-369:in_reversesequence,_2899-
3043,gene_for_uterine_bombesin_receptor
all_x78520_3490-3935,_hsapiens_rna_for_clcn3
all_x81636_2127-2329,clathrin_light_chain_a_gene_
all_x81637_5805-5938,clathrin_light_chain_b_gene_
all_x91992_1340-1929,mrna_for_alkb_protein_homolog_
x93017exon_1293-1797,ncx2_gene_(exon_2)/gb=x93017_/ntype=dna_/annot=exon_
all_x96753_7313-7896,mrna_for_melanoma-
associated_chondroitin_sulfate_proteoglycan_(mcsp)
all_y00064_1931-2418,mrna_for_secretogranin_i_(chromogranin_b)_

y08991cds_3846-4038:in_reversesequence,_4743-
 4845,mrna_for_adaptor_protein_p150_
 z34897_1138-1654,mrna_for_h1_histamine_receptor

Metagene 480

d38500_574-
 958,pms6_mrna_(yeast_mismatch_repair_gene_pms1_homologue),_partial_cds_(c-
 terminal_region
 hg1751-ht1768_s_at_hg1751-ht1768_chorionic_somatotropin_hormone_cs-5
 hg1783-ht1803_s_at_hg1783-ht1803_islet_amyloid_polypeptide_
 hg4116-ht4386_s_at_hg4116-ht4386_olfactory_receptor_or17-219_
 l14813_856-1147,carboxyl_ester_lipase_like_protein_(cell)_mrna,_complete_cds_
 l76703mrna_2687-3245,b56epsilon_mrna,_complete_cds
 m26856cds_1126-1456:in_reversesequence,_3467-3600,21-
 hydroxylase_b_gene,_complete_cds_
 all_m60746_531-844,histone_h3.1_(h1f3)_gene,_complete_cds
 s52028_582-1141,_cystathionine_gamma-lyase_{clone_hcl-
 1}_[human,_liver,_mrna,_1194_nt]
 s68271_891-1191,_crem=cyclic_amp-
 responsive_element_modulator_[human,_mrna,_1431_nt]
 u03886_2214-2730,gs2_mrna,_complete_cds
 u10685exon#2_992-1142:in_reversesequence,_3043-3271,mage-
 10_antigen_(mage10)_gene,_complete_cds_
 u47050_2888-3296,putative_calcium_influx_channel_(htrp3)_mrna,_complete_cds
 u49114_2196-2700,prohormone_convertaseprecursor_(pc5)_mrna,_partial_cds_
 u58522_1608-2124,huntingtin_interacting_protein_(hip2)_mrna,_complete_cds
 u66036_732-1236,sulfotransferase_mrna,_complete_cds
 u74382_1317-1900,telomeric_repeat_dna-binding_protein_(pin2)_mrna,_complete_cds
 u84573_2882-3422,lysyl_hydroxylase_isoform(plod2)_mrna,_complete_cds_
 u87593_f_at_u87593_u87593,_4040_in_u87593_31-
 568,endogenous_retrovirus_clone_pl.8_polymerase_mrna,_p
 all_x16546_724-1319,dna_for_eosinophil_derived_neurotoxin
 x17576cds_802-1078:in_reversesequence,_1233-
 1389,melanoma_mrna_for_nck_protein,_showing_homology_to_
 all_z22970_4355-4674,mrna_for_ml30_antigen_cytoplasmic_variant_2_

Metagene 481

l75847_1808-2330,zinc_finger_protein_45_(znf45)_mrna,_complete_cds_
 l76465_1929-2493,nad+-
 dependenthydroxyprostaglandin_dehydrogenase_(pgdh)_mrna,_complete_cds_
 m28585_329-839,leukocyte_interferon-alpha_mrna,_complete_cds,_clone_pifn105
 u50196_1238-1760,adenosine_kinase_mrna,_complete_cds_
 u92458_3747-4269,metabotropic_glutamate_receptormrna,_complete_cds

Metagene 482

l07515_253-790,heterochromatin_protein_homologue_(hp1)_mrna,_complete_cds
 l36051exon#6_678-1086,thrombopoietin_gene,_complete_cds
 u04811_1931-2375,trophinin_mrna,_complete_cds

u09646exon_358-874,carnitine_palmitoyltransferase_ii_precursor_(cpt1)_gene_
u11701_1316-1862,lim-homeobox_domain_protein_(hlh-2)_mrna,_complete_cds
u23946_1986-2496,putative_tumor_suppressor_(luca15)_mrna,_complete_cds_
u42359mrna_1197-
1217,n33_protein_form(n33)_gene,_exonand_complete_cds/gb=u42359_/ntype=dna_/ann
ot=ex
u49973cds#2_37-
367,_orf1;_mer37;_putative_transposase_similar_to_pogo_element_fromtiger1_tran
sposab
u79263_995-1535,clone_23760_mrna,_partial_cds
u86529_584-
1130,glutathione_transferase_zeta(gstz1)_mrna,_complete_cds/gb=u86529_/ntype=rn
a_
all_x52943_2163-2728,mrna_for_atf-a_transcription_factor_
x98266cds#2_1028-1340:in_reversesequence,_2103-2223,_ligase-
like_protein_gene_extracted_frommrna_for
z83802_133-511,mrna_for_axonemal_dynein_heavy_chain_(partial,_id_hdhc3)

Metagene 483

m60094mrna_196-640,testicular_h1_histone_(h1)_gene,_complete_cds
x00948cds_65-503,mrna_for_prepro-relaxin_h2/gb=x00948_/ntype=rna_

Metagene 484

ab003177_604-1096,mrna_for_proteasome_subunit_p27,_complete_cds
hg3187-ht3366_s_at_hg3187-ht3366_tyrosine_phosphatase_1,_non-
receptor,_altsplice_3_
hg3546-ht3744_s_at_hg3546-ht3744_pre-
mrna_splicing_factor_sf2p33,_altsplice_form_1_
m19650_1446-1700,2',3'-cyclic_nucleotide_3'-
phosphodiesterase_mrna,_complete_cds
s62904_2130-
2523,_thiopurine_methyltransferase_[human,t84_colon_carcinoma_cell,_mrna,_2742
_ntl]
u47007_1818-2250,transcriptional_repressor_(nab1)_nab1_mrna,_complete_cds
u51004_166-508,putative_protein_kinase_c_inhibitor_(pkci-1)_mrna,_complete_cds_
u90304_1272-1782,iroquois-class_homeodomain_protein_irx-2a_mrna,_complete_cds_
z93784cds_702-
1008:in_reversesequence,_58791:not_in_gb_record,dna_sequence_from_pac_398c22_on
_chromo

Metagene 485

d87682_5800-6286,mrna_for_kiaa0241_gene,_partial_cds_
d87742_5513-5921,mrna_for_kiaa0268_gene,_partial_cds_
d89050_691-1219,mrna_for_lectin-like_oxidized_ldl_receptor,_complete_cds_
l20688_864-1188,gdp-dissociation_inhibitor_protein_(ly-gdi)_mrna,_complete_cds_
m31158_2670-3216,camp-dependent_protein_kinase_subunit_rii-
beta_mrna,_complete_cds_
u63542_303-750,putative_fap_protein_mrna,_partial_cds

u95740mrna#2_1995-
 2457,_362g6.1_gene_(unknown_protein_cit987sk_362g6_1)_extracted_fromchromosome_
 16p
 all_x05409_1388-
 1965,rna_for_mitochondrial_aldehyde_dehydrogenase_i_aldh_i_(ec_1.2.1.3)

Metagene 486

all_m60751_910-1163,histone_h2b.1_(h2b)_gene,_complete_cds_
 x81333cds_1730-2078:in_reversesequence,_2130-
 2220,mrna_for_pph_beta_subunit_protein_
 all_y00317_1618-2081,mrna_for_liver_microsomal_udp-
 glucuronosyltransferase_(udpgt)_

Metagene 487

s76067cds_405-759,_cng2=cyclic_nucleotide-
 gated_cation_channel_[human,_peripheral_leucocytes,_genomi
 u13021_844-1392,positive_regulator_of_programmed_cell_death_ich-11_(ich-
 1)_mrna,_complete_cds
 u72508_757-1105,b7_mrna,_complete_cds
 x83490exon_3-34:in_reversesequence,_389,mrna_for_fas/apo-1_(clone_pcrtm11-
 fasdelta(3,4))/gb=x83490_
 z31690cds_838-1129:in_reversesequence,_1226-
 1445,(hepg2)_lal_mrna_for_lyosomal_acid_lipase_

Metagene 488

reverse_ac002076_127531-127606,_wugsc:gs345d13.2_gene_(g-protein_gamma-
 1_subunit)_extracted_frombac_
 d13637_2062-2566,mrna_for_kiaa0012_gene,_complete_cds
 d28915cds_1002-1272:in_reversesequence,_114-186,gene_for_hepatitis_c-
 associated_microtubular_aggrega
 hg2705-ht2801_s_at_hg2705-ht2801_serine/threonine_kinase_
 k02765_4466-
 4916,complement_component_c3_mrna,_alpha_and_beta_subunits,_complete_cds_
 l06175_1924-2482,p5-1_mrna,_complete_cds
 l12535_1641-2151,rsu-1/rsp-1_mrna,_complete_cds
 m11147mrna_251-689,ferritin_l_chain_mrna,_complete_cds_
 m13699mrna_2810-3278,ceruloplasmin_(ferroxidase)_mrna,_complete_cds
 m30818mrna_2384-2888,interferon-
 induced_cellular_resistance_mediator_protein_(mxh)_mrna,_complete_cd
 m33195_13-457,fc-epsilon-receptor_gamma-chain_mrna,_complete_cds_
 m37435_3368-3914,macrophage-specific_colony-stimulating_factor_(csf-
 1)_mrna,_complete_cds
 m55542mrna_2310-2802,guanylate_binding_protein_isoform_i_(gbp-
 2)_mrna,_complete_cds
 m68874_2293-2779,phosphatidylcholine_2-acylhydrolase_(cpla2)_mrna,_complete_cds
 m81750mrna_1132-
 1645,myeloid_cell_nuclear_differentiation_antigen_mrna,_complete_cds_
 u52101_61-451,ymp_mrna,_complete_cds_

all_x02530_571-1118,mrna_for_gamma-
interferon_inducible_early_response_gene_(with_homology_to_platel
all_x99886_601-2202:in_x99886cds_96-127,mcp-2_gene
all_z83735_344-817,hh3/k_gene

Metagene 489

m92287_1531-1999,cyclin_d3_(ccnd3)_mrna,_complete_cds_
u32989_1109-1559,tryptophan_oxygenase_(tdo)_mrna,_complete_cds_
u90907_1150-1612,clone_23907_mrna_sequence_
all_x99268_928-1367,mrna_for_b-hlh_dna_binding_protein_

Metagene 490

af005775_275-755,caspase-
like_apoptosis_regulatory_protein(clarp)_mrna,_alternatively_spliced,_compl
l35269exon_1602-2040,zinc_finger_protein_35_(znf35)_gene
u32499_848-929,d3_dopamine_receptor_mrna,_complete_cds.
u78107_667-1105,gamma_snap_mrna,_complete_cds
u85946_2030-2288,brain_secretory_protein_hsec10p_(hsec10)_mrna,_complete_cds_

Metagene 491

hg3510-ht3704_at_hg3510-ht3704_v-erba_related_ear-3_protein
hg880-ht880_s_at_hg880-ht880_mucin_6,_gastric
u37519_2304-2784,aldehyde_dehydrogenase_(aldh8)_mrna,_complete_cds_
all_x98263_520-1019,mrna_for_m-phase_phosphoprotein,_mpp6

DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT
(PCT Article 17(2)(a) and Rule 39)


Applicant's or agent's file reference 5251.01	IMPORTANT DECLARATION	Date of mailing (day/month/year) 15. 07. 2003
International application No. PCT/US02/038222	International filing date (day/month/year) 12-11-2002	(Earliest) Priority Date (day/month/year) ---
International Patent Classification (IPC) or both national classification and IPC G06N 3/00		
Applicant DUKE UNIVERSITY		

This International Searching Authority hereby declares, according to Article 17(2)(a), that **no international search report will be established** on the international application for the reasons indicated below.

1. ☒ The subject matter of the international application relates to:
 - a. ☐ scientific theories.
 - b. ☒ mathematical theories.
 - c. ☐ plant varieties.
 - d. ☐ animal varieties.
 - e. ☐ essentially biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
 - f. ☐ schemes, rules or methods of doing business.
 - g. ☐ schemes, rules or methods of performing purely mental acts.
 - h. ☐ schemes, rules or methods of playing games.
 - i. ☐ methods for treatment of the human body by surgery or therapy.
 - j. ☐ methods for treatment of the animal body by surgery or therapy.
 - k. ☐ diagnostic methods practised on the human or animal body.
 - l. ☐ mere presentations of information.
 - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.
2. ☐ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:

☐ the description
 ☐ the claims
 ☐ the drawings
3. ☐ The failure of the nucleotide and/or amino acid sequence listing to comply with the prescribed requirements prevents a meaningful search from being carried out:

☐ it does not comply with the prescribed standard
☐ it is not in the prescribed machine readable form
4. Further comments:
see extra sheet

Name and mailing address of the International Searching Authority  European Patent Office, P.B. 5818 Patentlaan 2 NL-2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Authorized officer Anders Edlund /LR Telephone no. 08-450 3674
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The claims relate to subject matter for which no search is required according to Rule 39 PCT. Given that the claims are formulated in terms of such subject matter or merely specify commonplace features relating to its technological implementation, the search examiner could not establish any technical problem which might potentially have required an inventive step to overcome. Hence it was not possible to carry out a meaningful search into the state of the art (Art. 17(2)(a)(i) and (ii) PCT; see EPO Guidelines Part B Chapter VIII, 1-6).

The applicant's attention is drawn to the fact that claims relating to inventions in respect of which no international search report has been established need not be subject of an international preliminary examination (Rule 66.1 (e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following the receipt of the search report or during any Chapter II procedure. If the application proceeds into the regional phase before the EPO, the applicant is reminded that a search may be carried out during examination of the EPO (see EPO Guideline C-VI, 8.5), should the problems which led to the Article 17(2) declaration be overcome.